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(71) Applicant (for all designated States except US): **EPIM-
MUNE INC.** [US/US]; 5820 Nancy Ridge Drive, San
Diego, CA 92121 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **SETTE, Alessandro**
[IT/US]; 5551 Linda Rosa Avenue, La Jolla, CA 92037
(US). **SIDNEY, John** [US/US]; 4218 Corte de la Siena,
San Diego, CA 92130 (US). **SOUTHWOOD, Scott**
[US/US]; 19679 Strathmore Drive, Santee, CA 92071
(US). **LIVINGSTON, Brian, D.** [US/US]; 13555 Chaco
Court, San Diego, CA 92129 (US). **CHESNUT, Robert**
[US/US]; 1473 Kings Cross Drive, Cardiff-by-the-Sea,
CA 92007 (US). **BAKER, Denise, Marie** [US/US]; 11575
Caminito LaBar #21, San Diego, CA 92126 (US). **CELIS,
Esteban** [US/US]; 3683 Wright Road S.W., Rochester,

MN 55902 (US). **KUBO, Ralph, T.** [US/US]; 6921 Pear
Tree Drive, Carlsbad, CA 92009 (US). **GREY, Howard,
M.** [US/US]; 1461 Caminito Batea, La Jolla, CA 92037
(US).

(74) Agents: **LOCKYER, Jean, M.** et al.; Townsend and
Townsend and Crew LLP, Eighth Floor, Two Embarcadero
Center, San Francisco, CA 94111 (US).

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(57) Abstract: This invention uses our knowledge of the mechanisms by which antigen is recognized by T cells to identify and pre-
pare human immunodeficiency virus (HIV) epitopes, and to develop epitope-based vaccines directed towards HIV. More specifically,
this application communicates our discovery of pharmaceutical compositions and methods of use in the prevention and treatment of
HIV infection.

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**INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN
IMMUNODEFICIENCY VIRUS-1 USING PEPTIDE AND NUCLEIC ACID
COMPOSITIONS**

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CROSS-REFERENCE TO RELATED APPLICATIONS

The present application claims priority to U.S. Application No. 09/412,863 filed October 5, 1999, which is herein incorporated by reference.

FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

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I. BACKGROUND OF THE INVENTION

Acquired immunodeficiency syndrome (AIDS) caused by infection with human immunodeficiency virus-1 (HIV-1) represents a major world health problem. Estimates indicate that about 16,000 people worldwide are infected with HIV each day.

5 The development of anti-viral drugs has been a major advancement in reducing viral loads in HIV infected patients. Highly active retroviral therapy (HAART) has been shown to reduce viremia to nearly undetectable levels. However, current drug therapies are not practicable as a long term solution to the HIV epidemic. HAART therapy is severely limited due to poor tolerance for the drugs and the emergence of drug-resistant virus. Moreover, replication competent HIV persists in the lymphoid tissue of patients
10 who have responded to HAART, thus serving as a reservoir of virus. Lastly, current anti-retroviral drug therapies have little impact upon the global epidemic: almost 90% of the world's HIV infected population resides within countries lacking financial resources for these drugs. Thus, a need exists for an efficacious vaccine to both prevent and treat HIV
15 infection.

Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections in vivo (Oldstone *et al.*, Nature 321:239, 1989; Jamieson *et al.*, J. Virol. 61:3930, 1987; Yap *et al.*, Nature 273:238, 1978; Lukacher *et al.*, J. Exp. Med. 160:814,
20 1994; McMichael *et al.*, N. Engl. J. Med. 309:13, 1983; Sethi *et al.*, J. Gen. Virol. 64:443, 1983; Watari *et al.*, J. Exp. Med. 165:459, 1987; Yasukawa *et al.*, J. Immunol. 143:2051, 1989; Tigges *et al.*, J. Virol. 66:1622, 1993; Reddenhase *et al.*, J. Virol. 55:263, 1985; Quinnan *et al.*, N. Engl. J. Med. 307:6, 1982). HLA class I molecules are expressed on the surface of almost all nucleated cells. Following intracellular processing of antigens,
25 epitopes from the antigens are presented as a complex with the HLA class I molecules on the surface of such cells. CTL recognize the peptide-HLA class I complex, which then results in the destruction of the cell bearing the HLA-peptide complex directly by the CTL and/or via the activation of non-destructive mechanisms *e.g.*, the production of interferon, that inhibit viral replication.

30 While immune correlates of protective immunity against HIV infection are not well defined, there is a growing body of evidence that suggests CTL are important in controlling HIV infection. HIV-specific CTL responses can be detected early in infection and the appearance of the responses corresponds to the time in infection at which initial viremia is reduced (Pantaleo *et al.*, Nature 370:463, 1994; Walker *et al.*, Proc. Natl.

Acad. Sci. 86:9514, 1989). In addition, HIV replication in infected lymphocytes can be inhibited by incubation with autologous CTL (*see, e.g., Tsubota et al., J. Exp. Med.* 169:1421, 1989). These data are supported by recent studies that indicate CTL are required for controlling viral replication in a SIV/rhesus animal model (Schmitz *et al.*,
5 *Science* 283:857, 1999), and additionally supported by studies that demonstrate that CTL exert selective pressure on HIV populations as evidenced by the eventual predominance of viruses with amino acid replacements in those regions of the virus to which CTL responses are directed (*see, e.g., Borrow et al., Nature Med.* 3:205-211, 1997; Price *et al., Proc. Nat. Acad. Sci.* 94:12890-1895, 1997; Koenig *et al., Nature Med.* 1:330-336, 1995;
10 and Haas *et al., J. Immunol.* 157:4212-4221, 1996)

Virus-specific T helper lymphocytes are also known to be critical for maintaining effective immunity in chronic viral infections. Historically, HTL responses were viewed as primarily supporting the expansion of specific CTL and B cell populations; however, more recent data indicate that HTL may directly contribute to the control of virus
15 replication. For example, a decline in CD4⁺ T cells and a corresponding loss in HTL function characterize infection with HIV (Lane *et al., New Engl. J. Med.* 313:79, 1985). Furthermore, studies in HIV infected patients have also shown that there is an inverse relationship between virus-specific HTL responses and viral load, suggesting that HTL play a role in viremia (*see, e.g., Rosenberg et al., Science* 278:1447, 1997).

20 A fundamental challenge in the development of an efficacious HIV vaccine is the heterogeneity observed in HIV. The virus, like other retroviruses, rapidly mutates during replication resulting in the generation of virus that can escape anti-viral therapy and immune recognition (Borrow *et al., Nature Med.* 3:205, 1997). In addition, HIV can be classified into a variety of subtypes that exhibit significant sequence divergence (*see, e.g.,*
25 Lukashov *et al., AIDS* 12:S43, 1998). In view of the heterogeneous nature of HIV, and the heterogeneous immune response observed with HIV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple HIV epitopes appears to be important for the development of an efficacious vaccine against HIV. There is a need to establish such vaccine embodiments which elicit immune responses of
30 sufficient breadth and vigor to prevent and/or clear HIV infection.

The epitope approach, as we have described, may represent a solution to this challenge, in that it allows the incorporation of various antibody, CTL and HTL epitopes, from various proteins, in a single vaccine compositions. Such a composition may

simultaneously target multiple dominant and subdominant epitopes and thereby be used to achieve effective immunization in a diverse population.

The information provided in this section is intended to disclose the presently understood state of the art as of the filing date of the present application. Information is included in this section which was generated subsequent to the priority date of this application. Accordingly, information in this section is not intended, in any way, to delineate the priority date for the invention.

II. SUMMARY OF THE INVENTION

This invention applies our knowledge of the mechanisms by which antigen is recognized by T cells, for example, to develop epitope-based vaccines directed towards HIV. More specifically, this application communicates our discovery of specific epitope pharmaceutical compositions and methods of use in the prevention and treatment of HIV infection.

Upon development of appropriate technology, the use of epitope-based vaccines has several advantages over current vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The epitopes for inclusion in an epitope-based vaccine may be selected from conserved regions of viral or tumor-associated antigens, which thereby reduces the likelihood of escape mutants. Furthermore, immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-based vaccines.

An additional advantage of an epitope-based vaccine approach is the ability to combine selected epitopes (CTL and HTL), and further, to modify the composition of the epitopes, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches.

Another major benefit of epitope-based immune-stimulating vaccines is their safety. The possible pathological side effects caused by infectious agents or whole protein antigens, which might have their own intrinsic biological activity, is eliminated.

An epitope-based vaccine also provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Thus, patient-by-patient variability in the immune response to a particular pathogen may be alleviated by inclusion

of epitopes from multiple antigens from the pathogen in a vaccine composition. In the case of HIV, epitopes derived from multiple strains may also be included. A "pathogen" may be an infectious agent or a tumor associated molecule.

One of the most formidable obstacles to the development of broadly efficacious epitope-based immunotherapeutics, however, has been the extreme polymorphism of HLA molecules. To date, effective non-genetically biased coverage of a population has been a task of considerable complexity; such coverage has required that epitopes be used that are specific for HLA molecules corresponding to each individual HLA allele. Impractically large numbers of epitopes would therefore have to be used in order to cover ethnically diverse populations. Thus, there has existed a need for peptide epitopes that are bound by multiple HLA antigen molecules for use in epitope-based vaccines. The greater the number of HLA antigen molecules bound, the greater the breadth of population coverage by the vaccine.

Furthermore, as described herein in greater detail, a need has existed to modulate peptide binding properties, *e.g.*, so that peptides that are able to bind to multiple HLA antigens do so with an affinity that will stimulate an immune response. Identification of epitopes restricted by more than one HLA allele at an affinity that correlates with immunogenicity is important to provide thorough population coverage, and to allow the elicitation of responses of sufficient vigor to prevent or clear an infection in a diverse segment of the population. Such a response can also target a broad array of epitopes. The technology disclosed herein provides for such favored immune responses.

In a preferred embodiment, epitopes for inclusion in vaccine compositions of the invention are selected by a process whereby protein sequences of known antigens are evaluated for the presence of motif or supermotif-bearing epitopes. Peptides corresponding to a motif- or supermotif-bearing epitope are then synthesized and tested for the ability to bind to the HLA molecule that recognizes the selected motif. Those peptides that bind at an intermediate or high affinity *i.e.*, an IC_{50} (or a K_D value) of 500 nM or less for HLA class I molecules or an IC_{50} of 1000 nM or less for HLA class II molecules, are further evaluated for their ability to induce a CTL or HTL response. Immunogenic peptide epitopes are selected for inclusion in vaccine compositions.

Supermotif-bearing peptides may additionally be tested for the ability to bind to multiple alleles within the HLA supertype family. Moreover, peptide epitopes may be analogued to modify binding affinity and/or the ability to bind to multiple alleles within an HLA supertype.

The invention also includes embodiments comprising methods for monitoring or evaluating an immune response to HIV in a patient having a known HLA-type. Such methods comprise incubating a T lymphocyte sample from the patient with a peptide composition comprising an HIV epitope that has an amino acid sequence described in
5 Tables VII to Table XX which binds the product of at least one HLA allele present in the patient, and detecting for the presence of a T lymphocyte that binds to the peptide. A CTL peptide epitope may, for example, be used as a component of a tetrameric complex for this type of analysis.

An alternative modality for defining the peptide epitopes in accordance with the
10 invention is to recite the physical properties, such as length; primary structure; or charge, which are correlated with binding to a particular allele-specific HLA molecule or group of allele-specific HLA molecules. A further modality for defining peptide epitopes is to recite the physical properties of an HLA binding pocket, or properties shared by several allele-specific HLA binding pockets (*e.g.* pocket configuration and charge distribution)
15 and reciting that the peptide epitope fits and binds to the pocket or pockets.

As will be apparent from the discussion below, other methods and embodiments are also contemplated. Further, novel synthetic peptides produced by any of the methods described herein are also part of the invention.

20 III. BRIEF DESCRIPTION OF THE FIGURES

Figure 1: Figure 1 provides a graph of total frequency of genotypes as a function of the number of PF candidate epitopes bound by HLA-A and B molecules, in an average population.

Figure 2: Figure 2 illustrates the position of peptide epitopes in an experimental
25 model minigene construct.

IV. DETAILED DESCRIPTION OF THE INVENTION

The peptide epitopes and corresponding nucleic acid compositions of the present invention are useful for stimulating an immune response to HIV by stimulating the
30 production of CTL or HTL responses. The peptide epitopes, which are derived directly or indirectly from native HIV protein amino acid sequences, are able to bind to HLA molecules and stimulate an immune response to HIV. The complete sequence of the HIV proteins to be analyzed can be obtained from Genbank. Peptide epitopes and analogs thereof can also be readily determined from sequence information that may subsequently

be discovered for heretofore unknown variants of HIV, as will be clear from the disclosure provided below.

The peptide epitopes of the invention have been identified in a number of ways, as will be discussed below. Also discussed in greater detail is that analog peptides have been derived and the binding activity for HLA molecules modulated by modifying specific amino acid residues to create peptide analogs exhibiting altered immunogenicity. Further, the present invention provides compositions and combinations of compositions that enable epitope-based vaccines that are capable of interacting with HLA molecules encoded by various genetic alleles to provide broader population coverage than prior vaccines.

IV.A. Definitions

The invention can be better understood with reference to the following definitions, which are listed alphabetically:

A "computer" or "computer system" generally includes: a processor; at least one information storage/retrieval apparatus such as, for example, a hard drive, a disk drive or a tape drive; at least one input apparatus such as, for example, a keyboard, a mouse, a touch screen, or a microphone; and display structure. Additionally, the computer may include a communication channel in communication with a network. Such a computer may include more or less than what is listed above.

A "construct" as used herein generally denotes a composition that does not occur in nature. A construct can be produced by synthetic technologies, *e.g.*, recombinant DNA preparation and expression or chemical synthetic techniques for nucleic or amino acids. A construct can also be produced by the addition or affiliation of one material with another such that the result is not found in nature in that form.

"Cross-reactive binding" indicates that a peptide is bound by more than one HLA molecule; a synonym is degenerate binding.

A "cryptic epitope" elicits a response by immunization with an isolated peptide, but the response is not cross-reactive *in vitro* when intact whole protein which comprises the epitope is used as an antigen.

A "dominant epitope" is an epitope that induces an immune response upon immunization with a whole native antigen (*see, e.g.*, Sercarz, *et al.*, *Annu. Rev. Immunol.* 11:729-766, 1993). Such a response is cross-reactive *in vitro* with an isolated peptide epitope.

With regard to a particular amino acid sequence, an "epitope" is a set of amino acid residues which is involved in recognition by a particular immunoglobulin, or in the context of T cells, those residues necessary for recognition by T cell receptor proteins and/or Major Histocompatibility Complex (MHC) receptors. In an immune system setting, *in vivo* or *in vitro*, an epitope is the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Throughout this disclosure epitope and peptide are often used interchangeably. It is to be appreciated, however, that isolated or purified protein or peptide molecules larger than and comprising an epitope of the invention are still within the bounds of the invention.

It is to be appreciated that protein or peptide molecules that comprise an epitope of the invention as well as additional amino acid(s) are still within the bounds of the invention. In certain embodiments, there is a limitation on the length of a peptide of the invention which is not otherwise a construct. An embodiment that is length-limited occurs when the protein/peptide comprising an epitope of the invention comprises a region (i.e., a contiguous series of amino acids) having 100% identity with a native sequence. In order to avoid the definition of epitope from reading, *e.g.*, on whole natural molecules, there is a limitation on the length of any region that has 100% identity with a native peptide sequence. Thus, for a peptide comprising an epitope of the invention and a region with 100% identity with a native peptide sequence (and is not otherwise a construct), the region with 100% identity to a native sequence generally has a length of: less than or equal to 600 amino acids, often less than or equal to 500 amino acids, often less than or equal to 400 amino acids, often less than or equal to 250 amino acids, often less than or equal to 100 amino acids, often less than or equal to 85 amino acids, often less than or equal to 75 amino acids, often less than or equal to 65 amino acids, and often less than or equal to 50 amino acids. In certain embodiments, an "epitope" of the invention is comprised by a peptide having a region with less than 51 amino acids that has 100% identity to a native peptide sequence, in any increment of (49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5) down to 5 amino acids.

Accordingly, peptide or protein sequences longer than 600 amino acids are within the scope of the invention, so long as they do not comprise any contiguous sequence of more than 600 amino acids that have 100% identity with a native peptide sequence, if they are not otherwise a construct. For any peptide that has five contiguous residues or

less that correspond to a native sequence, there is no limitation on the maximal length of that peptide in order to fall within the scope of the invention. It is presently preferred that a CTL epitope be less than 600 residues long in any increment down to eight amino acid residues.

5 "Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (*see, e.g., Stites, et al., IMMUNOLOGY*, 8TH ED., Lange Publishing, Los Altos, CA (1994).

10 An "HLA supertype or family", as used herein, describes sets of HLA molecules grouped on the basis of shared peptide-binding specificities. HLA class I molecules that share somewhat similar binding affinity for peptides bearing certain amino acid motifs are grouped into HLA supertypes. The terms HLA superfamily, HLA supertype family, HLA family, and HLA xx-like molecules (where xx denotes a particular HLA type), are synonyms.

15 Throughout this disclosure, results are expressed in terms of "IC₅₀'s." IC₅₀ is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.,* limiting HLA proteins and labeled peptide concentrations), these values approximate K_D values. Assays for determining binding are described in detail, *e.g.,* in PCT publications WO 94/20127 and WO 94/03205. It should be noted that IC₅₀ values can change, often
20 dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g.,* HLA preparation, *etc.*). For example, excessive concentrations of HLA molecules will increase the apparent measured IC₅₀ of a given ligand.

25 Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC₅₀'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC₅₀ of the reference peptide increases 10-fold, the IC₅₀ values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good, intermediate, weak, or negative binder is generally based on its IC₅₀, relative to the IC₅₀
30 of a standard peptide.

Binding may also be determined using other assay systems including those using: live cells (*e.g., Ceppellini et al., Nature* 339:392, 1989; Christnick *et al., Nature* 352:67, 1991; Busch *et al., Int. Immunol.* 2:443, 1990; Hill *et al., J. Immunol.* 147:189, 1991; del Guercio *et al., J. Immunol.* 154:685, 1995), cell free systems using detergent lysates (*e.g.,*

Cerundolo *et al.*, *J. Immunol.* 21:2069, 1991), immobilized purified MHC (*e.g.*, Hill *et al.*, *J. Immunol.* 152, 2890, 1994; Marshall *et al.*, *J. Immunol.* 152:4946, 1994), ELISA systems (*e.g.*, Reay *et al.*, *EMBO J.* 11:2829, 1992), surface plasmon resonance (*e.g.*, Khilko *et al.*, *J. Biol. Chem.* 268:15425, 1993); high flux soluble phase assays (Hammer
5 *et al.*, *J. Exp. Med.* 180:2353, 1994), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, *Nature* 346:476, 1990; Schumacher *et al.*, *Cell* 62:563, 1990; Townsend *et al.*, *Cell* 62:285, 1990; Parker *et al.*, *J. Immunol.* 149:1896, 1992).

As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC_{50} , or K_D value, of 50 nM or less; "intermediate affinity" is binding
10 with an IC_{50} or K_D value of between about 50 and about 500 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or K_D value of 100 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 100 and about 1000 nM.

The terms "identical" or percent "identity," in the context of two or more peptide
15 sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection.

An "immunogenic peptide" or "peptide epitope" is a peptide that comprises an
20 allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL and/or HTL response. Thus, immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and thereafter inducing a cytotoxic T cell response, or a helper T cell response, to the antigen from which the immunogenic peptide is derived.

25 The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment.

30 "Link" or "join" refers to any method known in the art for functionally connecting peptides, including, without limitation, recombinant fusion, covalent bonding, disulfide bonding, ionic bonding, hydrogen bonding, and electrostatic bonding.

"Major Histocompatibility Complex" or "MHC" is a cluster of genes that plays a role in control of the cellular interactions responsible for physiologic immune responses.

In humans, the MHC complex is also known as the HLA complex. For a detailed description of the MHC and HLA complexes, see, Paul, FUNDAMENTAL IMMUNOLOGY, 3RD ED., Raven Press, New York, 1993.

The term "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I HLA motif and from about 6 to about 25 amino acids for a class II HLA motif, which is recognized by a particular HLA molecule. Peptide motifs are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues.

A "negative binding residue" or "deleterious residue" is an amino acid which, if present at certain positions (typically not primary anchor positions) in a peptide epitope, results in decreased binding affinity of the peptide for the peptide's corresponding HLA molecule.

A "non-native" sequence or "construct" refers to a sequence that is not found in nature, *i.e.*, is "non-naturally occurring". Such sequences include, *e.g.*, peptides that are lipidated or otherwise modified, and polyepitopic compositions that contain epitopes that are not contiguous in a native protein sequence.

The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α -amino and carboxyl groups of adjacent amino acids. The preferred CTL-inducing peptides of the invention are 13 residues or less in length and usually consist of between about 8 and about 11 residues, preferably 9 or 10 residues. The preferred HTL-inducing oligopeptides are less than about 50 residues in length and usually consist of between about 6 and about 30 residues, more usually between about 12 and 25, and often between about 15 and 20 residues.

"Pharmaceutically acceptable" refers to a generally non-toxic, inert, and/or physiologically compatible composition.

A "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One to three, usually two, primary anchor residues within a peptide of defined length generally defines a "motif" for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding grooves of an HLA molecule, with their side chains buried in specific pockets of the binding grooves themselves. In one embodiment, for example, the primary anchor

residues are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a 9-residue peptide epitope in accordance with the invention. The primary anchor positions for each motif and supermotif are set forth in Table 1. For example, analog peptides can be created by altering the presence or absence of particular residues in these primary anchor positions. Such analogs are used to modulate the binding affinity of a peptide comprising a particular motif or supermotif.

"Promiscuous recognition" is where a distinct peptide is recognized by the same T cell clone in the context of various HLA molecules. Promiscuous recognition or binding is synonymous with cross-reactive binding.

A "protective immune response" or "therapeutic immune response" refers to a CTL and/or an HTL response to an antigen derived from an infectious agent or a tumor antigen, which prevents or at least partially arrests disease symptoms or progression. The immune response may also include an antibody response which has been facilitated by the stimulation of helper T cells.

The term "residue" refers to an amino acid or amino acid mimetic incorporated into an oligopeptide by an amide bond or amide bond mimetic.

A "secondary anchor residue" is an amino acid at a position other than a primary anchor position in a peptide which may influence peptide binding. A secondary anchor residue occurs at a significantly higher frequency amongst bound peptides than would be expected by random distribution of amino acids at one position. The secondary anchor residues are said to occur at "secondary anchor positions." A secondary anchor residue can be identified as a residue which is present at a higher frequency among high or intermediate affinity binding peptides, or a residue otherwise associated with high or intermediate affinity binding. For example, analog peptides can be created by altering the presence or absence of particular residues in these secondary anchor positions. Such analogs are used to finely modulate the binding affinity of a peptide comprising a particular motif or supermotif.

A "subdominant epitope" is an epitope which evokes little or no response upon immunization with whole antigens which comprise the epitope, but for which a response can be obtained by immunization with an isolated peptide, and this response (unlike the case of cryptic epitopes) is detected when whole protein is used to recall the response *in vitro* or *in vivo*.

A "supermotif" is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Preferably, a supermotif-bearing peptide is recognized with high or intermediate affinity (as defined herein) by two or more HLA antigens.

"Synthetic peptide" refers to a peptide that is man-made using such methods as
5 chemical synthesis or recombinant DNA technology.

As used herein, a "vaccine" is a composition that contains one or more peptides of the invention. There are numerous embodiments of vaccines in accordance with the invention, such as by a cocktail of one or more peptides; one or more epitopes of the invention comprised by a polyepitopic peptide; or nucleic acids that encode such peptides
10 or polypeptides, *e.g.*, a minigene that encodes a polyepitopic peptide. The "one or more peptides" can include any whole unit integer from 1-150, *e.g.*, at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 or more peptides of the invention. The peptides or
15 polypeptides can optionally be modified, such as by lipidation, addition of targeting or other sequences. HLA class I-binding peptides of the invention can be admixed with, or linked to, HLA class II-binding peptides, to facilitate activation of both cytotoxic T lymphocytes and helper T lymphocytes. Vaccines can also comprise peptide-pulsed antigen presenting cells, *e.g.*, dendritic cells.

20 The nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in a peptide epitope they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal
25 end of the epitope, or the peptide or protein of which it may be a part. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter
30 designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G. Symbols for the amino acids are shown below.

Single Letter Symbol	Three Letter Symbol	Amino Acids
A	Ala	Alanine
C	Cys	Cysteine
D	Asp	Aspartic Acid
E	Glu	Glutamic Acid
F	Phe	Phenylalanine
G	Gly	Glycine
H	His	Histidine
I	Ile	Isoleucine
K	Lys	Lysine
L	Leu	Leucine
M	Met	Methionine
N	Asn	Asparagine
P	Pro	Proline
Q	Gln	Glutamine
R	Arg	Arginine
S	Ser	Serine
T	Thr	Threonine
V	Val	Valine
W	Trp	Tryptophan
Y	Tyr	Tyrosine

IV.B. Stimulation of CTL and HTL responses

5 The mechanism by which T cells recognize antigens has been delineated during
the past ten years. Based on our understanding of the immune system we have developed
efficacious peptide epitope vaccine compositions that can induce a therapeutic or
prophylactic immune response to HIV in a broad population. For an understanding of the
value and efficacy of the claimed compositions, a brief review of immunology-related
10 technology is provided.

A complex of an HLA molecule and a peptidic antigen acts as the ligand
recognized by HLA-restricted T cells (Buus, S. *et al.*, *Cell* 47:1071, 1986; Babbitt, B. P.

- et al.*, *Nature* 317:359, 1985; Townsend, A. and Bodmer, H., *Annu. Rev. Immunol.* 7:601, 1989; Germain, R. N., *Annu. Rev. Immunol.* 11:403, 1993). Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues that correspond to motifs required for specific binding to HLA antigen molecules have been identified and are described herein and are set forth in Tables I, II, and III (*see also, e.g.*, Southwood, *et al.*, *J. Immunol.* 160:3363, 1998; Rammensee, *et al.*, *Immunogenetics* 41:178, 1995; Rammensee *et al.*, SYFPEITHI, access via web at : <http://134.2.96.221/scripts.hlaserver.dtl/home.htm>; Sette, A. and Sidney, J. *Curr. Opin. Immunol.* 10:478, 1998; Engelhard, V. H., *Curr. Opin. Immunol.* 6:13, 1994; Sette, A. and Grey, H. M., *Curr. Opin. Immunol.* 4:79, 1992; Sinigaglia, F. and Hammer, J. *Curr. Biol.* 6:52, 1994; Ruppert *et al.*, *Cell* 74:929-937, 1993; Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; Sidney *et al.*, *J. Immunol.* 157:3480-3490, 1996; Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; Sette, A. and Sidney, J. *Immunogenetics*, in press, 1999).
- Furthermore, x-ray crystallographic analysis of HLA-peptide complexes has revealed pockets within the peptide binding cleft of HLA molecules which accommodate, in an allele-specific mode, residues borne by peptide ligands; these residues in turn determine the HLA binding capacity of the peptides in which they are present. (*See, e.g.*, Madden, D.R. *Annu. Rev. Immunol.* 13:587, 1995; Smith, *et al.*, *Immunity* 4:203, 1996; Fremont *et al.*, *Immunity* 8:305, 1998; Stern *et al.*, *Structure* 2:245, 1994; Jones, E.Y. *Curr. Opin. Immunol.* 9:75, 1997; Brown, J. H. *et al.*, *Nature* 364:33, 1993; Guo, H. C. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:8053, 1993; Guo, H. C. *et al.*, *Nature* 360:364, 1992; Silver, M. L. *et al.*, *Nature* 360:367, 1992; Matsumura, M. *et al.*, *Science* 257:927, 1992; Madden *et al.*, *Cell* 70:1035, 1992; Fremont, D. H. *et al.*, *Science* 257:919, 1992; Saper, M. A., Bjorkman, P. J. and Wiley, D. C., *J. Mol. Biol.* 219:277, 1991.)

Accordingly, the definition of class I and class II allele-specific HLA binding motifs, or class I or class II supermotifs allows identification of regions within a protein that have the potential of binding particular HLA antigen(s).

- The present inventors have found that the correlation of binding affinity with immunogenicity, which is disclosed herein, is an important factor to be considered when evaluating candidate peptides. Thus, by a combination of motif searches and HLA-peptide binding assays, candidates for epitope-based vaccines have been identified. After determining their binding affinity, additional confirmatory work can be performed to

select, amongst these vaccine candidates, epitopes with preferred characteristics in terms of population coverage, antigenicity, and immunogenicity.

Various strategies can be utilized to evaluate immunogenicity, including:

- 1) Evaluation of primary T cell cultures from normal individuals (*see, e.g.,*
5 Wentworth, P. A. *et al.*, *Mol. Immunol.* 32:603, 1995; Celis, E. *et al.*, *Proc. Natl. Acad. Sci. USA* 91:2105, 1994; Tsai, V. *et al.*, *J. Immunol.* 158:1796, 1997; Kawashima, I. *et al.*, *Human Immunol.* 59:1, 1998); This procedure involves the stimulation of peripheral blood lymphocytes (PBL) from normal subjects with a test peptide in the presence of antigen presenting cells *in vitro* over a period of several weeks. T cells specific for the
10 peptide become activated during this time and are detected using, *e.g.*, a ^{51}Cr -release assay involving peptide sensitized target cells.
- 2) Immunization of HLA transgenic mice (*see, e.g.,* Wentworth, P. A. *et al.*, *J. Immunol.* 26:97, 1996; Wentworth, P. A. *et al.*, *Int. Immunol.* 8:651, 1996; Alexander, J. *et al.*, *J. Immunol.* 159:4753, 1997); In this method, peptides in incomplete Freund's
15 adjuvant are administered subcutaneously to HLA transgenic mice. Several weeks following immunization, splenocytes are removed and cultured *in vitro* in the presence of test peptide for approximately one week. Peptide-specific T cells are detected using, *e.g.*, a ^{51}Cr -release assay involving peptide sensitized target cells and target cells expressing endogenously generated antigen.
- 3) Demonstration of recall T cell responses from immune individuals who have
20 effectively been vaccinated, recovered from infection, and/or from chronically infected patients (*see, e.g.,* Rehermann, B. *et al.*, *J. Exp. Med.* 181:1047, 1995; Doolan, D. L. *et al.*, *Immunity* 7:97, 1997; Bertoni, R. *et al.*, *J. Clin. Invest.* 100:503, 1997; Threlkeld, S. C. *et al.*, *J. Immunol.* 159:1648, 1997; Diepolder, H. M. *et al.*, *J. Virol.* 71:6011, 1997);
25 In applying this strategy, recall responses are detected by culturing PBL from subjects that have been naturally exposed to the antigen, for instance through infection, and thus have generated an immune response "naturally", or from patients who were vaccinated against the infection. PBL from subjects are cultured *in vitro* for 1-2 weeks in the presence of test peptide plus antigen presenting cells (APC) to allow activation of
30 "memory" T cells, as compared to "naive" T cells. At the end of the culture period, T cell activity is detected using assays for T cell activity including ^{51}Cr release involving peptide-sensitized targets, T cell proliferation, or lymphokine release.

The following describes the peptide epitopes and corresponding nucleic acids of the invention.

IV.C. Binding Affinity of Peptide Epitopes for HLA Molecules

5 As indicated herein, the large degree of HLA polymorphism is an important factor to be taken into account with the epitope-based approach to vaccine development. To address this factor, epitope selection encompassing identification of peptides capable of binding at high or intermediate affinity to multiple HLA molecules is preferably utilized, most preferably these epitopes bind at high or intermediate affinity to two or more allele-specific HLA molecules.

10 CTL-inducing peptides of interest for vaccine compositions preferably include those that have an IC_{50} or binding affinity value for class I HLA molecules of 500 nM or better (*i.e.*, the value is ≤ 500 nM). HTL-inducing peptides preferably include those that have an IC_{50} or binding affinity value for class II HLA molecules of 1000 nM or better, 15 (*i.e.*, the value is $\leq 1,000$ nM). For example, peptide binding is assessed by testing the capacity of a candidate peptide to bind to a purified HLA molecule *in vitro*. Peptides exhibiting high or intermediate affinity are then considered for further analysis. Selected peptides are tested on other members of the supertype family. In preferred embodiments, peptides that exhibit cross-reactive binding are then used in cellular screening analyses or 20 vaccines.

As disclosed herein, higher HLA binding affinity is correlated with greater immunogenicity. Greater immunogenicity can be manifested in several different ways. Immunogenicity corresponds to whether an immune response is elicited at all, and to the vigor of any particular response, as well as to the extent of a population in which a 25 response is elicited. For example, a peptide might elicit an immune response in a diverse array of the population, yet in no instance produce a vigorous response. In accordance with these principles, close to 90% of high binding peptides have been found to be immunogenic, as contrasted with about 50% of the peptides which bind with intermediate affinity. Moreover, higher binding affinity peptides lead to more vigorous immunogenic 30 responses. As a result, less peptide is required to elicit a similar biological effect if a high affinity binding peptide is used. Thus, in preferred embodiments of the invention, high affinity binding epitopes are particularly useful.

The relationship between binding affinity for HLA class I molecules and immunogenicity of discrete peptide epitopes on bound antigens has been determined for the first time in the art by the present inventors. The correlation between binding affinity and immunogenicity was analyzed in two different experimental approaches (*see, e.g.,* 5 Sette, *et al.*, *J. Immunol.* 153:5586-5592, 1994). In the first approach, the immunogenicity of potential epitopes ranging in HLA binding affinity over a 10,000-fold range was analyzed in HLA-A*0201 transgenic mice. In the second approach, the antigenicity of approximately 100 different hepatitis B virus (HBV)-derived potential epitopes, all carrying A*0201 binding motifs, was assessed by using PBL from acute 10 hepatitis patients. Pursuant to these approaches, it was determined that an affinity threshold value of approximately 500 nM (preferably 50 nM or less) determines the capacity of a peptide epitope to elicit a CTL response. These data are true for class I binding affinity measurements for naturally processed peptides and for synthesized T cell epitopes. These data also indicate the important role of determinant selection in the 15 shaping of T cell responses (*see, e.g.,* Schaeffer *et al. Proc. Natl. Acad. Sci. USA* 86:4649-4653, 1989).

An affinity threshold associated with immunogenicity in the context of HLA class II DR molecules has also been delineated (*see, e.g.,* Southwood *et al. J. Immunology* 160:3363-3373, 1998, and co-pending U.S.S.N. 09/009,953 filed 1/21/98). In order to 20 define a biologically significant threshold of DR binding affinity, a database of the binding affinities of 32 DR-restricted epitopes for their restricting element (*i.e.*, the HLA molecule that binds the motif) was compiled. In approximately half of the cases (15 of 32 epitopes), DR restriction was associated with high binding affinities, *i.e.* binding affinity values of 100 nM or less. In the other half of the cases (16 of 32), DR restriction was 25 associated with intermediate affinity (binding affinity values in the 100-1000 nM range). In only one of 32 cases was DR restriction associated with an IC₅₀ of 1000 nM or greater. Thus, 1000 nM can be defined as an affinity threshold associated with immunogenicity in the context of DR molecules.

The binding affinity of peptides for HLA molecules can be determined as 30 described in Example 1, below.

IV.D. Peptide Epitope Binding Motifs and Supermotifs

Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues

required for allele-specific binding to HLA molecules have been identified. The presence of these residues correlates with binding affinity for HLA molecules. The identification of motifs and/or supermotifs that correlate with high and intermediate affinity binding is an important issue with respect to the identification of immunogenic peptide epitopes for the inclusion in a vaccine. Kast *et al.* (*J. Immunol.* 152:3904-3912, 1994) have shown that motif-bearing peptides account for 90% of the epitopes that bind to allele-specific HLA class I molecules. In this study all possible peptides of 9 amino acids in length and overlapping by eight amino acids (240 peptides), which cover the entire sequence of the E6 and E7 proteins of human papillomavirus type 16, were evaluated for binding to five allele-specific HLA molecules that are expressed at high frequency among different ethnic groups. This unbiased set of peptides allowed an evaluation of the predictive value of HLA class I motifs. From the set of 240 peptides, 22 peptides were identified that bound to an allele-specific HLA molecule with high or intermediate affinity. Of these 22 peptides, 20 (*i.e.* 91%) were motif-bearing. Thus, this study demonstrates the value of motifs for the identification of peptide epitopes for inclusion in a vaccine: application of motif-based identification techniques will identify about 90% of the potential epitopes in a target antigen protein sequence.

Such peptide epitopes are identified in the Tables described below.

Peptides of the present invention may also comprise epitopes that bind to MHC class II DR molecules. A greater degree of heterogeneity in both size and binding frame position of the motif, relative to the N and C termini of the peptide, exists for class II peptide ligands. This increased heterogeneity of HLA class II peptide ligands is due to the structure of the binding groove of the HLA class II molecule which, unlike its class I counterpart, is open at both ends. Crystallographic analysis of HLA class II DRB*0101-peptide complexes showed that the major energy of binding is contributed by peptide residues complexed with complementary pockets on the DRB*0101 molecules. An important anchor residue engages the deepest hydrophobic pocket (*see, e.g.*, Madden, D.R. *Ann. Rev. Immunol.* 13:587, 1995) and is referred to as position 1 (P1). P1 may represent the N-terminal residue of a class II binding peptide epitope, but more typically is flanked towards the N-terminus by one or more residues. Other studies have also pointed to an important role for the peptide residue in the 6th position towards the C-terminus, relative to P1, for binding to various DR molecules.

In the past few years evidence has accumulated to demonstrate that a large fraction of HLA class I and class II molecules can be classified into a relatively few

supertypes, each characterized by largely overlapping peptide binding repertoires, and consensus structures of the main peptide binding pockets. Thus, peptides of the present invention are identified by any one of several HLA-specific amino acid motifs (*see, e.g.*, Tables I-III), or if the presence of the motif corresponds to the ability to bind several
5 allele-specific HLA antigens, a supermotif. The HLA molecules that bind to peptides that possess a particular amino acid supermotif are collectively referred to as an HLA "supertype."

The peptide motifs and supermotifs described below, and summarized in Tables I-III, provide guidance for the identification and use of peptide epitopes in accordance with
10 the invention.

Examples of peptide epitopes bearing a respective supermotif or motif are included in Tables as designated in the description of each motif or supermotif below. The Tables include a binding affinity ratio listing for some of the peptide epitopes. The ratio may be converted to IC_{50} by using the following formula: IC_{50} of the standard
15 peptide/ratio = IC_{50} of the test peptide (*i.e.*, the peptide epitope). The IC_{50} values of standard peptides used to determine binding affinities for Class I peptides are shown in Table IV. The IC_{50} values of standard peptides used to determine binding affinities for Class II peptides are shown in Table V. The peptides used as standards for the binding assays described herein are examples of standards; alternative standard peptides can also
20 be used when performing binding studies.

To obtain the peptide epitope sequences listed in each Table, protein sequence data for all of the HIV-1 isolates present in the 1999 Los Alamos database (<http://hiv-web.lanl.gov>) were evaluated for the presence of the designated supermotif or motif. A listing of the strains is provided in Table XXVI. Nine HIV-1 structural and regulatory
25 proteins, gag, pol, env, nef, rev, tat, vif, vpr, and vpu, were included in the analysis. Peptide epitopes were additionally evaluated on the basis of their conservancy (*i.e.*, the amount of variance) among the available protein sequences for each HIV antigen. A criterion for conservancy used to generate the peptides set out in Tables VII-XX requires that the entire sequence of an HLA class I binding peptide be totally conserved in 15% of
30 the sequences available for a specific HIV antigen. Similarly, a criterion for conservancy requires that the entire 9-mer core region of an HLA class II binding peptide be totally conserved in 15% of the sequences available for a specific protein. The percent conservancy of the selected peptide epitopes is indicated on the Tables. The frequency, *i.e.* the number of sequences of the HIV protein antigen in which the totally conserved

peptide sequence was identified, is also shown. The "pos" (position) column in the Tables designates the amino acid position in the HIV protein that corresponds to the first amino acid residue of the epitope. The "number of amino acids" indicates the number of residues in the epitope sequence.

5

HLA Class I Motifs Indicative of CTL Inducing Peptide Epitopes:

The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs delineated below are summarized in Table I. The HLA class I motifs set out in Table I(a) are those most particularly relevant to the invention claimed here. Primary and
10 secondary anchor positions are summarized in Table II. Allele-specific HLA molecules that comprise HLA class I supertype families are listed in Table VI. In some cases, peptide epitopes may be listed in both a motif and a supermotif Table. The relationship of a particular motif and respective supermotif is indicated in the description of the individual motifs.

15

IV.D.1. HLA-A1 supermotif

The HLA-A1 supermotif is characterized by the presence in peptide ligands of a small (T or S) or hydrophobic (L, I, V, or M) primary anchor residue in position 2, and an aromatic (Y, F, or W) primary anchor residue at the C-terminal position of the epitope.
20 The corresponding family of HLA molecules that bind to the A1 supermotif (*i.e.*, the HLA-A1 supertype) is comprised of at least A*0101, A*2601, A*2602, A*2501, and A*3201 (*see, e.g.*, DiBrino, M. *et al.*, *J. Immunol.* 151:5930, 1993; DiBrino, M. *et al.*, *J. Immunol.* 152:620, 1994; Kondo, A. *et al.*, *Immunogenetics* 45:249, 1997). Other allele-specific HLA molecules predicted to be members of the A1 superfamily are shown in
25 Table VI. Peptides binding to each of the individual HLA proteins can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A1 supermotif are set forth in Table VII.

30

IV.D.2. HLA-A2 supermotif

Primary anchor specificities for allele-specific HLA-A2.1 molecules (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991; Hunt *et al.*, *Science* 255:1261-1263, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992; Ruppert *et al.*, *Cell* 74:929-937, 1993) and

cross-reactive binding among HLA-A2 and -A28 molecules have been described. (See, e.g., Fruci *et al.*, *Human Immunol.* 38:187-192, 1993; Tanigaki *et al.*, *Human Immunol.* 39:155-162, 1994; Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994 for reviews of relevant data.) These primary anchor residues define the HLA-A2 supermotif; which presence in peptide ligands corresponds to the ability to bind several different HLA-A2 and -A28 molecules. The HLA-A2 supermotif comprises peptide ligands with L, I, V, M, A, T, or Q as a primary anchor residue at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope.

- 10 The corresponding family of HLA molecules (*i.e.*, the HLA-A2 supertype that binds these peptides) is comprised of at least: A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, and A*6901. Other allele-specific HLA molecules predicted to be members of the A2 superfamily are shown in Table VI. As explained in detail below, binding to each of the individual allele-specific
- 15 HLA molecules can be modulated by substitutions at the primary anchor and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

- Representative peptide epitopes that comprise an A2 supermotif are set forth in Table VIII. The motifs comprising the primary anchor residues V, A, T, or Q at position
- 20 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

IV.D.3. HLA-A3 supermotif

- The HLA-A3 supermotif is characterized by the presence in peptide ligands of A, L, I, V, M, S, or, T as a primary anchor at position 2, and a positively charged residue, R or K, at the C-terminal position of the epitope, *e.g.*, in position 9 of 9-mers (*see, e.g.*, Sidney *et al.*, *Hum. Immunol.* 45:79, 1996). Exemplary members of the corresponding family of HLA molecules (the HLA-A3 supertype) that bind the A3 supermotif include at least A*0301, A*1101, A*3101, A*3301, and A*6801. Other allele-specific HLA
- 25 molecules predicted to be members of the A3 supertype are shown in Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions of amino acids at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.
- 30

Representative peptide epitopes that comprise the A3 supermotif are set forth in Table IX.

IV.D.4. HLA-A24 supermotif

5 The HLA-A24 supermotif is characterized by the presence in peptide ligands of an aromatic (F, W, or Y) or hydrophobic aliphatic (L, I, V, M, or T) residue as a primary anchor in position 2, and Y, F, W, L, I, or M as primary anchor at the C-terminal position of the epitope (*see, e.g.,* Sette and Sidney, *Immunogenetics*, in press, 1999). The corresponding family of HLA molecules that bind to the A24 supermotif (*i.e.,* the A24
10 supertype) includes at least A*2402, A*3001, and A*2301. Other allele-specific HLA molecules predicted to be members of the A24 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

15 Representative peptide epitopes that comprise the A24 supermotif are set forth in Table X.

IV.D.5. HLA-B7 supermotif

 The HLA-B7 supermotif is characterized by peptides bearing proline in position 2
20 as a primary anchor, and a hydrophobic or aliphatic amino acid (L, I, V, M, A, F, W, or Y) as the primary anchor at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind the B7 supermotif (*i.e.,* the HLA-B7 supertype) is comprised of at least twenty six HLA-B proteins including: B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507,
25 B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, and B*7801 (*see, e.g.,* Sidney, *et al., J. Immunol.* 154:247, 1995; Barber, *et al., Curr. Biol.* 5:179, 1995; Hill, *et al., Nature* 360:434, 1992; Rammensee, *et al., Immunogenetics* 41:178, 1995 for reviews of relevant data). Other allele-specific HLA molecules predicted to be members of the B7 supertype are shown in
30 Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B7 supermotif are set forth in Table XI.

IV.D.6. HLA-B27 supermotif

- 5 The HLA-B27 supermotif is characterized by the presence in peptide ligands of a positively charged (R, H, or K) residue as a primary anchor at position 2, and a hydrophobic (F, Y, L, W, M, I, A, or V) residue as a primary anchor at the C-terminal position of the epitope (*see, e.g.,* Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B27 supermotif (*i.e.,* the B27 supertype) include at least B*1401, B*1402, B*1509, B*2702, 10 B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, and B*7301. Other allele-specific HLA molecules predicted to be members of the B27 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably 15 choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B27 supermotif are set forth on Table XII.

IV.D.7. HLA-B44 supermotif

- 20 The HLA-B44 supermotif is characterized by the presence in peptide ligands of negatively charged (D or E) residues as a primary anchor in position 2, and hydrophobic residues (F, W, Y, L, I, M, V, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.,* Sidney et al., *Immunol. Today* 17:261, 1996). Exemplary members of the corresponding family of HLA molecules that bind to the B44 supermotif (*i.e.,* the B44 25 supertype) include at least: B*1801, B*1802, B*3701, B*4001, B*4002, B*4006, B*4402, B*4403, and B*4006. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the supermotif.

30 IV.D.8. HLA-B58 supermotif

The HLA-B58 supermotif is characterized by the presence in peptide ligands of a small aliphatic residue (A, S, or T) as a primary anchor residue at position 2, and an aromatic or hydrophobic residue (F, W, Y, L, I, V, M, or A) as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.,* Sidney and Sette, *Immunogenetics*, in

press, 1999 for reviews of relevant data). Exemplary members of the corresponding family of HLA molecules that bind to the B58 supermotif (*i.e.*, the B58 supertype) include at least: B*1516, B*1517, B*5701, B*5702, and B*5801. Other allele-specific HLA molecules predicted to be members of the B58 supertype are shown in Table VI.

- 5 Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B58 supermotif are set forth on Table XIII.

10

IV.D.9. HLA-B62 supermotif

The HLA-B62 supermotif is characterized by the presence in peptide ligands of the polar aliphatic residue Q or a hydrophobic aliphatic residue (L, V, M, I, or P) as a primary anchor in position 2, and a hydrophobic residue (F, W, Y, M, I, V, L, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B62 supermotif (*i.e.*, the B62 supertype) include at least: B*1501, B*1502, B*1513, and B5201. Other allele-specific HLA molecules predicted to be members of the B62 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

20

Representative peptide epitopes that comprise the B62 supermotif are set forth on Table XIV.

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IV.D.10. HLA-A1 motif

The HLA-A1 motif is characterized by the presence in peptide ligands of T, S, or M as a primary anchor residue at position 2 and the presence of Y as a primary anchor residue at the C-terminal position of the epitope. An alternative allele-specific A1 motif is characterized by a primary anchor residue at position 3 rather than position 2. This motif is characterized by the presence of D, E, A, or S as a primary anchor residue in position 3, and a Y as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, DiBrino *et al.*, *J. Immunol.*, 152:620, 1994; Kondo *et al.*, *Immunogenetics* 45:249, 1997; and Kubo *et al.*, *J. Immunol.* 152:3913, 1994 for reviews of relevant data).

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Peptide binding to HLA A1 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise either A1 motif are set forth on Table XV. Those epitopes comprising T, S, or M at position 2 and Y at the C-terminal position are also included in the listing of HLA-A1 supermotif-bearing peptide epitopes listed in Table VII, as these residues are a subset of the A1 supermotif primary anchors.

IV.D.11. HLA-A*0201 motif

An HLA-A2*0201 motif was determined to be characterized by the presence in peptide ligands of L or M as a primary anchor residue in position 2, and L or V as a primary anchor residue at the C-terminal position of a 9-residue peptide (*see, e.g., Falk et al., Nature* 351:290-296, 1991) and was further found to comprise an I at position 2 and I or A at the C-terminal position of a nine amino acid peptide (*see, e.g., Hunt et al., Science* 255:1261-1263, March 6, 1992; Parker *et al., J. Immunol.* 149:3580-3587, 1992). The A*0201 allele-specific motif has also been defined by the present inventors to additionally comprise V, A, T, or Q as a primary anchor residue at position 2, and M or T as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., Kast et al., J. Immunol.* 152:3904-3912, 1994). Thus, the HLA-A*0201 motif comprises peptide ligands with L, I, V, M, A, T, or Q as primary anchor residues at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope. The preferred and tolerated residues that characterize the primary anchor positions of the HLA-A*0201 motif are identical to the residues describing the A2 supermotif. (For reviews of relevant data, *see, e.g., Del Guercio et al., J. Immunol.* 154:685-693, 1995; Ruppert *et al., Cell* 74:929-937, 1993; Sidney *et al., Immunol. Today* 17:261-266, 1996; Sette and Sidney, *Curr. Opin. in Immunol.* 10:478-482, 1998). Secondary anchor residues that characterize the A*0201 motif have additionally been defined (*see, e.g., Ruppert et al., Cell* 74:929-937, 1993). These are shown in Table II. Peptide binding to HLA-A*0201 molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise an A*0201 motif are set forth on Table VIII. The A*0201 motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

IV.D.12. HLA-A3 motif

The HLA-A3 motif is characterized by the presence in peptide ligands of L, M, V, I, S, A, T, F, C, G, or D as a primary anchor residue at position 2, and the presence of K, Y, R, H, F, or A as a primary anchor residue at the C-terminal position of the epitope (see, e.g., DiBrino *et al.*, *Proc. Natl. Acad. Sci USA* 90:1508, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A3 motif are set forth on Table XVI. Those peptide epitopes that also comprise the A3 supermotif are also listed in Table IX. The A3 supermotif primary anchor residues comprise a subset of the A3- and A11-allele specific motif primary anchor residues.

IV.D.13. HLA-A11 motif

The HLA-A11 motif is characterized by the presence in peptide ligands of V, T, M, L, I, S, A, G, N, C, D, or F as a primary anchor residue in position 2, and K, R, Y, or H as a primary anchor residue at the C-terminal position of the epitope (see, e.g., Zhang *et al.*, *Proc. Natl. Acad. Sci USA* 90:2217-2221, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A11 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A11 motif are set forth on Table XVII; peptide epitopes comprising the A3 allele-specific motif are also present in this Table because of the extensive overlap between the A3 and A11 motif primary anchor specificities. Further, those peptide epitopes that comprise the A3 supermotif are also listed in Table IX.

IV.D.14. HLA-A24 motif

The HLA-A24 motif is characterized by the presence in peptide ligands of Y, F, W, or M as a primary anchor residue in position 2, and F, L, I, or W as a primary anchor residue at the C-terminal position of the epitope (see, e.g., Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A24 molecules can be modulated by substitutions at primary and/or

secondary anchor positions; preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A24 motif are set forth on Table XVIII. These epitopes are also listed in Table X, which sets forth HLA-A24-supermotif-bearing peptide epitopes, as the primary anchor residues characterizing the A24 allele-specific motif comprise a subset of the A24 supermotif primary anchor residues.

Motifs Indicative of Class II HTL Inducing Peptide Epitopes

The primary and secondary anchor residues of the HLA class II peptide epitope supermotifs and motifs delineated below are summarized in Table III.

IV.D.15. HLA DR-1-4-7 supermotif

Motifs have also been identified for peptides that bind to three common HLA class II allele-specific HLA molecules: HLA DRB1*0401, DRB1*0101, and DRB1*0701 (see, e.g., the review by Southwood *et al. J. Immunology* 160:3363-3373,1998). Collectively, the common residues from these motifs delineate the HLA DR-1-4-7 supermotif. Peptides that bind to these DR molecules carry a supermotif characterized by a large aromatic or hydrophobic residue (Y, F, W, L, I, V, or M) as a primary anchor residue in position 1, and a small, non-charged residue (S, T, C, A, P, V, I, L, or M) as a primary anchor residue in position 6 of a 9-mer core region. Allele-specific secondary effects and secondary anchors for each of these HLA types have also been identified (Southwood *et al., supra*). These are set forth in Table III. Peptide binding to HLA-DRB1*0401, DRB1*0101, and/or DRB1*0701 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Conserved 9-mer core regions (*i.e.*, sequences that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis), comprising the DR-1-4-7 supermotif, wherein position 1 of the supermotif is at position 1 of the nine-residue core, are set forth in Table XIXa. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in section "a" of the Table. Cross-reactive binding data for exemplary 15-residue supermotif-bearing peptides are shown in Table XIXb.

IV.D.16. HLA DR3 motifs

Two alternative motifs (*i.e.*, submotifs) characterize peptide epitopes that bind to HLA-DR3 molecules (*see, e.g.*, Geluk *et al.*, *J. Immunol.* 152:5742, 1994). In the first motif (submotif DR3A) a large, hydrophobic residue (L, I, V, M, F, or Y) is present in anchor position 1 of a 9-mer core, and D is present as an anchor at position 4, towards the carboxyl terminus of the epitope. As in other class II motifs, core position 1 may or may not occupy the peptide N-terminal position.

The alternative DR3 submotif provides for lack of the large, hydrophobic residue at anchor position 1, and/or lack of the negatively charged or amide-like anchor residue at position 4, by the presence of a positive charge at position 6 towards the carboxyl terminus of the epitope. Thus, for the alternative allele-specific DR3 motif (submotif DR3B): L, I, V, M, F, Y, A, or Y is present at anchor position 1; D, N, Q, E, S, or T is present at anchor position 4; and K, R, or H is present at anchor position 6. Peptide binding to HLA-DR3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Conserved 9-mer core regions (*i.e.*, those sequences that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis) corresponding to a nine residue sequence comprising the DR3A submotif (wherein position 1 of the motif is at position 1 of the nine residue core) are set forth in Table XXa. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in Table XXa. Table XXb shows binding data of exemplary DR3 submotif A-bearing peptides.

Conserved 9-mer core regions (*i.e.*, those that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis) comprising the DR3B submotif and respective exemplary 15-mer peptides comprising the DR3 submotif-B epitope are set forth in Table XXc. Table XXd shows binding data of exemplary DR3 submotif B-bearing peptides.

Each of the HLA class I or class II peptide epitopes set out in the Tables herein are deemed singly to be an inventive aspect of this application. Further, it is also an inventive aspect of this application that each peptide epitope may be used in combination with any other peptide epitope.

IV.E. Enhancing Population Coverage of the Vaccine

Vaccines that have broad population coverage are preferred because they are more commercially viable and generally applicable to the most people. Broad population coverage can be obtained using the peptides of the invention (and nucleic acid compositions that encode such peptides) through selecting peptide epitopes that bind to HLA alleles which, when considered in total, are present in most of the population. Table XXI lists the overall frequencies of the HLA class I supertypes in various ethnicities (Table XXIa) and the combined population coverage achieved by the A2-, A3-, and B7-supertypes (Table XXIb). The A2-, A3-, and B7 supertypes are each present on the average of over 40% in each of these five major ethnic groups. Coverage in excess of 80% is achieved with a combination of these supermotifs. These results suggest that effective and non-ethnically biased population coverage is achieved upon use of a limited number of cross-reactive peptides. Although the population coverage reached with these three main peptide specificities is high, coverage can be expanded to reach 95% population coverage and above, and more easily achieve truly multispecific responses upon use of additional supermotif or allele-specific motif bearing peptides.

The B44-, A1-, and A24-supertypes are each present, on average, in a range from 25% to 40% in these major ethnic populations (Table XXIa). While less prevalent overall, the B27-, B58-, and B62 supertypes are each present with a frequency >25% in at least one major ethnic group (Table XXIa). Table XXIb summarizes the estimated prevalence of combinations of HLA supertypes that have been identified in five major ethnic groups. The incremental coverage obtained by the inclusion of A1-, A24-, and B44-supertypes to the A2, A3, and B7 coverage and coverage obtained with all of the supertypes described herein, is shown.

The data presented herein, together with the previous definition of the A2-, A3-, and B7-supertypes, indicates that all antigens, with the possible exception of A29, B8, and B46, can be classified into a total of nine HLA supertypes. By including epitopes from the six most frequent supertypes, an average population coverage of 99% is obtained for five major ethnic groups..

IV.F. Immune Response-Stimulating Peptide Analogs

In general, CTL and HTL responses are not directed against all possible epitopes. Rather, they are restricted to a few "immunodominant" determinants (Zinkernagel, *et al.*, *Adv. Immunol.* 27:5159, 1979; Bennink, *et al.*, *J. Exp. Med.* 168:19351939, 1988; Rawle,

et al., *J. Immunol.* 146:3977-3984, 1991). It has been recognized that immunodominance (Benacerraf, *et al.*, *Science* 175:273-279, 1972) could be explained by either the ability of a given epitope to selectively bind a particular HLA protein (determinant selection theory) (Vitiello, *et al.*, *J. Immunol.* 131:1635, 1983); Rosenthal, *et al.*, *Nature* 267:156-158, 1977), or to be selectively recognized by the existing TCR (T cell receptor) specificities (repertoire theory) (Klein, J., *IMMUNOLOGY, THE SCIENCE OF SELF/NONSELF DISCRIMINATION*, John Wiley & Sons, New York, pp. 270-310, 1982). It has been demonstrated that additional factors, mostly linked to processing events, can also play a key role in dictating, beyond strict immunogenicity, which of the many potential determinants will be presented as immunodominant (Sercarz, *et al.*, *Annu. Rev. Immunol.* 11:729-766, 1993).

The concept of dominance and subdominance is relevant to immunotherapy of both infectious diseases and cancer. For example, in the course of chronic viral disease, recruitment of subdominant epitopes can be important for successful clearance of the infection, especially if dominant CTL or HTL specificities have been inactivated by functional tolerance, suppression, mutation of viruses and other mechanisms (Franco, *et al.*, *Curr. Opin. Immunol.* 7:524-531, 1995). In the case of cancer and tumor antigens, CTLs recognizing at least some of the highest binding affinity peptides might be functionally inactivated. Lower binding affinity peptides are preferentially recognized at these times, and may therefore be preferred in therapeutic or prophylactic anti-cancer vaccines.

In particular, it has been noted that a significant number of epitopes derived from known non-viral tumor associated antigens (TAA) bind HLA class I with intermediate affinity (IC_{50} in the 50-500 nM range). For example, it has been found that 8 of 15 known TAA peptides recognized by tumor infiltrating lymphocytes (TIL) or CTL bound in the 50-500 nM range. (These data are in contrast with estimates that 90% of known viral antigens were bound by HLA class I molecules with IC_{50} of 50 nM or less, while only approximately 10% bound in the 50-500 nM range (Sette, *et al.*, *J. Immunol.*, 153:558-5592, 1994). In the cancer setting this phenomenon is probably due to elimination or functional inhibition of the CTL recognizing several of the highest binding peptides, presumably because of T cell tolerization events.

Without intending to be bound by theory, it is believed that because T cells to dominant epitopes may have been clonally deleted, selecting subdominant epitopes may allow existing T cells to be recruited, which will then lead to a therapeutic or prophylactic

response. However, the binding of HLA molecules to subdominant epitopes is often less vigorous than to dominant ones. Accordingly, there is a need to be able to modulate the binding affinity of particular immunogenic epitopes for one or more HLA molecules, and thereby to modulate the immune response elicited by the peptide, for example to prepare
5 analog peptides which elicit a more vigorous response. This ability would greatly enhance the usefulness of peptide epitope-based vaccines and therapeutic agents.

Although peptides with suitable cross-reactivity among all alleles of a superfamily are identified by the screening procedures described above, cross-reactivity is not always as complete as possible, and in certain cases procedures to increase cross-reactivity of
10 peptides can be useful; moreover, such procedures can also be used to modify other properties of the peptides such as binding affinity or peptide stability. Having established the general rules that govern cross-reactivity of peptides for HLA alleles within a given motif or supermotif, modification (*i.e.*, analoging) of the structure of peptides of particular interest in order to achieve broader (or otherwise modified) HLA binding
15 capacity can be performed. More specifically, peptides which exhibit the broadest cross-reactivity patterns, can be produced in accordance with the teachings herein. The present concepts related to analog generation are set forth in greater detail in co-pending U.S.S.N. 09/226,775 filed 1/6/99.

In brief, the strategy employed utilizes the motifs or supermotifs which correlate
20 with binding to certain HLA molecules. The motifs or supermotifs are defined by having primary anchors, and in many cases secondary anchors. Analog peptides can be created by substituting amino acid residues at primary anchor, secondary anchor, or at primary and secondary anchor positions. Generally, analogs are made for peptides that already bear a motif or supermotif. Preferred secondary anchor residues of supermotifs and
25 motifs that have been defined for HLA class I and class II binding peptides are shown in Tables II and III, respectively.

For a number of the motifs or supermotifs in accordance with the invention, residues are defined which are deleterious to binding to allele-specific HLA molecules or members of HLA supertypes that bind the respective motif or supermotif (Tables II and
30 III). Accordingly, removal of such residues that are detrimental to binding can be performed in accordance with the present invention. For example, in the case of the A3 supertype, when all peptides that have such deleterious residues are removed from the population of peptides used in the analysis, the incidence of cross-reactivity increased from 22% to 37% (*see, e.g.*, Sidney, J. *et al.*, *Hu. Immunol.* 45:79, 1996). Thus, one

strategy to improve the cross-reactivity of peptides within a given supermotif is simply to delete one or more of the deleterious residues present within a peptide and substitute a small "neutral" residue such as Ala (that may not influence T cell recognition of the peptide). An enhanced likelihood of cross-reactivity is expected if, together with
5 elimination of detrimental residues within a peptide, "preferred" residues associated with high affinity binding to an allele-specific HLA molecule or to multiple HLA molecules within a superfamily are inserted.

To ensure that an analog peptide, when used as a vaccine, actually elicits a CTL response to the native epitope *in vivo* (or, in the case of class II epitopes, elicits helper T
10 cells that cross-react with the wild type peptides), the analog peptide may be used to immunize T cells *in vitro* from individuals of the appropriate HLA allele. Thereafter, the immunized cells' capacity to induce lysis of wild type peptide sensitized target cells is evaluated. It will be desirable to use as antigen presenting cells, cells that have been either infected, or transfected with the appropriate genes, or, in the case of class II
15 epitopes only, cells that have been pulsed with whole protein antigens, to establish whether endogenously produced antigen is also recognized by the relevant T cells.

Another embodiment of the invention is to create analogs of weak binding peptides, to thereby ensure adequate numbers of cross-reactive cellular binders. Class I binding peptides exhibiting binding affinities of 500-5000 nM, and carrying an acceptable
20 but suboptimal primary anchor residue at one or both positions can be "fixed" by substituting preferred anchor residues in accordance with the respective supertype. The analog peptides can then be tested for crossbinding activity.

Another embodiment for generating effective peptide analogs involves the substitution of residues that have an adverse impact on peptide stability or solubility in,
25 *e.g.*, a liquid environment. This substitution may occur at any position of the peptide epitope. For example, a cysteine (C) can be substituted out in favor of α -amino butyric acid. Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substituting α -amino butyric acid for C not only alleviates this problem, but actually improves binding
30 and crossbinding capability in certain instances (*see, e.g.*, the review by Sette *et al.*, In: Persistent Viral Infections, Eds. R. Ahmed and I. Chen, John Wiley & Sons, England, 1999). Substitution of cysteine with α -amino butyric acid may occur at any residue of a peptide epitope, *i.e.* at either anchor or non-anchor positions.

IV.G. Computer Screening of Protein Sequences from Disease-Related Antigens for Supermotif- or Motif-Bearing Peptides

In order to identify supermotif- or motif-bearing epitopes in a target antigen, a native protein sequence, *e.g.*, a tumor-associated antigen, or sequences from an infectious organism, or a donor tissue for transplantation, is screened using a means for computing, such as an intellectual calculation or a computer, to determine the presence of a supermotif or motif within the sequence. The information obtained from the analysis of native peptide can be used directly to evaluate the status of the native peptide or may be utilized subsequently to generate the peptide epitope.

Computer programs that allow the rapid screening of protein sequences for the occurrence of the subject supermotifs or motifs are encompassed by the present invention; as are programs that permit the generation of analog peptides. These programs are implemented to analyze any identified amino acid sequence or operate on an unknown sequence and simultaneously determine the sequence and identify motif-bearing epitopes thereof; analogs can be simultaneously determined as well. Generally, the identified sequences will be from a pathogenic organism or a tumor-associated peptide. For example, the target molecules considered herein include, without limitation, the gag, pol, env, nef, rev, tat, vif, vpr, and vpu proteins of HIV.

In cases where the sequence of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide, be conserved in a designated percentage, of the sequences evaluated for a specific protein antigen.

Because HIV rapidly mutates thereby resulting in the generation of virus strains that have divergent amino acid sequences, an alternative method of selecting epitopes for inclusion in a vaccine composition is employed herein. In order to target a broad population that may be infected with a number of different strains, it is preferable to include in vaccine compositions epitopes that are representative of HIV antigen sequences from different HIV strains. For example, by selecting 5 epitopes from the same region, each of which is 20% conserved among HIV strains, the combination of the epitopes achieves 100% coverage of that region. As appreciated by those in the art, lower or higher degrees of conservancy, such as the 15% conservancy used for identification of

the epitopes set out in Tables VII-XX, can be employed as appropriate for a given antigenic target.

It is important that the selection criteria utilized for prediction of peptide binding are as accurate as possible, to correlate most efficiently with actual binding. Prediction of peptides that bind, for example, to HLA-A*0201, on the basis of the presence of the appropriate primary anchors, is positive at about a 30% rate (*see, e.g., Ruppert, J. et al. Cell* 74:929, 1993). However, by extensively analyzing peptide-HLA binding data disclosed herein, data in related patent applications, and data in the art, the present inventors have developed a number of allele-specific polynomial algorithms that dramatically increase the predictive value over identification on the basis of the presence of primary anchor residues alone. These algorithms take into account not only the presence or absence of primary anchors, but also consider the positive or deleterious presence of secondary anchor residues (to account for the impact of different amino acids at different positions). The algorithms are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA interactions can be approximated as a linear polynomial function of the type:

$$\Delta G = a_{1i} \times a_{2i} \times a_{3i} \dots \times a_{ni}$$

where a_{ji} is a coefficient that represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. An important assumption of this method is that the effects at each position are essentially independent of each other. This assumption is justified by studies that demonstrated that peptides are bound to HLA molecules and recognized by T cells in essentially an extended conformation. Derivation of specific algorithm coefficients has been described, for example, in Gulukota, K. *et al., J. Mol. Biol.* 267:1258, 1997.

Additional methods to identify preferred peptide sequences, which also make use of specific motifs, include the use of neural networks and molecular modeling programs (*see, e.g., Milik et al., Nature Biotechnology* 16:753, 1998; Altuvia *et al., Hum. Immunol.* 58:1, 1997; Altuvia *et al., J. Mol. Biol.* 249:244, 1995; Buus, S. *Curr. Opin. Immunol.* 11:209-213, 1999; Brusic, V. *et al., Bioinformatics* 14:121-130, 1998; Parker *et al., J. Immunol.* 152:163, 1993; Meister *et al., Vaccine* 13:581, 1995; Hammer *et al., J. Exp. Med.* 180:2353, 1994; Sturniolo *et al., Nature Biotechnol.* 17:555 1999).

For example, it has been shown that in sets of A*0201 motif-bearing peptides containing at least one preferred secondary anchor residue while avoiding the presence of

any deleterious secondary anchor residues, 69% of the peptides will bind A*0201 with an IC_{50} less than 500 nM (Ruppert, J. *et al. Cell* 74:929, 1993). These algorithms are also flexible in that cut-off scores may be adjusted to select sets of peptides with greater or lower predicted binding properties, as desired.

5 In utilizing computer screening to identify peptide epitopes, a protein sequence or translated sequence may be analyzed using software developed to search for motifs, for example the "FINDPATTERNS" program (Devereux, *et al. Nucl. Acids Res.* 12:387-395, 1984) or MotifSearch 1.4 software program (D. Brown, San Diego, CA) to identify potential peptide sequences containing appropriate HLA binding motifs. The identified
10 peptides can be scored using customized polynomial algorithms to predict their capacity to bind specific HLA class I or class II alleles. As appreciated by one of ordinary skill in the art, a large array of computer programming software and hardware options are available in the relevant art which can be employed to implement the motifs of the invention in order to evaluate (*e.g.*, without limitation, to identify epitopes, identify
15 epitope concentration per peptide length, or to generate analogs) known or unknown peptide sequences.

 In accordance with the procedures described above, HIV peptide epitopes and analogs thereof that are able to bind HLA supertype groups or allele-specific HLA molecules have been identified (Tables VII-XX).

20

IV.H. Preparation of Peptide Epitopes

 Peptides in accordance with the invention can be prepared synthetically, by recombinant DNA technology or chemical synthesis, or from natural sources such as native tumors or pathogenic organisms. Peptide epitopes may be synthesized individually
25 or as polyepitopic peptides. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides may be synthetically conjugated to native fragments or particles.

 The peptides in accordance with the invention can be a variety of lengths, and either in their neutral (uncharged) forms or in forms which are salts. The peptides in
30 accordance with the invention are either free of modifications such as glycosylation, side chain oxidation, or phosphorylation; or they contain these modifications, subject to the condition that modifications do not destroy the biological activity of the peptides as described herein.

When possible, it may be desirable to optimize HLA class I binding peptide epitopes of the invention to a length of about 8 to about 13 amino acid residues, preferably 9 to 10. HLA class II binding peptide epitopes may be optimized to a length of about 6 to about 30 amino acids in length, preferably to between about 13 and about 20 residues. Preferably, the peptide epitopes are commensurate in size with endogenously processed pathogen-derived peptides or tumor cell peptides that are bound to the relevant HLA molecules.

In alternative embodiments, epitopes of the invention can be linked as a polyepitopic peptide, or as a minigene that encodes a polyepitopic peptide.

In another embodiment, it is preferred to identify native peptide regions that contain a high concentration of class I and/or class II epitopes. Such a sequence is generally selected on the basis that it contains the greatest number of epitopes per amino acid length. It is to be appreciated that epitopes can be present in a nested or overlapping manner, *e.g.* a 10 amino acid long peptide could contain two 9 amino acid long epitopes and one 10 amino acid long epitope; upon intracellular processing, each epitope can be exposed and bound by an HLA molecule upon administration of such a peptide. This larger, preferably multi-epitopic, peptide can be generated synthetically, recombinantly, or via cleavage from the native source.

The peptides of the invention can be prepared in a wide variety of ways. For the preferred relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. (*See, for example, Stewart & Young, SOLID PHASE PEPTIDE SYNTHESIS, 2D. ED., Pierce Chemical Co., 1984*). Further, individual peptide epitopes can be joined using chemical ligation to produce larger peptides that are still within the bounds of the invention.

Alternatively, recombinant DNA technology can be employed wherein a nucleotide sequence which encodes an immunogenic peptide of interest is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art, as described generally in Sambrook *et al.*, *MOLECULAR CLONING, A LABORATORY MANUAL*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989). Thus, recombinant polypeptides which comprise one or more peptide sequences of the invention can be used to present the appropriate T cell epitope.

The nucleotide coding sequence for peptide epitopes of the preferred lengths contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci, *et al.*, *J. Am. Chem. Soc.* 103:3185 (1981). Peptide analogs can be made simply by substituting the appropriate and desired nucleic acid base(s) for those that encode the native peptide sequence; exemplary nucleic acid substitutions are those that encode an amino acid defined by the motifs/super motifs herein. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired fusion protein. A number of such vectors and suitable host systems are now available. For expression of the fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts. Of course, yeast, insect or mammalian cell hosts may also be used, employing suitable vectors and control sequences.

IV.I. Assays to Detect T-Cell Responses

Once HLA binding peptides are identified, they can be tested for the ability to elicit a T-cell response. The preparation and evaluation of motif-bearing peptides are described in PCT publications WO 94/20127 and WO 94/03205. Briefly, peptides comprising epitopes from a particular antigen are synthesized and tested for their ability to bind to the appropriate HLA proteins. These assays may involve evaluating the binding of a peptide of the invention to purified HLA class I molecules in relation to the binding of a radioiodinated reference peptide. Alternatively, cells expressing empty class I molecules (*i.e.* lacking peptide therein) may be evaluated for peptide binding by immunofluorescent staining and flow microfluorimetry. Other assays that may be used to evaluate peptide binding include peptide-dependent class I assembly assays and/or the inhibition of CTL recognition by peptide competition. Those peptides that bind to the class I molecule, typically with an affinity of 500 nM or less, are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary *in vitro* or *in vivo* CTL responses that can give rise to CTL populations capable of reacting with selected target cells associated with

a disease. Corresponding assays are used for evaluation of HLA class II binding peptides. HLA class II motif-bearing peptides that are shown to bind, typically at an affinity of 1000 nM or less, are further evaluated for the ability to stimulate HTL responses.

Conventional assays utilized to detect T cell responses include proliferation
5 assays, lymphokine secretion assays, direct cytotoxicity assays, and limiting dilution assays. For example, antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells. Alternatively, mutant non-human mammalian cell lines that are
10 deficient in their ability to load class I molecules with internally processed peptides and that have been transfected with the appropriate human class I gene, may be used to test for the capacity of the peptide to induce *in vitro* primary CTL responses.

Peripheral blood mononuclear cells (PBMCs) may be used as the responder cell source of CTL precursors. The appropriate antigen-presenting cells are incubated with
15 peptide, after which the peptide-loaded antigen-presenting cells are then incubated with the responder cell population under optimized culture conditions. Positive CTL activation can be determined by assaying the culture for the presence of CTLs that kill radio-labeled target cells, both specific peptide-pulsed targets as well as target cells expressing endogenously processed forms of the antigen from which the peptide sequence
20 was derived.

More recently, a method has been devised which allows direct quantification of antigen-specific T cells by staining with Fluorescein-labelled HLA tetrameric complexes (Altman, J. D. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:10330, 1993; Altman, J. D. *et al.*, *Science* 274:94, 1996). Other relatively recent technical developments include staining
25 for intracellular lymphokines, and interferon release assays or ELISPOT assays. Tetramer staining, intracellular lymphokine staining and ELISPOT assays all appear to be at least 10-fold more sensitive than more conventional assays (Lalvani, A. *et al.*, *J. Exp. Med.* 186:859, 1997; Dunbar, P. R. *et al.*, *Curr. Biol.* 8:413, 1998; Murali-Krishna, K. *et al.*, *Immunity* 8:177, 1998).

30 HTL activation may also be assessed using such techniques known to those in the art such as T cell proliferation and secretion of lymphokines, *e.g.* IL-2 (*see, e.g.* Alexander *et al.*, *Immunity* 1:751-761, 1994).

Alternatively, immunization of HLA transgenic mice can be used to determine immunogenicity of peptide epitopes. Several transgenic mouse models including mice

with human A2.1, A11 (which can additionally be used to analyze HLA-A3 epitopes), and B7 alleles have been characterized and others (e.g., transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed. Additional transgenic mouse models with other HLA alleles may be generated as necessary. Mice may be immunized with peptides emulsified in Incomplete Freund's Adjuvant and the resulting T cells tested for their capacity to recognize peptide-pulsed target cells and target cells transfected with appropriate genes. CTL responses may be analyzed using cytotoxicity assays described above. Similarly, HTL responses may be analyzed using such assays as T cell proliferation or secretion of lymphokines.

Exemplary immunogenic peptide epitopes are set out in Table XXIII.

IV.J. Use of Peptide Epitopes as Diagnostic Agents and for Evaluating Immune Responses

HLA class I and class II binding peptides as described herein are used, in one embodiment of the invention, as reagents to evaluate an immune response. The immune response to be evaluated may be induced by using as an immunogen any agent that may result in the production of antigen-specific CTLs or HTLs that recognize and bind to the peptide epitope(s) to be employed as the reagent. The peptide reagent need not be used as the immunogen. Assay systems that may be used for such an analysis include relatively recent technical developments such as tetramers, staining for intracellular lymphokines and interferon release assays, or ELISPOT assays.

For example, a peptide of the invention can be used in a tetramer staining assay to assess peripheral blood mononuclear cells for the presence of antigen-specific CTLs following exposure to a pathogen or immunogen. The HLA-tetrameric complex is used to directly visualize antigen-specific CTLs (*see, e.g., Ogg et al., Science* 279:2103-2106, 1998; and Altman *et al., Science* 174:94-96, 1996) and determine the frequency of the antigen-specific CTL population in a sample of peripheral blood mononuclear cells.

A tetramer reagent using a peptide of the invention can typically be generated as follows: A peptide that binds to an HLA molecule is refolded in the presence of the corresponding HLA heavy chain and β_2 -microglobulin to generate a trimolecular complex. The complex is biotinylated at the carboxyl terminal end of the heavy chain at a site that was previously engineered into the protein. Tetramer formation is then induced by the addition of streptavidin. By means of fluorescently labeled streptavidin, the

tetramer can be used to stain antigen-specific cells. The cells may then be identified, for example, by flow cytometry. Such an analysis may be used for diagnostic or prognostic purposes.

Peptides of the invention are also used as reagents to evaluate immune recall
5 responses. (see, *e.g.*, Bertoni *et al.*, *J. Clin. Invest.* 100:503-513, 1997 and Penna *et al.*, *J. Exp. Med.* 174:1565-1570, 1991.) For example, patient PBMC samples from individuals infected with HIV may be analyzed for the presence of antigen-specific CTLs or HTLs using specific peptides. A blood sample containing mononuclear cells may be evaluated by cultivating the PBMCs and stimulating the cells with a peptide of the invention. After
10 an appropriate cultivation period, the expanded cell population may be analyzed, for example, for CTL or for HTL activity.

The peptides are also used as reagents to evaluate the efficacy of a vaccine. PBMCs obtained from a patient vaccinated with an immunogen may be analyzed using, for example, either of the methods described above. The patient is HLA typed, and
15 peptide epitope reagents that recognize the allele-specific molecules present in that patient are selected for the analysis. The immunogenicity of the vaccine is indicated by the presence of HIV epitope-specific CTLs and/or HTLs in the PBMC sample.

The peptides of the invention are also used to make antibodies, using techniques well known in the art (see, *e.g.* *CURRENT PROTOCOLS IN IMMUNOLOGY*, Wiley/Greene, NY;
20 and *Antibodies A Laboratory Manual* Harlow, Harlow and Lane, Cold Spring Harbor Laboratory Press, 1989), which may be useful as reagents to diagnose HIV infection. Such antibodies include those that recognize a peptide in the context of an HLA molecule, *i.e.*, antibodies that bind to a peptide-MHC complex.

25 IV.K. Vaccine Compositions

Vaccines and methods of preparing vaccines that contain an immunogenically effective amount of one or more peptides as described herein are further embodiments of the invention. Once appropriately immunogenic epitopes have been defined, they can be sorted and delivered by various means, herein referred to as "vaccine" compositions.
30 Such vaccine compositions can include, for example, lipopeptides (*e.g.*, Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, *e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, *e.g.*,

Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998), multiple antigen peptide systems (MAPs) (*see e.g.*, Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990), particles of viral or synthetic origin (*e.g.*, Kofler, N. *et al.*, *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995), adjuvants (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993), liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996), or, naked or particle absorbed cDNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions of the invention include nucleic acid-mediated modalities. DNA or RNA encoding one or more of the peptides of the invention can also be administered to a patient. This approach is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, for example, as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a non-infected host, the recombinant vaccinia virus expresses the

immunogenic peptide, and thereby elicits a host CTL and/or HTL response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors
5 useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein.

Furthermore, vaccines in accordance with the invention encompass compositions
10 of one or more of the claimed peptides. A peptide can be present in a vaccine individually. Alternatively, the peptide can exist as a homopolymer comprising multiple copies of the same peptide, or as a heteropolymer of various peptides. Polymers have the advantage of increased immunological reaction and, where different peptide epitopes are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that
15 react with different antigenic determinants of the pathogenic organism or tumor-related peptide targeted for an immune response. The composition can be a naturally occurring region of an antigen or can be prepared, *e.g.*, recombinantly or by chemical synthesis.

Carriers that can be used with vaccines of the invention are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid,
20 polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza, hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable (*i.e.*, acceptable) diluent such as water, or saline, preferably phosphate buffered saline. The vaccines also typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials
25 well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glycerylcysteinylserine (P₃CSS).

Upon immunization with a peptide composition in accordance with the invention, via injection, aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other
30 suitable routes, the immune system of the host responds to the vaccine by producing large amounts of CTLs and/or HTLs specific for the desired antigen. Consequently, the host becomes at least partially immune to later infection, or at least partially resistant to developing an ongoing chronic infection, or derives at least some therapeutic benefit when the antigen was tumor-associated.

In some embodiments, it may be desirable to combine the class I peptide components with components that induce or facilitate neutralizing antibody and or helper T cell responses to the target antigen of interest. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. An
5 alternative embodiment of such a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PanDR molecule, *e.g.*, PADRE™ (Epimmune, San Diego, CA; described, *e.g.*, in U.S. Patent Number 5,736,142).

A vaccine of the invention can also include antigen-presenting cells (APC), such as dendritic cells (DC), as a vehicle to present peptides of the invention. Vaccine
10 compositions can be created *in vitro*, following dendritic cell mobilization and harvesting, whereby loading of dendritic cells occurs *in vitro*. For example, dendritic cells are transfected, *e.g.*, with a minigene in accordance with the invention, or are pulsed with peptides. The dendritic cell can then be administered to a patient to elicit immune responses *in vivo*.

15 Vaccine compositions, either DNA- or peptide-based, can also be administered *in vivo* in combination with dendritic cell mobilization whereby loading of dendritic cells occurs *in vivo*.

Antigenic peptides are used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTL or HTL cells, can be used to treat chronic infections, or tumors in
20 patients that do not respond to other conventional forms of therapy, or will not respond to a therapeutic vaccine peptide or nucleic acid in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular antigen (infectious or tumor-associated antigen) are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and the appropriate
25 immunogenic peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy or facilitate destruction of their specific target cell (an infected cell or a tumor cell). Transfected dendritic cells may also be used as antigen presenting cells.

30 The vaccine compositions of the invention can also be used in combination with other treatments used for HIV infection, including use in combination with therapy regimens including protease inhibitors and other immune adjuvants such as IL-2.

Preferably, the following principles are utilized when selecting an array of epitopes for inclusion in a polypeptidic composition for use in a vaccine, or for selecting discrete epitopes to be included in a vaccine and/or to be encoded by nucleic acids such as a minigene. Exemplary epitopes that may be utilized in a vaccine to treat or prevent HIV infection are set out in Tables XXXVII and XXXVIII. It is preferred that each of the following principles are balanced in order to make the selection. The multiple epitopes to be incorporated in a given vaccine composition can be, but need not be, contiguous in sequence in the native antigen from which the epitopes are derived.

1.) Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with HIV clearance. For HLA Class I this includes 3-4 epitopes that come from at least one antigen of HIV. For HLA Class II a similar rationale is employed; again 3-4 epitopes are selected from at least one HIV antigen (*see e.g., Rosenberg et al., Science 278:1447-1450*).

2.) Epitopes are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC_{50} of 500 nM or less, or for Class II an IC_{50} of 1000 nM or less.

3.) Sufficient supermotif bearing-peptides, or a sufficient array of allele-specific motif-bearing peptides, are selected to give broad population coverage. For example, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth, or redundancy of, population coverage.

4.) When selecting epitopes from cancer-related antigens it is often useful to select analogs because the patient may have developed tolerance to the native epitope. When selecting epitopes for infectious disease-related antigens it is preferable to select either native or analoged epitopes.

5.) Of particular relevance are epitopes referred to as "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. A nested peptide sequence can comprise both HLA class I and HLA class II epitopes. When providing nested epitopes, a general objective is to provide the greatest number of epitopes per sequence. Thus, an aspect is to avoid providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a multi-epitopic sequence, such as a sequence comprising nested epitopes, it is generally important to screen the sequence

in order to insure that it does not have pathological or other deleterious biological properties.

6.) If a polyepitopic protein is created, or when creating a minigene, an objective is to generate the smallest peptide that encompasses the epitopes of interest.

5 This principle is similar, if not the same as that employed when selecting a peptide comprising nested epitopes. However, with an artificial polyepitopic peptide, the size minimization objective is balanced against the need to integrate any spacer sequences between epitopes in the polyepitopic protein. Spacer amino acid residues can, for example, be introduced to avoid junctional epitopes (an epitope recognized by the
10 immune system, not present in the target antigen, and only created by the man-made juxtaposition of epitopes), or to facilitate cleavage between epitopes and thereby enhance epitope presentation. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may
15 lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

7.) In cases where the sequences of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire
20 sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.

IV.K.1. Minigene Vaccines

25 A number of different approaches are available which allow simultaneous delivery of multiple epitopes. Nucleic acids encoding the peptides of the invention are a particularly useful embodiment of the invention. Epitopes for inclusion in a minigene are preferably selected according to the guidelines set forth in the previous section. A preferred means of administering nucleic acids encoding the peptides of the invention
30 uses minigene constructs encoding a peptide comprising one or multiple epitopes of the invention.

The use of multi-epitope minigenes is described below and in, *e.g.*, co-pending application U.S.S.N. 09/311,784; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822,

1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998.

For example, a multi-epitope DNA plasmid encoding nine dominant HLA-A*0201- and A11-restricted epitopes derived from the polymerase, envelope, and core proteins of HBV and human immunodeficiency virus (HIV), a PADRE™ universal helper T cell (HTL)

5 epitope, and an endoplasmic reticulum-translocating signal sequence was engineered.

The immunogenicity of a multi-epitopic minigene can be tested in transgenic mice to evaluate the magnitude of CTL induction responses against the epitopes tested.

Further, the immunogenicity of DNA-encoded epitopes *in vivo* can be correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA

10 plasmid. Thus, these experiments can show that the minigene serves to both: 1.) generate a CTL response and 2.) that the induced CTLs recognized cells expressing the encoded epitopes.

For example, to create a DNA sequence encoding the selected epitopes (minigene)

for expression in human cells, the amino acid sequences of the epitopes may be reverse

15 translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that

when translated, a continuous polypeptide sequence is created. To optimize expression

and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequences that can be reverse translated and included in

20 the minigene sequence include: HLA class I epitopes, HLA class II epitopes, a ubiquitination signal sequence, and/or an endoplasmic reticulum targeting signal. In

addition, HLA presentation of CTL and HTL epitopes may be improved by including synthetic (*e.g.* poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger peptides comprising the epitope(s) are within the

25 scope of the invention.

The minigene sequence may be converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides

(30-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides

30 can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope polypeptide, can then be cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are

preferably included in the vector to ensure expression in the target cells. Several vector

elements are desirable: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing minigene expression.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence, if desired to enhance immunogenicity.

In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (included to enhance or decrease immunogenicity) can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (*e.g.*, IL-2, IL-12, GM-CSF), cytokine-inducing molecules (*e.g.*, LeIF), costimulatory molecules, or for HTL responses, pan-DR binding proteins (PADRE™, Epimmune, San Diego, CA). Helper (HTL) epitopes can be joined to intracellular targeting signals and expressed separately from expressed CTL epitopes; this allows direction of the HTL epitopes to a cell compartment different than that of the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the HLA class II pathway, thereby improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune

response by co-expression of immunosuppressive molecules (e.g. TGF- β) may be beneficial in certain diseases.

Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of minigene DNA vaccines, an alternative method for formulating purified plasmid DNA may be desirable. A variety of methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, e.g., as described by WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Pat No. 5,279,833; WO 91/06309; and Felgner, *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and HLA class I presentation of minigene-encoded CTL epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 (^{51}Cr) labeled and used as target cells for epitope-specific CTL lines; cytolysis, detected by ^{51}Cr release, indicates both production of, and HLA presentation of, minigene-encoded CTL epitopes. Expression of

HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (*e.g.*, IM for DNA in PBS, intraperitoneal (IP) for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTL effector cells, assays are conducted for cytolysis of peptide-loaded, ⁵¹Cr-labeled target cells using standard techniques. Lysis of target cells that were sensitized by HLA loaded with peptide epitopes, corresponding to minigene-encoded epitopes, demonstrates DNA vaccine function for *in vivo* induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.

Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of DNA are administered. In a further alternative embodiment, DNA can be adhered to particles, such as gold particles.

IV.K.2. Combinations of CTL Peptides with Helper Peptides

Vaccine compositions comprising the peptides of the present invention, or analogs thereof, which have immunostimulatory activity may be modified to provide desired attributes, such as improved serum half life, or to enhance immunogenicity.

For instance, the ability of a peptide to induce CTL activity can be enhanced by linking the peptide to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. The use of T helper epitopes in conjunction with CTL epitopes to enhance immunogenicity is illustrated, for example, in the co-pending applications U.S.S.N. 08/820,360, U.S.S.N. 08/197,484, and U.S.S.N. 08/464,234.

Although a CTL peptide can be directly linked to a T helper peptide, often CTL epitope/HTL epitope conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer.

When present, the spacer will usually be at least one or two residues, more usually three to six residues and sometimes 10 or more residues. The CTL peptide epitope can be linked to the T helper peptide epitope either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic
5 peptide or the T helper peptide may be acylated.

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in the majority of the population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. These are known as "loosely HLA-restricted" or "promiscuous" T helper sequences. Examples of amino
10 acid sequences that are promiscuous include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; SEQ ID NO: 51484), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; SEQ ID NO: 51485), and *Streptococcus* 18kD protein at positions 116 (GAVDSILGGVATYGAA; SEQ ID NO: 51486). Other
15 examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are
20 designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAWTLKAAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type.
25 An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

HTL peptide epitopes can also be modified to alter their biological properties. For example, they can be modified to include D-amino acids to increase their resistance to proteases and thus extend their serum half life, or they can be conjugated to other
30 molecules such as lipids, proteins, carbohydrates, and the like to increase their biological activity. For example, a T helper peptide can be conjugated to one or more palmitic acid chains at either the amino or carboxyl termini.

III.K.3. Combinations of CTL Peptides with T Cell Priming Agents

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes cytotoxic T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. For example, palmitic acid residues can be attached to the ϵ - and α - amino groups of a lysine residue and then linked, *e.g.*, via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant. In a preferred embodiment, a particularly effective immunogenic composition comprises palmitic acid attached to ϵ - and α - amino groups of Lys, which is attached via linkage, *e.g.*, Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinylserine (P₃CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide (*see, e.g.*, Deres, *et al.*, *Nature* 342:561, 1989). Peptides of the invention can be coupled to P₃CSS, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P₃CSS-conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses.

CTL and/or HTL peptides can also be modified by the addition of amino acids to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or the like, can be introduced at the C- or N-terminus of the peptide or oligopeptide, particularly class I peptides. However, it is to be noted that modification at the carboxyl terminus of a CTL epitope may, in some cases, alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH₂ acylation, *e.g.*, by alkanoyl (C1-C20) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule.

IV.K.4. Vaccine Compositions Comprising DC Pulsed with CTL and/or HTL Peptides

An embodiment of a vaccine composition in accordance with the invention comprises *ex vivo* administration of a cocktail of epitope-bearing peptides to PBMC, or
5 isolated DC therefrom, from the patient's blood. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides. In this embodiment, a vaccine comprises peptide-pulsed DCs which present the pulsed peptide epitopes complexed with HLA molecules on
10 their surfaces.

The DC can be pulsed *ex vivo* with a cocktail of peptides, some of which stimulate CTL responses to one or more HIV antigens of interest. Optionally, a helper T cell (HTL) peptide such as a PADRE family molecule, can be included to facilitate the CTL response. Thus, a vaccine in accordance with the invention, preferably comprising
15 epitopes from multiple HIV antigens, is used to treat HIV infection.

IV.L. Administration of Vaccines for Therapeutic or Prophylactic Purposes

The peptides of the present invention and pharmaceutical and vaccine compositions of the invention are useful for administration to mammals, particularly
20 humans, to treat and/or prevent HIV infection. Vaccine compositions containing the peptides of the invention are administered to a patient infected with HIV or to an individual susceptible to, or otherwise at risk for, HIV infection to elicit an immune response against HIV antigens and thus enhance the patient's own immune response capabilities.

As discussed herein, peptides comprising CTL and/or HTL epitopes of the invention induce immune responses when presented by HLA molecules and contacted with a CTL or HTL specific for an epitope comprised by the peptide. The peptides (or DNA encoding them) can be administered individually or as fusions of one or more peptide sequences. The manner in which the peptide is contacted with the CTL or HTL is
30 not critical to the invention. For instance, the peptide can be contacted with the CTL or HTL either *in vivo* or *in vitro*. If the contacting occurs *in vivo*, the peptide itself can be administered to the patient, or other vehicles, *e.g.*, DNA vectors encoding one or more

peptides, viral vectors encoding the peptide(s), liposomes and the like, can be used, as described herein.

When the peptide is contacted *in vitro*, the vaccinating agent can comprise a population of cells, *e.g.*, peptide-pulsed dendritic cells, or HIV-specific CTLs, which have
5 been induced by pulsing antigen-presenting cells *in vitro* with the peptide or by transfecting antigen-presenting cells with a minigene of the invention. Such a cell population is subsequently administered to a patient in a therapeutically effective dose.

In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective CTL and/or HTL
10 response to the virus antigen and to cure or at least partially arrest or slow symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, *e.g.*, the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the
15 judgment of the prescribing physician.

The vaccine compositions of the invention can also be used purely as prophylactic agents. Generally the dosage for an initial prophylactic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg . Dosage values for a human
20 typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 μg to about 50,000 μg of peptide administered at defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine may be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's
25 blood.

Where susceptible individuals are identified prior to infection, the composition can be targeted to them, thus minimizing the need for administration to a larger population.

For pharmaceutical compositions, the immunogenic peptides of the invention, or
30 DNA encoding them, are generally administered to an individual already infected with HIV. The peptides or DNA encoding them can be administered individually or as fusions of one or more peptide sequences. HIV-infected patients can be treated with the immunogenic peptides separately or in conjunction with other treatments as appropriate.

For therapeutic use, administration should generally begin at the first diagnosis of HIV infection. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. The embodiment of the vaccine composition (*i.e.*, including, but not limited to embodiments such as peptide cocktails, polyepitopic polypeptides, minigenes, or HIV antigen-specific CTLs or pulsed dendritic cells) delivered to the patient may vary according to the stage of the disease or the patient's health status. For example, in some patients, a vaccine comprising HIV-specific CTL may be more efficacious in killing HIV-infected cells than alternative embodiments.

The peptide or other compositions used for the treatment or prophylaxis of HIV infection can be used, *e.g.*, in persons who have not manifested symptoms of disease but who act as a disease vector. In this context, it is generally important to provide an amount of the peptide epitope delivered by a mode of administration sufficient to effectively stimulate a cytotoxic T cell response; compositions which stimulate helper T cell responses can also be given in accordance with this embodiment of the invention.

The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg . Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. Boosting dosages of between about 1.0 μg to about 50,000 μg of peptide pursuant to a boosting regimen over weeks to months, *e.g.*, from four weeks to six months, may be required, possibly for a prolonged period of time to effectively immunize an individual. Boosting doses may be administered depending upon the patient's response and condition as determined by measuring the specific activity of CTL and HTL obtained from the patient's blood.

The peptides and compositions of the present invention may be employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides in preferred compositions of the invention, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

Administration should continue until at least clinical symptoms or laboratory tests indicate that the viral infection has been eliminated or substantially abated and for a period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, intrathecal, or local administration. Preferably, the pharmaceutical compositions are administered parentally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides

5 compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The

10 resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like, for example, sodium

15 acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, *etc.*

The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, *i.e.*, from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes,

20 viscosities, *etc.*, in accordance with the particular mode of administration selected.

A human unit dose form of the peptide composition is typically included in a pharmaceutical composition that comprises a human unit dose of an acceptable carrier, preferably an aqueous carrier, and is administered in a volume of fluid that is known by those of skill in the art to be used for administration of such compositions to humans (*see*,

25 *e.g.*, Remington's Pharmaceutical Sciences, 17th Edition, A. Gennaro, Editor, Mack Publishing Co., Easton, Pennsylvania, 1985).

The peptides of the invention may also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or to target selectively to infected cells, as well as to increase the half-life of the peptide composition.

30 Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to a receptor prevalent among lymphoid cells, such as monoclonal antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic

compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively
5 charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka, *et al.*, *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

10 For targeting cells of the immune system, a ligand to be incorporated into the liposome can include, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the
15 stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is
20 formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of
25 peptides are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or
30 natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, *e.g.*, lecithin for intranasal delivery.

IV.M. Kits

The peptide and nucleic acid compositions of this invention can be provided in kit form together with instructions for vaccine administration. Typically the kit would include desired peptide compositions in a container, preferably in unit dosage form and instructions for administration. An alternative kit would include a minigene construct with desired nucleic acids of the invention in a container, preferably in unit dosage form together with instructions for administration. Lymphokines such as IL-2 or IL-12 may also be included in the kit. Other kit components that may also be desirable include, for example, a sterile syringe, booster dosages, and other desired excipients.

Summary

Epitopes in accordance with the present invention were successfully used to induce an immune response. Immune responses with these epitopes have been induced by administering the epitopes in various forms. The epitopes have been administered as peptides, as nucleic acids, and as viral vectors comprising nucleic acids that encode the epitope(s) of the invention. Upon administration of peptide-based epitope forms, immune responses have been induced by direct loading of an epitope onto an empty HLA molecule that is expressed on a cell, and via internalization of the epitope and processing via the HLA class I pathway; in either event, the HLA molecule expressing the epitope was then able to interact with and induce a CTL response. Peptides can be delivered directly or using such agents as liposomes. They can additionally be delivered using ballistic delivery, in which the peptides are typically in a crystalline form. When DNA is used to induce an immune response, it is administered either as naked DNA, generally in a dose range of approximately 1-5mg, or via the ballistic "gene gun" delivery, typically in a dose range of approximately 10-100 µg. The DNA can be delivered in a variety of conformations, *e.g.*, linear, circular *etc.* Various viral vectors have also successfully been used that comprise nucleic acids which encode epitopes in accordance with the invention.

Accordingly compositions in accordance with the invention exist in several forms. Embodiments of each of these composition forms in accordance with the invention have been successfully used to induce an immune response.

One composition in accordance with the invention comprises a plurality of peptides. This plurality or cocktail of peptides is generally admixed with one or more pharmaceutically acceptable excipients. The peptide cocktail can comprise multiple

copies of the same peptide or can comprise a mixture of peptides. The peptides can be analogs of naturally occurring epitopes. The peptides can comprise artificial amino acids and/or chemical modifications such as addition of a surface active molecule, *e.g.*, lipidation; acetylation, glycosylation, biotinylation, phosphorylation etc. The peptides
5 can be CTL or HTL epitopes. In a preferred embodiment the peptide cocktail comprises a plurality of different CTL epitopes and at least one HTL epitope. The HTL epitope can be naturally or non-naturally (*e.g.*, PADRE®, Epimmune Inc., San Diego, CA). The number of distinct epitopes in an embodiment of the invention is generally a whole unit integer from one through one hundred fifty (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14,
10 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, or 150).

An additional embodiment of a composition in accordance with the invention
15 comprises a polypeptide multi-epitope construct, *i.e.*, a polyepitopic peptide. Polyepitopic peptides in accordance with the invention are prepared by use of technologies well-known in the art. By use of these known technologies, epitopes in accordance with the invention are connected one to another. The polyepitopic peptides can be linear or non-linear, *e.g.*, multivalent. These polyepitopic constructs can comprise
20 artificial amino acids, spacing or spacer amino acids, flanking amino acids, or chemical modifications between adjacent epitope units. The polyepitopic construct can be a heteropolymer or a homopolymer. The polyepitopic constructs generally comprise epitopes in a quantity of any whole unit integer between 2-150 (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33,
25 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, or 150). The polyepitopic construct can comprise CTL and/or HTL epitopes. One or more of the epitopes in the construct can be modified, *e.g.*, by addition of a surface active material,
30 *e.g.* a lipid, or chemically modified, *e.g.*, acetylation, *etc.* Moreover, bonds in the multiepitopic construct can be other than peptide bonds, *e.g.*, covalent bonds, ester or ether bonds, disulfide bonds, hydrogen bonds, ionic bonds *etc.*

Alternatively, a composition in accordance with the invention comprises construct which comprises a series, sequence, stretch, *etc.*, of amino acids that have homology to (

i.e., corresponds to or is contiguous with) to a native sequence. This stretch of amino acids comprises at least one subsequence of amino acids that, if cleaved or isolated from the longer series of amino acids, functions as an HLA class I or HLA class II epitope in accordance with the invention. In this embodiment, the peptide sequence is modified, so
5 as to become a construct as defined herein, by use of any number of techniques known or to be provided in the art. The polyepitopic constructs can contain homology to a native sequence in any whole unit integer increment from 70-100%, e.g., 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or, 100 percent.

10 A further embodiment of a composition in accordance with the invention is an antigen presenting cell that comprises one or more epitopes in accordance with the invention. The antigen presenting cell can be a "professional" antigen presenting cell, such as a dendritic cell. The antigen presenting cell can comprise the epitope of the invention by any means known or to be determined in the art. Such means include
15 pulsing of dendritic cells with one or more individual epitopes or with one or more peptides that comprise multiple epitopes, by nucleic acid administration such as ballistic nucleic acid delivery or by other techniques in the art for administration of nucleic acids, including vector-based, *e.g.* viral vector, delivery of nucleic acids.

Further embodiments of compositions in accordance with the invention comprise
20 nucleic acids that encode one or more peptides of the invention, or nucleic acids which encode a polyepitopic peptide in accordance with the invention. As appreciated by one of ordinary skill in the art, various nucleic acids compositions will encode the same peptide due to the redundancy of the genetic code. Each of these nucleic acid compositions falls within the scope of the present invention. This embodiment of the invention comprises
25 DNA or RNA, and in certain embodiments a combination of DNA and RNA. It is to be appreciated that any composition comprising nucleic acids that will encode a peptide in accordance with the invention or any other peptide based composition in accordance with the invention, falls within the scope of this invention.

It is to be appreciated that peptide-based forms of the invention (as well as the
30 nucleic acids that encode them) can comprise analogs of epitopes of the invention generated using principles already known, or to be known, in the art. Principles related to analoging are now known in the art, and are disclosed herein; moreover, analoging principles (heteroclitic analoging) are disclosed in co-pending application serial number

U.S.S.N. 09/226,775 filed 6 January 1999. Generally the compositions of the invention are isolated or purified.

The invention will be described in greater detail by way of specific examples.

The following examples are offered for illustrative purposes, and are not intended to limit the invention in any manner. Those of skill in the art will readily recognize a variety of non-critical parameters that can be changed or modified to yield alternative embodiments in accordance with the invention.

V. EXAMPLES

The following examples illustrate identification, selection, and use of immunogenic Class I and Class II peptide epitopes for inclusion in vaccine compositions.

Example 1. HLA Class I and Class II Binding Assays

The following example of peptide binding to HLA molecules demonstrates quantification of binding affinities of HLA class I and class II peptides. Binding assays can be performed with peptides that are either motif-bearing or not motif-bearing.

Cell lysates were prepared and HLA molecules purified in accordance with disclosed protocols (Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); Sette, *et al.*, *Mol. Immunol.* 31:813 (1994)).

The cell lines used as sources of HLA molecules (Table XXIV) and the antibodies used for the extraction of the HLA molecules from the cell lysates (Table XXV) are also described in these publications.

Epstein-Barr virus (EBV)-transformed homozygous cell lines, fibroblasts, CIR, or 721.221-transfectants were used as sources of HLA class I molecules. These cells were cultured in RPMI 1640 medium supplemented with 2mM L-glutamine (GIBCO, Grand Island, NY), 50μM 2-ME, 100μg/ml of streptomycin, 100U/ml of penicillin (Irvine Scientific) and 10% heat-inactivated FCS (Irvine Scientific, Santa Ana, CA).

Cell lysates were prepared as follows. Briefly, cells were lysed at a concentration of 10⁸ cells/ml in 50 mM Tris-HCl, pH 8.5, containing 1% Nonidet P-40 (Fluka Biochemika, Buchs, Switzerland), 150 mM NaCl, 5 mM EDTA, and 2 mM PMSF. Lysates were cleared of debris and nuclei by centrifugation at 15,000 x g for 30min.

HLA molecules were purified from lysates by affinity chromatography. Lysates were passed twice through two pre-columns of inactivated Sepharose CL4-B and protein

A-Sepharose. Next, the lysate was passed over a column of Sepharose CL-4B beads coupled to an appropriate antibody. The anti-HLA column was then washed with 10-column volumes of 10mM Tris-HCL, pH 8.0, in 1% NP-40, PBS, 2-column volumes of PBS, and 2-column volumes of PBS containing 0.4% n-octylglucoside. Finally, MHC molecules were eluted with 50mM diethylamine in 0.15M NaCl containing 0.4% n-octylglucoside, pH 11.5. A 1/25 volume of 2.0M Tris, pH 6.8, was added to the eluate to reduce the pH to ~8.0. Eluates were then concentrated by centrifugation in Centriprep 30 concentrators at 2000 rpm (Amicon, Beverly, MA). Protein content was evaluated by a BCA protein assay (Pierce Chemical Co., Rockford, IL) and confirmed by SDS-PAGE.

A detailed description of the protocol utilized to measure the binding of peptides to Class I and Class II MHC has been published (Sette *et al.*, *Mol. Immunol.* 31:813, 1994; Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998). Briefly, purified MHC molecules (5 to 500nM) were incubated with various unlabeled peptide inhibitors and 1-10nM ¹²⁵I-radiolabeled probe peptides for 48h in PBS containing 0.05% Nonidet P-40 (NP40) (or 20% w/v digitonin for H-2 IA assays) in the presence of a protease inhibitor cocktail. The final concentrations of protease inhibitors (each from CalBioChem, La Jolla, CA) were 1 mM PMSF, 1.3 nM 1.10 phenanthroline, 73 μM pepstatin A, 8mM EDTA, 6mM N-ethylmaleimide (for Class II assays), and 200 μM N alpha-p-tosyl-L-lysine chloromethyl ketone (TLCK). All assays were performed at pH 7.0 with the exception of DRB1*0301, which was performed at pH 4.5, and DRB1*1601 (DR2w21β₁) and DRB4*0101 (DRw53), which were performed at pH 5.0. pH was adjusted as described elsewhere (*see* Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998).

Following incubation, MHC-peptide complexes were separated from free peptide by gel filtration on 7.8 mm x 15 cm TSK200 columns (TosoHaas 16215, Montgomeryville, PA), eluted at 1.2 mls/min with PBS pH 6.5 containing 0.5% NP40 and 0.1% NaN₃. Because the large size of the radiolabeled peptide used for the DRB1*1501 (DR2w2β₁) assay makes separation of bound from unbound peaks more difficult under these conditions, all DRB1*1501 (DR2w2β₁) assays were performed using a 7.8mm x 30cm TSK2000 column eluted at 0.6 mls/min. The eluate from the TSK columns was passed through a Beckman 170 radioisotope detector, and radioactivity was plotted and

integrated using a Hewlett-Packard 3396A integrator, and the fraction of peptide bound was determined.

Radiolabeled peptides were iodinated using the chloramine-T method.

Representative radiolabeled probe peptides utilized in each assay, and its assay specific

5 IC_{50} nM, are summarized in Tables IV and V. Typically, in preliminary experiments, each MHC preparation was titrated in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of the total radioactivity. All subsequent inhibition and direct binding assays were performed using these HLA concentrations.

10 Since under these conditions $[label] < [HLA]$ and $IC_{50} \geq [HLA]$, the measured IC_{50} values are reasonable approximations of the true K_D values. Peptide inhibitors are typically tested at concentrations ranging from 120 μ g/ml to 1.2 ng/ml, and are tested in two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide
15 by dividing the IC_{50} of a positive control for inhibition by the IC_{50} for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For inter-experiment comparisons, relative binding values are compiled. These values can subsequently be converted back into IC_{50} nM values by dividing the IC_{50} nM of the positive controls for inhibition by the relative binding of the peptide of interest. This method of data
20 compilation has proven to be the most accurate and consistent for comparing peptides that have been tested on different days, or with different lots of purified MHC.

Because the antibody used for HLA-DR purification (LB3.1) is α -chain specific, β_1 molecules are not separated from β_3 (and/or β_4 and β_5) molecules. The β_1 specificity of the binding assay is obvious in the cases of DRB1*0101 (DR1), DRB1*0802 (DR8w2),
25 and DRB1*0803 (DR8w3), where no β_3 is expressed. It has also been demonstrated for DRB1*0301 (DR3) and DRB3*0101 (DR52a), DRB1*0401 (DR4w4), DRB1*0404 (DR4w14), DRB1*0405 (DR4w15), DRB1*1101 (DR5), DRB1*1201 (DR5w12), DRB1*1302 (DR6w19) and DRB1*0701 (DR7). The problem of β chain specificity for DRB1*1501 (DR2w2 β_1), DRB5*0101 (DR2w2 β_2), DRB1*1601 (DR2w21 β_1),
30 DRB5*0201 (DR51Dw21), and DRB4*0101 (DRw53) assays is circumvented by the use of fibroblasts. Development and validation of assays with regard to DR β molecule specificity have been described previously (*see, e.g., Southwood et al., J. Immunol.* 160:3363-3373, 1998).

Binding assays as outlined above may be used to analyze supermotif and/or motif-bearing epitopes as, for example, described in Example 2.

Example 2. Identification of HLA Supermotif- and Motif-Bearing CTL Candidate

5 Epitopes

Vaccine compositions of the invention may include multiple epitopes that comprise multiple HLA supermotifs or motifs to achieve broad population coverage. This example illustrates the identification of supermotif- and motif-bearing epitopes for the inclusion in such a vaccine composition. Calculation of population coverage was
10 performed using the strategy described below.

Computer searches and algorithms for identification of supermotif and/or motif-bearing epitopes

The searches performed to identify the motif-bearing peptide sequences in
15 Examples 2 and 5 employed the protein sequence data from HIV-1 clade B virus strains that were available in the 1994 Los Alamos database.

Computer searches for epitopes bearing HLA Class I or Class II supermotifs or motifs were performed as follows. All translated HIV protein sequences were analyzed using a text string search software program, e.g., MotifSearch 1.4 (D. Brown, San Diego)
20 to identify potential peptide sequences containing appropriate HLA binding motifs; alternative programs are readily produced in accordance with information in the art in view of the motif/supermotif disclosure herein. Furthermore, such calculations can be made mentally. Identified A2-, A3-, and DR-supermotif sequences were scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II
25 molecules. These polynomial algorithms take into account both extended and refined motifs (that is, to account for the impact of different amino acids at different positions), and are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$\text{"}\Delta G\text{"} = a_{1i} \times a_{2i} \times a_{3i} \dots \times a_{ni}$$

30 where a_{ji} is a coefficient which represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (i.e., independent binding of individual side-chains). When residue j occurs

at position i in the peptide, it is assumed to contribute a constant amount j_i to the free energy of binding of the peptide irrespective of the sequence of the rest of the peptide. This assumption is justified by studies from our laboratories that demonstrated that peptides are bound to MHC and recognized by T cells in essentially an extended
5 conformation (data omitted herein).

The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (see also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all i positions, anchor and non-anchor alike, the geometric mean of the
10 average relative binding (ARB) of all peptides carrying j is calculated relative to the remainder of the group, and used as the estimate of j_i . For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product
15 exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

Selection of HLA-A2 supertype cross-reactive peptides

Complete protein sequences from nine HIV structural and regulatory proteins
20 were aligned, then scanned, utilizing motif identification software, to identify conserved 9- and 10-mer sequences containing the HLA-A2-supermotif main anchor specificity. The analysis included all isolates in the 1994 Los Alamos database. The conservation criteria varied according to antigen: greater than 80% of clade B isolates for gag, pol, env; greater than 70% for nef, rev, tat, vif, vpr; great than 60% for vpu.)

25 A total of 233 conserved, HLA-A2 supermotif-positive sequences were identified. The peptides corresponding to the sequences were then synthesized and tested for their capacity to bind purified HLA-A*0201 molecules *in vitro* (HLA-A*0201 is considered a prototype A2 supertype molecule). Thirty peptides bound A*0201 with IC_{50} values ≤ 500 nM; of these 30, 5 bound with high binding affinities (IC_{50} values ≤ 50 nM) and 25 bound
30 with intermediate binding affinities, in the 50-500 nM range (Table XXVII).

The thirty A*0201-binding peptides were subsequently tested for the capacity to bind to additional A2-supertype molecules (A*0202, A*0203, A*0206, and A*6802). As

shown in Table XXVII, 20 of the 30 peptides were found to be A2-supertype cross-reactive binders, binding at least 3 of the 5 A2-supertype alleles tested.

Selection of HLA-A3 supermotif-bearing epitopes

5 The HIV protein sequences scanned above were also examined for the presence of peptides with the HLA-A3-supermotif primary anchors. A total of 353 conserved 9- or 10-mer motif-containing sequences were identified. The corresponding peptides were synthesized and tested for binding to HLA-A*0301 and HLA-A*1101 molecules, the two most prevalent A3-supertype alleles. Sixty-six of the peptides were found to bind one of 10 the two alleles with binding affinities of ≤ 500 nM (Table XXVIII). These peptides were then tested for binding cross-reactivity to the other common A3-supertype alleles (A*3101, A*3301, and A*6801). Twenty one of the peptides bound at least three of the five HLA-A3-supertype molecules tested (Table XXVIII). Table XXVIII also includes two 11-mer peptides that were not selected using the search criteria outlined above, but 15 have been shown to be A3-supertype cross-reactive binders.

Selection of HLA-B7 supermotif bearing epitopes

When the same HIV target antigen protein sequences were also analyzed for the presence of conserved 9- or 10-mer peptides with the HLA-B7-supermotif, 54 sequences 20 were identified. The corresponding peptides were synthesized and tested for binding to HLA-B*0702, the most common B7-supertype allele (*i.e.*, the prototype B7 supertype allele). Sixteen peptides bound B*0702 with IC_{50} of ≤ 500 nM (Table XXIX). These peptides were then tested for binding to other common B7-supertype molecules (B*3501, B*5101, B*5301, and B*5401). As shown in Table XXIX, eight of the sixteen peptides 25 were capable of binding to three or more of the five B7-supertype alleles tested.

Selection of A1 and A24 motif-bearing epitopes

To further increase population coverage, HLA-A1 and -A24 epitopes can also be incorporated into vaccine constructs. An analysis of the protein sequence data from the 30 HIV target antigens utilized above is also performed to identify HLA-A1- and A24-motif-containing conserved sequences.

Five conserved HIV-derived peptides that bind to A*0101 with an IC_{50} of 500 nM or less (Table XXX) have been identified. Eleven conserved HLA-A*2402-binding HIV-

derived peptides have also been identified, five of which bind with an IC_{50} of 100 nM or less (Table XXXI).

Example 3. Confirmation of Immunogenicity

5 *Evaluation of A*0201 immunogenicity*

It has been shown that CTL induced in A*0201/K^b transgenic mice exhibit specificity similar to CTL induced in the human system (*see, e.g., Vitiello et al., J. Exp. Med.* 173:1007-1015, 1991; Wentworth *et al., Eur. J. Immunol.* 26:97-101, 1996).

Accordingly, these mice were used to evaluate the immunogenicity of 19 of the 20 A2-
10 supertype cross-reactive peptides identified in Example 2 above.

CTL induction in transgenic mice following peptide immunization has been described (Vitiello *et al., J. Exp. Med.* 173:1007-1015, 1991; Alexander *et al., J. Immunol.* 159:4753-4761, 1997). In these studies, mice were injected subcutaneously at the base of the tail with each peptide (50 μ g/mouse) emulsified in IFA in the presence of
15 an excess of an IA^b-restricted helper peptide (140 μ g/mouse) (HBV core 128-140, Sette *et al., J. Immunol.* 153:5586-5592, 1994). Eleven days after injection, splenocytes were incubated in the presence of peptide-loaded syngenic LPS blasts. After six days, cultures were assayed for cytotoxic activity using peptide-pulsed targets. The data, summarized in Table XXXII, indicate that eight peptides were capable of inducing primary CTL
20 responses in A*0201/K^b transgenic mice. (For these studies, a peptide was considered positive if it induced CTL (L.U. 30/10⁶ cells \geq 2 in at least two transgenic animals (Wentworth *et al., Eur. J. Immunol.* 26:97-101, 1996).

The cross-reactive candidate CTL epitopes were also tested for the ability to stimulate recall CTL responses HIV-infected patients. Briefly, PBMC from patients
25 infected with HIV were cultured in the presence of 10 μ g/ml of synthetic peptide. After 7 and 14 days, the cultures were restimulated with peptide. The cultures were assayed for cytolytic activity on day 21 using target cells pulsed with the specific peptide in a ⁵¹Cr release assay. These data are also summarized in Table XXXII. As shown, 15 of the 19 peptides analyzed were recognized in recall CTL responses using PBMC from HIV-
30 infected patients.

The set of peptides screened for immunogenicity contained two redundant peptides, 1261.14 and 1261.04, which differ in length by a single amino acid. While both peptides exhibit supertype degenerate binding, only the short of the two peptides

exhibited immunogenicity. One supertype peptide not tested, 1211.09, has been reported to be recognized by CTL lines isolated from HIV-infected patients.

In summary, 16 A2-supertype cross-reactive peptides have been identified that are immunogenic in humans; 53% of these peptides are also recognized in HLA-A2 transgenic mice. The sixteen peptides represent epitopes from five HIV antigens: env, gag, pol, vpr, and nef.

*Evaluation of A*03/A11 immunogenicity*

Twenty one of the A3-supertype cross-reactive peptides identified in Example 2 above were evaluated for immunogenicity (Table XXXIII). Peptides were screened using HLA-A11/K^b transgenic mice, using the protocol described above for HLA-A2 transgenic mice (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997) and using PBMC obtained from HIV-infected patients to test for the ability to stimulate CTL recall responses. Ten peptides that were capable of inducing CTL in HLA-A11 transgenic mice were identified.

Three peptides, 966.01, 940.03, and 1069.47, have been shown by collaborators to be immunogenic in HIV-infected patients. Peptides 966.01 and 1069.47 also induced CTL responses in transgenic mice, peptide 940.03 exhibited immunogenicity in patients only.

In summary, 11 of 23 A3-supertype cross-reactive binding peptides were found to be immunogenic in either HLA-A11 transgenic mice or HIV-infected patients. These peptides represent epitopes from three HIV antigens: pol, env, and nef.

Evaluation of B7 immunogenicity

Immunogenicity screening of the B7-supertype cross-reactive binding peptides identified in Example 2 is used to evaluate immunogenicity using HLA-B7 transgenic mice and PBMC from HIV-infected patients in a manner analogous to the evaluation of A2-and A3-supermotif-bearing peptides. Three of these peptides have been reported as being immunogenic in HIV-infected patients.

Example 4. Implementation of the Extended Supermotif to Improve the Binding Capacity of Native Epitopes by Creating Analogs

HLA motifs and supermotifs (comprising primary and/or secondary residues) are useful in the identification and preparation of highly cross-reactive native peptides, as demonstrated herein. Moreover, the definition of HLA motifs and supermotifs also

allows one to engineer highly cross-reactive epitopes by identifying residues within a native peptide sequence which can be analoged, or “fixed” to confer upon the peptide certain characteristics, *e.g.* greater cross-reactivity within the group of HLA molecules that comprise a supertype, and/or greater binding affinity for some or all of those HLA molecules. Examples of analog peptides that exhibit modulated binding affinity are set forth in this example.

Analoging at Primary Anchor Residues

As shown in Example 2, twenty HIV-derived, A2-supertype-restricted epitopes were identified. Peptide engineering strategies are implemented to further increase the cross-reactivity of the candidate epitopes identified above which bind 3/5 of the A2 supertype alleles tested. On the basis of the data disclosed, *e.g.*, in related and co-pending U.S.S.N 09/226,775, the main anchors of A2-supermotif-bearing peptides are altered, for example, to introduce a preferred L, I, V, or M at position 2, and I or V at the C-terminus.

To analyze the cross-reactivity of the analog peptides, each engineered analog is initially tested for binding to the prototype A2 supertype allele A*0201, then, if A*0201 binding capacity is maintained, for A2-supertype cross-reactivity.

Alternatively, a peptide can be tested for binding to one or all supertype members and then analogued to modulate binding affinity to any one (or more) of the supertype members to add population coverage.

Similarly, analogs of HLA-A3 supermotif-bearing epitopes are also generated. For example, peptides binding to 3/5 of the A3-supertype molecules can be engineered at primary anchor residues to possess a preferred residue (V, S, M, or A) at position 2.

The analog peptides are then tested for the ability to bind A*03 and A*11 (prototype A3 supertype alleles). Typically, those peptides that demonstrate ≤ 500 nM binding capacity are then tested for A3-supertype cross-reactivity.

Similarly to the A2- and A3- motif bearing peptides, B7 supermotif-bearing peptide are also analoged. For example, peptides binding 3 or more B7-supertype alleles are modulated to achieve increased cross-reactive binding. B7 supermotif-bearing peptides can, for example, be engineered to possess a preferred residue (V, I, L, or F) at the C-terminal primary anchor position, as demonstrated by Sidney *et al.* (*J. Immunol.* 157:3480-3490, 1996).

Analoging at Secondary Anchor Residues

Secondary anchor residues defined for HLA motifs and/or supermotifs are also used to engineer peptide with modified binding activity, typically increased cross-reactive binding and/or increased affinity. For example, the binding capacity of a B7 supermotif-
5 bearing peptide representing a discreet single amino acid substitution at position 1 is analyzed. A peptide such as Peptide 1261.01 (Table XXIX), can, for example, be analogued to substitute L for F at position 1 and subsequently be evaluated for modulated binding activity, e.g., increased binding affinity/ and or increased cross-reactivity. This procedure identifies analoged peptides with modified binding properties.

10 Engineered analogs with improved binding capacity or cross-reactivity are tested for immunogenicity in HLA-B7-transgenic mice, following for example, IFA immunization or lipopeptide immunization. The analoged peptides are typically additionally tested for the ability to stimulate a recall response using PBMC from HIV-infected patients.

15 Thus, by the use of even single amino acid substitutions, it is possible to increase the binding affinity and/or cross-reactivity of peptide ligands for HLA supertype molecules.

Example 5. Identification of HIV-derived sequences with HLA-DR binding motifs

20 Peptide epitopes bearing an HLA class II supermotif or motif are identified as outlined below using methodology similar to that described in Examples 1-3.

Selection of HLA-DR-supermotif-bearing epitopes.

To identify HIV-derived, HLA class II HTL epitopes, the protein sequences from
25 the same HIV antigens used for the identification of HLA Class I supermotif/motif sequences were analyzed for the presence of sequences bearing an HLA-DR-motif or supermotif. Specifically, 15-mer sequences were selected comprising a DR-supermotif, further comprising a 9-mer core, and three-residue N- and C-terminal flanking regions (15 amino acids total).

30 Protocols for predicting peptide binding to DR molecules have been developed (Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). These protocols, specific for individual DR molecules, allow the scoring, and ranking, of 9-mer core regions. Each protocol not only scores peptide sequences for the presence of DR-supermotif primary anchors (i.e., at position 1 and position 6) within a 9-mer core, but additionally evaluates

sequences for the presence of secondary anchors. Using allele specific selection tables (see, *e.g.*, Southwood *et al.*, *ibid.*), it has been found that these protocols efficiently select peptide sequences with a high probability of binding a particular DR molecule.

Additionally, it has been found that performing these protocols in tandem, specifically
5 those for DR1, DR4w4, and DR7, can efficiently select DR cross-reactive peptides.

The HIV-derived peptides identified above were tested for their binding capacity for various common HLA-DR molecules. All peptides were initially tested for binding to the DR molecules in the primary panel: DR1, DR4w4, and DR7. Peptides binding at least 2 of these 3 DR molecules were then tested for binding to DR2w2 β 1, DR2w2 β 2,
10 DR6w19, and DR9 molecules in secondary assays. Finally, peptides binding at least 2 of the 4 secondary panel DR molecules, and thus cumulatively at least 4 of 7 different DR molecules, were screened for binding to DR4w15, DR5w11, and DR8w2 molecules in tertiary assays. Peptides binding at least 7 of the 10 DR molecules comprising the primary, secondary, and tertiary screening assays were considered cross-reactive DR
15 binders. The composition of these screening panels, and the phenotypic frequency of associated antigens, are shown in Table XXXIV.

Thirteen HIV-derived peptides were found to bind at least 7 of 10 common HLA-DR alleles. The sequence of these 13 peptides, and their binding capacity for each assay in the primary through tertiary panels, are shown in Table XXXV. This set of peptide
20 epitopes is predominantly derived from pol, but also includes epitopes from gag and env.

Selection of DR3 motif peptides

Because HLA-DR3 is an allele that is prevalent in Caucasian, Black, and Hispanic populations, DR3 binding capacity is an important criterion in the selection of HTL
25 epitopes. However, data generated previously indicated that DR3 only rarely cross-reacts with other DR alleles (Sidney *et al.*, *J. Immunol.* 149:2634-2640, 1992; Geluk *et al.*, *J. Immunol.* 152:5742-5748, 1994; Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). This is not entirely surprising in that the DR3 peptide-binding motif appears to be distinct from the specificity of most other DR alleles. For maximum efficiency in developing
30 vaccine candidates it would be desirable for DR3 motifs to be clustered in proximity with DR supermotif regions. Thus, peptides shown to be candidates may also be assayed for their DR3 binding capacity. However, in view of the distinct binding specificity of the

DR3 motif, peptides binding only to DR3 can also be considered as candidates for inclusion in a vaccine formulation.

To efficiently identify peptides that bind DR3, the nine target HIV antigens were analyzed for conserved sequences carrying one of the two DR3 specific binding motifs reported by Geluk *et al.* (*J. Immunol.* 152:5742-5748, 1994). The corresponding peptides were then synthesized and tested for the ability to bind DR3 with an affinity of 1 μ M or better, *i.e.*, less than 1 μ M. Five peptides were found that met this binding criterion (Table XXXVI), and thereby qualify as HLA class II high affinity binders. Of these five, four represent epitopes from pol, and one is from vpu.

DR3 binding epitopes can also be included in vaccine compositions.

Example 6. Immunogenicity of HIV-derived HTL epitopes

Immunogenicity of HTL epitopes is typically evaluated in a manner analogous to the determination of immunogenicity of CTL epitopes using appropriate transgenic mice models and/or assessing the ability to stimulate recall responses using PBMC isolated from HIV-infected individuals.

The immunogenicity of 11 of the 13 HLA class II DR-supermotif binding epitopes identified in Example 5 was evaluated in a study testing PBMC isolated from HIV-infected individuals for recall proliferative responses. All eleven of these peptides were found to stimulate DR-restricted proliferative responses (Table XXXVII).

DR3-motif bearing peptides are typically evaluated in a similar manner. Such studies demonstrate the immunogenicity of class II epitopes derived from HIV proteins.

Example 7. Calculation of phenotypic frequencies of HLA-supertypes in various ethnic backgrounds to determine breadth of population coverage

This example illustrates the assessment of the breadth of population coverage of a vaccine composition comprised of multiple epitopes comprising multiple supermotifs and/or motifs.

In order to analyze population coverage, gene frequencies of HLA alleles were determined. Gene frequencies for each HLA allele were calculated from antigen or allele frequencies utilizing the binomial distribution formulae $gf=1-(SQRT(1-af))$ (see, *e.g.*, Sidney *et al.*, *Human Immunol.* 45:79-93, 1996). To obtain overall phenotypic frequencies, cumulative gene frequencies were calculated, and the cumulative antigen frequencies derived by the use of the inverse formula $[af=1-(1-Cgf)^2]$.

Where frequency data was not available at the level of DNA typing, correspondence to the serologically defined antigen frequencies was assumed. To obtain total potential supertype population coverage no linkage disequilibrium was assumed, and only alleles confirmed to belong to each of the superotypes were included (minimal estimates). Estimates of total potential coverage achieved by inter-loci combinations were made by adding to the A coverage the proportion of the non-A covered population that could be expected to be covered by the B alleles considered (e.g., $\text{total} = A + B \cdot (1 - A)$). Confirmed members of the A3-like supertype are A3, A11, A31, A*3301, and A*6801. Although the A3-like supertype may also include A34, A66, and A*7401, these alleles were not included in overall frequency calculations. Likewise, confirmed members of the A2-like supertype family are A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*6802, and A*6901. Finally, the B7-like supertype-confirmed alleles are: B7, B*3501-03, B51, B*5301, B*5401, B*5501-2, B*5601, B*6701, and B*7801 (potentially also B*1401, B*3504-06, B*4201, and B*5602).

Population coverage achieved by combining the A2-, A3- and B7-supertypes is approximately 86% in five major ethnic groups (see Table XXI). Coverage may be extended by including peptides bearing the A1 and A24 motifs. On average, A1 is present in 12% and A24 in 29% of the population across five different major ethnic groups (Caucasian, North American Black, Chinese, Japanese, and Hispanic). Together, these alleles are represented with an average frequency of 39% in these same ethnic populations. The total coverage across the major ethnicities when A1 and A24 are combined with the coverage of the A2-, A3- and B7-supertype alleles is >95%. An analagous approach can be used to estimate population coverage achieved with combinations of class II motif-bearing epitopes.

Summary of preferred HLA class I epitopes

In summary, on the basis of the data presented in the above examples, 47 immunogenic and/or cross-reactive binding preferred CTL peptide epitopes derived from HIV were identified (*see*, Table XXXVIII). Of these 47 eptiopes, 6 are derived from gag, 22 from pol, 10 from env, 3 from nef, and one epitope each from rev, vif, and vpr. This set of epitopes includes 16 HLA-A2 supermotif-bearing epitopes (two from gag, eight from pol, three from env, two from vpr, and one from nef), all of which are recognized in HIV-infected patients. The 10 HLA-A3 supermotif-bearing candidate epitopes include 6 pol-derived epitopes, two env-derived epitopes and one eptiope each from gag, vif, and

nef. With the exception of peptides 1273.08 and 1273.03, all of the epitopes are immunogenic in HLA transgenic mice. The two additional peptides are included to enhance antigen diversity.

5 The CTL epitope set also includes 8 B7-restricted peptides. Of these eight, 3 epitopes have been reported as immunogenic in patients. Five B7-supermotif-bearing peptides were included as candidates based on supertype binding. Immunogenicity studies in humans (*e.g.*, Bertoni *et al.*, *J. Clin. Invest.* 100:503, 1997; Doolan *et al.*, *Immunity* 7:97, 1997; and Threlkeld *et al.*, *J. Immunol.* 159:1648, 1997) have shown that highly cross-reactive binding peptides are almost always recognized as epitopes. Given
10 these results, and in view of the limited immunogenicity data available for B7 supermotif-bearing peptides, the use of B7-supertype binding affinity is an important selection criterion in identifying candidate epitopes for inclusion in a vaccine that is immunogenic in a diverse population.

Similarly, A1- and A24-restricted peptides were included on the basis of both
15 demonstrated immunogenicity of the candidate epitopes and on the basis of binding affinity. Five of the preferred epitopes have been reported to be recognized in recall CTL responses from HIV-infected patients. Because a high percentage of the peptides with binding affinities ≤ 100 nM are found to be immunogenic, four A24-restricted peptides were included as vaccine candidates. An additional five A24-restricted epitopes and four
20 A1-restricted epitopes that bound their respective alleles with an IC_{50} of ≤ 500 nM were also included to provide a greater degree of population coverage.

With these 47 CTL epitopes, an average population coverage is predicted to be greater than 95% in each of five major ethnic populations. Using the game theory Monte Carlo simulation analysis, which is known in the art (see *e.g.*, Osborne, M.J. and
25 Rubinstein, A. "A course in game theory" MIT Press, 1994), it is estimated that 90% of the individuals in a population comprised of the Caucasian, North American Black, Japanese, Chinese, and Hispanic ethnic groups would recognize 7 or more of the vaccine epitopes described herein (Figure 1)

30 *Summary of preferred HLA class II epitopes*

A list of preferred HIV-derived HTL epitopes for vaccine compositions is summarized in Table XXXIX. The set of HTL epitopes includes 13 DR supermotif-bearing peptides and 5 DR3 motif-bearing peptides. The majority of the epitopes are

derived from pol, 3 are from gag, 2 are from env and one is derived from vpu. The total estimated population coverage represented by this panel of HTL epitopes is estimated to be greater than 91% in each of five major ethnic groups (Table XL).

5 Example 8. CTL Recognition Of Endogenous Processed Antigens After Priming

This example determines that CTL induced by native or analoged peptide epitopes identified and selected as described in Examples 1-6 recognize endogenously synthesized, *i.e.*, native antigens.

Effector cells isolated from transgenic mice that are immunized with peptide
10 epitopes as in Example 3, for example HLA-A2 supermotif-bearing epitopes, are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on ⁵¹Cr labeled Jurkat-A2.1/K^b target cells in the absence or presence of
15 peptide, and also tested on ⁵¹Cr labeled target cells bearing the endogenously synthesized antigen, *i.e.* cells that are stably transfected with HIV expression vectors.

The result will demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized HIV antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that
20 is being evaluated. In addition to HLA-A*0201/K^b transgenic mice, several other transgenic mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

25

Example 9. Activity Of CTL-HTL Conjugated Epitopes In Transgenic Mice

This example illustrates the induction of CTLs and HTLs in transgenic mice by use of a HIV CTL/HTL peptide conjugate whereby the vaccine composition comprises peptides administered to an HIV-infected patient or an individual at risk for HIV. The
30 peptide composition can comprise multiple CTL and/or HTL epitopes. This analysis demonstrates enhanced immunogenicity that can be achieved by inclusion of one or more HTL epitopes in a vaccine composition. Such a peptide composition can comprise an HTL epitope conjugated to a preferred CTL epitope containing, for example, at least one CTL epitope selected from Table XXVI-XXIX, or an analog of that epitope. The HTL

epitope is, for example, selected from Table XXXII. The peptides may be lipidated, if desired.

Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K^b mice, which are transgenic for the human HLA A2.1 allele and are useful for the assessment of the immunogenicity of HLA-A*0201 motif- or HLA-A2 supermotif-bearing epitopes, are primed subcutaneously (base of the tail) with a 0.1 ml of peptide in Incomplete Freund's Adjuvant, or if the peptide composition is a lipidated CTL/HTL conjugate, in DMSO/saline or if the peptide composition is a polypeptide, in PBS or Incomplete Freund's Adjuvant. Seven days after priming, splenocytes obtained from these animals are restimulated with syngenic irradiated LPS-activated lymphoblasts coated with peptide.

Cell lines: Target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (*e.g.*, Vitiello *et al.*, *J. Exp. Med.* 173:1007, 1991).

In vitro CTL activation: One week after priming, spleen cells (30×10^6 cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated lymphoblasts (10×10^6 cells/flask) in 10 ml of culture medium/T25 flask. After six days, effector cells are harvested and assayed for cytotoxic activity.

Assay for cytotoxic activity: Target cells (1.0 to 1.5×10^6) are incubated at 37°C in the presence of 200 μ l of ^{51}Cr . After 60 minutes, cells are washed three times and resuspended in R10 medium. Peptide is added where required at a concentration of 1 μ g/ml. For the assay, 10^4 ^{51}Cr -labeled target cells are added to different concentrations of effector cells (final volume of 200 μ l) in U-bottom 96-well plates. After a 6 hour incubation period at 37°C, a 0.1 ml aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release = $100 \times (\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})$. To facilitate comparison between separate CTL assays run under the same conditions, % ^{51}Cr release data is expressed as lytic units/ 10^6 cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a 6 hour ^{51}Cr release assay. To obtain specific lytic units/ 10^6 , the lytic units/ 10^6 obtained in the absence of peptide is subtracted from the lytic units/ 10^6 obtained in the presence of peptide. For example, if 30% ^{51}Cr release is obtained at the effector (E): target (T) ratio

of 50:1 (i.e., 5×10^5 effector cells for 10,000 targets) in the absence of peptide and 5:1 (i.e., 5×10^4 effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be: $[(1/50,000) - (1/500,000)] \times 10^6 = 18 \text{ LU}$.

The results are analyzed to assess the magnitude of the CTL responses of animals
5 injected with the immunogenic CTL/HTL conjugate vaccine preparation and are compared to the magnitude of the CTL response achieved using the CTL epitope as outlined in Example 3. Analyses similar to this may be performed to evaluate the immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures it is found that a CTL response is
10 induced, and concomitantly that an HTL response is induced upon administration of such compositions.

Example 10. Selection of CTL and HTL epitopes for inclusion in an HIV-specific vaccine.

15 This example illustrates the procedure for the selection of peptide epitopes for vaccine compositions of the invention. The peptides in the composition can be in the form of a nucleic acid sequence, either single or one or more sequences (i.e., minigene) that encodes peptide(s), or can be single and/or polypeptidic peptides.

The following principles are utilized when selecting an array of epitopes for
20 inclusion in a vaccine composition. Each of the following principles is balanced in order to make the selection.

Epitopes are selected which, upon administration, mimic immune responses that correlate with virus clearance. For example, if it has been observed that patients who clear HIV generate an immune response to at least 3 epitopes on at least one HIV antigen,
25 then 3-4 epitopes should be included for HLA class I. A similar rationale is used to determine HLA class II epitopes.

When selecting an array of HIV epitopes, it is preferred that at least some of the epitopes are derived from early and late proteins. The early proteins of HIV are expressed when the virus is replicating, either following acute or dormant infection.
30 Therefore, it is particularly preferred to use epitopes from early stage proteins to alleviate disease manifestations at the earliest stage possible.

Epitopes are often selected that have a binding affinity of an IC_{50} of 500 nM or less for an HLA class I molecule, or for class II, an IC_{50} of 1000 nM or less.

Sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. For example, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess breadth, or redundancy, of population coverage.

When creating a polyepitopic compositions, *e.g.* a minigene, it is typically desirable to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same, as those employed when selecting a peptide comprising nested epitopes.

In cases where the sequences of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.

Peptide epitopes for inclusion in vaccine compositions are, for example, selected from those listed in Tables XXVI-XXIX and Table XXXII. A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response similar in magnitude of an immune response that clears an acute HIV infection.

Example 11. Construction of Minigene Multi-Epitope DNA Plasmids

This example provides general guidance for the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of CTL and/or HTL epitopes or epitope analogs as described herein. Expression plasmids have been constructed and evaluated as described, for example, in co-pending U.S.S.N. 09/311,784 filed 5/13/99 and in Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999. An example of such a plasmid for the expression of HIV epitopes is shown in Figure 2, which illustrates the orientation of HIV peptide epitopes in a minigene construct.

A minigene expression plasmid typically includes multiple CTL and HTL peptide epitopes. In the present example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes (Figure 2). Preferred epitopes are identified, for example, in Tables XXVI-XXIX and XXXII. HLA class I supermotif or

motif-bearing peptide epitopes derived from multiple HIV antigens, are selected such that multiple supermotifs/motifs are represented to ensure broad population coverage.

Similarly, HLA class II epitopes are selected from multiple HIV antigens to provide broad population coverage, *i.e.* both HLA DR-1-4-7 supermotif-bearing epitopes and

5 HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct.

The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

Such a construct may additionally include sequences that direct the HTL epitopes to the endoplasmic reticulum. For example, the Ii protein may be fused to one or more

10 HTL epitopes as described in co-pending application U.S.S.N. 09/311,784 filed 5/13/99, wherein the CLIP sequence of the Ii protein is removed and replaced with an HLA class II epitope sequence so that HLA class II epitope is directed to the endoplasmic reticulum, where the epitope binds to an HLA class II molecules.

This example illustrates the methods to be used for construction of a minigene-bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

The minigene DNA plasmid contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance with principles disclosed herein. The construct can also

20 include, for example, The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

Overlapping oligonucleotides, for example eight oligonucleotides, averaging approximately 70 nucleotides in length with 15 nucleotide overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as

25 appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multiepitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing temperature (5° below the lowest calculated T_m of each primer pair) for 30 sec, and 72°C

30 for 1 min.

For the first PCR reaction, 5 µg of each of two oligonucleotides are annealed and extended: Oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 µl reactions containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM (NH₄)₂SO₄, 20 mM Tris-chloride, pH 8.75, 2 mM MgSO₄, 0.1% Triton X-100, 100 µg/ml BSA), 0.25 mM each

dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to
5 amplify the full length product for 25 additional cycles. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

Example 12. The plasmid construct and the degree to which it induces immunogenicity.

10 The degree to which a plasmid construct, for example a plasmid constructed in accordance with Example 11, is able to induce immunogenicity can be evaluated *in vitro* by testing for epitope presentation by APC following transduction or transfection of the APC with an epitope-expressing nucleic acid construct. Such a study determines “antigenicity” and allows the use of human APC. The assay determines the ability of the
15 epitope to be presented by the APC in a context that is recognized by a T cell by quantifying the density of epitope-HLA class I complexes on the cell surface. Quantitation can be performed by directly measuring the amount of peptide eluted from the APC (*see, e.g.,* Sijts *et al.*, *J. Immunol.* 156:683-692, 1996; Demotz *et al.*, *Nature* 342:682-684, 1989); or the number of peptide-HLA class I complexes can be estimated
20 by measuring the amount of lysis or lymphokine release induced by infected or transfected target cells, and then determining the concentration of peptide necessary to obtained equivalent levels of lysis or lymphokine release (*see, e.g.,* Kageyama *et al.*, *J. Immunol.* 154:567-576, 1995).

Alternatively, immunogenicity can be evaluated through *in vivo* injections into
25 mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analysed using cytotoxicity and proliferation assays, respectively, as detailed *e.g.*, in copending U.S.S.N. 09/311,784 filed 5/13/99 and Alexander *et al.*, *Immunity* 1:751-761, 1994.

For example, to assess the capacity of a DNA minigene construct (*e.g.*, a pMin minigene construct generated as described in U.S.S.N. 09/311,784) containing at least one
30 HLA-A2 supermotif peptide to induce CTLs *in vivo*, HLA-A2.1/K^b transgenic mice, for example, are immunized intramuscularly with 100 µg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA immunization, a control group of animals is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.

Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polyepitopic peptide), then assayed for peptide-specific cytotoxic activity in a ^{51}Cr release assay. The results indicate the magnitude of the CTL response directed against the A2-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polyepitopic vaccine. It is, therefore, found that the minigene elicits immune responses directed toward the HLA-A2 supermotif peptide epitopes as does the polyepitopic peptide vaccine. A similar analysis is also performed using other HLA-A3 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes.

To assess the capacity of a class II epitope encoding minigene to induce HTLs *in vivo*, DR transgenic mice, or for those epitope that cross react with the appropriate mouse MHC molecule, I-A^b-restricted mice, for example, are immunized intramuscularly with 100 μg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant. CD4⁺ T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene). The HTL response is measured using a ^3H -thymidine incorporation proliferation assay, (*see, e.g.*, Alexander et al. *Immunity* 1:751-761, 1994). The results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

DNA minigenes, constructed as described in Example 11, may also be evaluated as a vaccine in combination with a boosting agent using a prime boost protocol. The boosting agent can consist of recombinant protein (*e.g.*, Barnett et al., *Aids Res. and Human Retroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (*see, e.g.*, Hanke et al., *Vaccine* 16:439-445, 1998; Sedegah et al., *Proc. Natl. Acad. Sci USA* 95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson et al., *Nature Med.* 5:526-34, 1999).

For example, the efficacy of the DNA minigene used in a prime boost protocol is initially evaluated in transgenic mice. In this example, A2.1/K^b transgenic mice are immunized IM with 100 μg of a DNA minigene encoding the immunogenic peptides including at least one HLA-A2 supermotif-bearing peptide. After an incubation period

(ranging from 3-9 weeks), the mice are boosted IP with 10^7 pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 μ g of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the minigene and recombinant vaccinia, then assayed for peptide-specific activity in an IFN- γ ELISA.

It is found that the minigene utilized in a prime-boost protocol elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis can also be performed using HLA-A11 or HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 or HLA-B7 motif or supermotif epitopes.

The use of prime boost protocols in humans is described in Example 20.

Example 13. Peptide Composition for Prophylactic Uses

Vaccine compositions of the present invention can be used to prevent HIV infection in persons who are at risk for such infection. For example, a polyepitopic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes such as those selected in Examples 9 and/or 10, which are also selected to target greater than 80% of the population, is administered to individuals at risk for HIV infection.

For example, a peptide-based composition can be provided as a single polypeptide that encompasses multiple epitopes. The vaccine is typically administered in a physiological solution that comprises an adjuvant, such as Incomplete Freund's Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 μ g, generally 100-5,000 μ g, for a 70 kg patient. The initial administration of vaccine is followed by booster dosages at 4 weeks followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against HIV infection.

Alternatively, a composition typically comprising transfecting agents can be used for the administration of a nucleic acid-based vaccine in accordance with methodologies known in the art and disclosed herein.

5 Example 14. Polyepitopic Vaccine Compositions Derived from Native HIV Sequences

A native HIV polyprotein sequence is screened, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify “relatively short” regions of the polyprotein that comprise multiple epitopes and is preferably less in length than an entire native antigen. This relatively short sequence that
10 contains multiple distinct, even overlapping, epitopes is selected and used to generate a minigene construct. The construct is engineered to express the peptide, which corresponds to the native protein sequence. The “relatively short” peptide is generally less than 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in
15 length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping, for example, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic
20 purposes.

The vaccine composition will preferably include, for example, three CTL epitopes and at least one HTL epitope from HIV. This polyepitopic native sequence is administered either as a peptide or as a nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the
25 epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide.

The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune
30 response-inducing vaccine compositions. Additionally such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent analogs) directs the immune response to multiple peptide sequences that are actually present in native HIV antigens thus avoiding the need

to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions.

Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of
5 epitopes per sequence length.

Example 15. Polyepitopic Vaccine Compositions Directed To Multiple Diseases

The HIV peptide epitopes of the present invention are used in conjunction with peptide epitopes from target antigens related to one or more other diseases, to create a
10 vaccine composition that is useful for the prevention or treatment of HIV as well as the one or more other disease(s). Examples of the other diseases include, but are not limited to, HCV and HBV.

For example, a polyepitopic peptide composition comprising multiple CTL and HTL epitopes that target greater than 98% of the population may be created for
15 administration to individuals at risk for both HBV and HIV infection. The composition can be provided as a single polypeptide that incorporates the multiple epitopes from the various disease-associated sources, or can be administered as a composition comprising one or more discrete epitopes.

20 Example 16. Use of peptides to evaluate an immune response

Peptides of the invention may be used to analyze an immune response for the presence of specific CTL or HTL populations directed to HIV. Such an analysis may be performed in a manner as that described by Ogg *et al.*, *Science* 279:2103-2106, 1998. In the following example, peptides in accordance with the invention are used as a reagent for
25 diagnostic or prognostic purposes, not as an immunogen.

In this example highly sensitive human leukocyte antigen tetrameric complexes ("tetramers") are used for a cross-sectional analysis of, for example, HIV HLA-A*0201-specific CTL frequencies from HLA A*0201-positive individuals at different stages of infection or following immunization using an HIV peptide containing an A*0201 motif.
30 Tetrameric complexes are synthesized as described (Musey *et al.*, *N. Engl. J. Med.* 337:1267, 1997). Briefly, purified HLA heavy chain (A*0201 in this example) and β 2-microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal

addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain, β 2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5'triphosphate and
5 magnesium. Streptavidin-phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300 x g for 5 minutes and resuspended in 50 μ l of cold phosphate-buffered
10 saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are applied to contain >99.98% of control samples. Controls for the tetramers include both A*0201-negative individuals and A*0201-positive uninfected donors. The percentage of
15 cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby readily indicating the extent of immune response to the HIV epitope, and thus the stage of infection with HIV, the status of exposure to HIV, or exposure to a vaccine that elicits a protective or therapeutic response.

20

Example 17. Use of Peptide Epitopes to Evaluate Recall Responses

The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who have recovered from infection, who are chronically infected
25 with HIV, or who have been vaccinated with an HIV vaccine.

For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any HIV vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA
30 supertype family members, are then used for analysis of samples derived from individuals who bear that HLA type.

PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO

Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 µg/ml), and Hepes (10mM) containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is
5 added at 10 µg/ml to each well and HBV core 128-140 epitope is added at 1 µg/ml to each well as a source of T cell help during the first week of stimulation.

In the microculture format, 4×10^5 PBMC are stimulated with peptide in 8 replicate cultures in 96-well round bottom plate in 100 µl/well of complete RPMI. On days 3 and 10, 100 ml of complete RPMI and 20 U/ml final concentration of rIL-2 are
10 added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and 10^5 irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response requires two or more of the eight replicate cultures to display greater than 10% specific ^{51}Cr release, based on comparison with uninfected control subjects as previously
15 described (Rehermann, *et al.*, *Nature Med.* 2:1104,1108, 1996; Rehermann *et al.*, *J. Clin. Invest.* 97:1655-1665, 1996; and Rehermann *et al.* *J. Clin. Invest.* 98:1432-1440, 1996).

Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics (ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al.*
20 *J. Virol.* 66:2670-2678, 1992).

Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10 µM, and labeled with 100 µCi of ^{51}Cr (Amersham Corp., Arlington Heights, IL) for 1
25 hour after which they are washed four times with HBSS.

Cytolytic activity is determined in a standard 4-h, split well ^{51}Cr release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula: $100 \times [(\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})]$. Maximum release is determined by
30 lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to HIV or an HIV vaccine.

The class II restricted HTL responses may also be analyzed. Purified PBMC are cultured in a 96-well flat bottom plate at a density of 1.5×10^5 cells/well and are stimulated with 10 µg/ml synthetic peptide, whole antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1 µCi ^3H -thymidine is added to each well and incubation is continued for an additional 18 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for ^3H -thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of ^3H -thymidine incorporation in the presence of antigen divided by the ^3H -thymidine incorporation in the absence of antigen.

Example 18. Induction Of Specific CTL Response In Humans

A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study and carried out as a randomized, double-blind, placebo-controlled trial. Such a trial is designed, for example, as follows:

A total of about 27 subjects are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 µg of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 µg peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 µg of peptide composition.

After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage.

The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the peptide composition are an index of the intrinsic activity of this the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.

Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.

Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

5 The vaccine is found to be both safe and efficacious.

Example 19. Phase II Trials In Patients Infected With HIV

Phase II trials are performed to study the effect of administering the CTL-HTL peptide compositions to HIV-infected patients. The main objectives of the trials are to
10 determine an effective dose and regimen for inducing CTLs in chronically infected HIV patients, to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of chronically infected HIV patients, as manifested by a reduction in viral load and an increase in CD4⁺ cells counts. Such a study is designed, for example, as follows:

15 The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.

20 There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group range in age from 21-65, include both males and females, and represent diverse ethnic backgrounds. All of them are infected with HIV for over five years and are HCV, HBV
25 and delta hepatitis virus (HDV) negative, but have positive levels of HIV antigen.

The viral load and CD4⁺ levels are monitored to assess the effects of administering the peptide compositions. The vaccine composition is found to be both safe and efficacious in the treatment of HIV infection.

30 Example 20. Induction of CTL Responses Using a Prime Boost Protocol

A prime boost protocol can also be used for the administration of the vaccine to humans. Such a vaccine regimen can include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.

For example, the initial immunization is performed using an expression vector, such as that constructed in Example 11, in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 μ g) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster is, for example, recombinant fowlpox virus administered at a dose of $5 \cdot 10^7$ to $5 \cdot 10^9$ pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polyepitopic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood samples are obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

Analysis of the results indicates that a magnitude of sufficient response to achieve protective immunity against HIV is generated.

Example 21. Administration of Vaccine Compositions Using Dendritic Cells

Vaccines comprising peptide epitopes of the invention can be administered using APCs, or "professional" APCs such as DC. In this example, the peptide-pulsed DC are administered to a patient to stimulate a CTL response *in vivo*. In this method, dendritic cells are isolated, expanded, and pulsed with a vaccine comprising peptide CTL and HTL epitopes of the invention. The dendritic cells are infused back into the patient to elicit CTL and HTL responses *in vivo*. The induced CTL and HTL then destroy or facilitate destruction of the specific target cells that bear the proteins from which the epitopes in the vaccine are derived.

For example, a cocktail of epitope-bearing peptides is administered *ex vivo* to PBMC, or isolated DC therefrom. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides.

As appreciated clinically, and readily determined by one of skill based on clinical outcomes, the number of DC reinfused into the patient can vary (*see, e.g., Nature Med.* 4:328, 1998; *Nature Med.* 2:52, 1996 and *Prostate* 32:272, 1997). Although $2 \cdot 50 \times 10^6$

DC per patient are typically administered, larger number of DC, such as 10^7 or 10^8 can also be provided. Such cell populations typically contain between 50-90% DC.

In some embodiments, peptide-loaded PBMC are injected into patients without purification of the DC. For example, PBMC containing DC generated after treatment
5 with an agent such as Progenipoiectin™ are injected into patients without purification of the DC. The total number of PBMC that are administered often ranges from 10^8 to 10^{10} . Generally, the cell doses injected into patients is based on the percentage of DC in the blood of each patient, as determined, for example, by immunofluorescence analysis with specific anti-DC antibodies. Thus, for example, if Progenipoiectin™ mobilizes 2% DC in
10 the peripheral blood of a given patient, and that patient is to receive 5×10^6 DC, then the patient will be injected with a total of 2.5×10^8 peptide-loaded PBMC. The percent DC mobilized by an agent such as Progenipoiectin™ is typically estimated to be between 2-10%, but can vary as appreciated by one of skill in the art.

15 *Ex vivo activation of CTL/HTL responses*

Alternatively, *ex vivo* CTL or HTL responses to HIV antigens can be induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and the appropriate immunogenic peptides. After an appropriate incubation time (typically about 7-28 days),
20 in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy or facilitate destruction of their specific target cells.

Example 22. Alternative Method of Identifying Motif-Bearing Peptides

25 Another way of identifying motif-bearing peptides is to elute them from cells bearing defined MHC molecules. For example, EBV transformed B cell lines used for tissue typing have been extensively characterized to determine which HLA molecules they express. In certain cases these cells express only a single type of HLA molecule. These cells can then be infected with a pathogenic organism or transfected with nucleic acids that express the antigen of interest, *e.g.* HIV regulatory or structural proteins.
30 Thereafter, peptides produced by endogenous antigen processing of peptides produced consequent to infection (or as a result of transfection) will bind to HLA molecules within the cell and be transported and displayed on the cell surface.

The peptides are then eluted from the HLA molecules by exposure to mild acid conditions and their amino acid sequence determined, *e.g.*, by mass spectral analysis (*e.g.*, Kubo *et al.*, *J. Immunol.* 152:3913, 1994). Because the majority of peptides that bind a particular HLA molecule are motif-bearing, this is an alternative modality for obtaining the motif-bearing peptides correlated with the particular HLA molecule expressed on the cell.

Alternatively, cell lines that do not express any endogenous HLA molecules can be transfected with an expression construct encoding a single HLA allele. These cells can then be used as described, *i.e.*, they can be infected with a pathogenic organism or transfected with nucleic acid encoding an antigen of interest to isolate peptides corresponding to the pathogen or antigen of interest that have been presented on the cell surface. Peptides obtained from such an analysis will bear motif(s) that correspond to binding to the single HLA allele that is expressed in the cell.

As appreciated by one in the art, one can perform a similar analysis on a cell bearing more than one HLA allele and subsequently determine peptides specific for each HLA allele expressed. Moreover, one of skill would also recognize that means other than infection or transfection, such as loading with a protein antigen, can be used to provide a source of antigen to the cell.

The above examples are provided to illustrate the invention but not to limit its scope. For example, the human terminology for the Major Histocompatibility Complex, namely HLA, is used throughout this document. It is to be appreciated that these principles can be extended to other species as well. Thus, other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent application cited herein are hereby incorporated by reference for all purposes.

TABLE I

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	T <i>L</i> V <i>M</i> S		F <i>W</i> Y
A2	L <i>I</i> V <i>M</i> A <i>T</i> Q		I <i>V</i> M <i>A</i> T <i>L</i>
A3	V <i>S</i> M <i>A</i> T <i>L</i> I		R <i>K</i>
A24	Y <i>F</i> W <i>I</i> V <i>L</i> M <i>T</i>		F <i>I</i> Y <i>W</i> L <i>M</i>
B7	P		V <i>L</i> F <i>M</i> W <i>YA</i>
B27	R <i>H</i> K		F <i>Y</i> L <i>W</i> M <i>IVA</i>
B44	E <i>D</i>		F <i>W</i> Y <i>L</i> I M <i>VA</i>
B58	A <i>T</i> S		F <i>W</i> Y <i>L</i> I V M A
B62	Q <i>L</i> I <i>VM<i>P</i></i>		F <i>W</i> Y <i>M</i> I <i>VLA</i>
MOTIFS			
A1	T S M		Y
A1		D E A S	Y
A2.1	L M <i>V</i> Q <i>IAT</i>		V L I M A T
A3	L M <i>V</i> I S A T F C G D		K Y R H F A
A11	V T M L I S A G N C D F		K R Y H
A24	Y F W M		F L I W
A*3101	M V T A L I S		R K
A*3301	M V A L F I S T		R K
A*6801	A V T M S L I		R K
B*0702	P		L M F W Y A I V
B*3501	P		L M F W Y I V A
B51	P		L I V F W Y A M
B*5301	P		I M F W Y A L V
B*5401	P		A T I V L M F W Y

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE Ia

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	T <i>L</i> V <i>M</i> S		F <i>W</i> Y
A2	<i>V</i> Q <i>A</i> T		<i>V</i> L <i>I</i> M <i>A</i> T
A3	V <i>S</i> M <i>A</i> T <i>L</i> I		R K
A24	Y <i>F</i> W <i>I</i> V <i>L</i> M <i>T</i>		F <i>I</i> Y <i>W</i> L <i>M</i>
B7	P		V <i>IL<i>F</i>M<i>W</i>Y<i>A</i></i>
B27	R H K		F <i>Y</i> L <i>W</i> M <i>IV<i>A</i></i>
B58	A T S		F <i>W</i> Y <i>L</i> I V M <i>A</i>
B62	Q <i>L</i> I V M P		F <i>W</i> Y <i>M</i> I V L <i>A</i>
MOTIFS			
A1	T S M		Y
A1		D E A S	Y
A2.1	<i>V</i> Q <i>A</i> T *		<i>V</i> L <i>IM<i>A</i>T</i>
A3.2	L M <i>V</i> I S <i>A</i> T <i>F</i> C G D		K Y R H F A
A11	V T M L I S A G N C D F		K R H Y
A24	Y F W		F L I W

*If 2 is V, or Q, the C-term is not L

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

		POSITION								
		1	2	3	4	5	6	7	8	C-terminus
<u>MOTIFS</u>										
A1 preferred 9-mer	GFYW		1°Anchor STM	DEA	YFW		P	DEQN	YFW	1°Anchor Y
deleterious	DE			RHKLIVM P	A	G	A			
A1 preferred 9-mer	GRHK		ASTCLIV M	1°Anchor DEAS	GSTC		ASTC	LIVM	DE	1°Anchor Y
deleterious	A		RHKDEPY I°W		DE	PQN	RHK	PG	GP	

MOTIFS

AI preferred GFYW
9-mer

deleterious DE

A1	preferred	GRHK
9-mer		

deleterious A

M:I

POSITION										
	1	2	3	4	5	6	7	8	9 or C-terminus	C-terminus
A1 preferred 10-mer	YFW	<u>1°Anchor</u> STM	DEAQN	A	YFWQN		PASTC	GDE	P	<u>1°Anchor</u> Y
deleterious	GP		RHKGLIV M	DE	RHK	QNA	RHKYFW	RHK	A	
A1 preferred 10-mer	YFW	STCLIVM	<u>1°Anchor</u> DE4S	A	YFW		PG	G	YFW	<u>1°Anchor</u> Y
deleterious	RHK	RHKDEPY FW			P	G		PRHK	QN	
A2.1 preferred 9-mer	YFW	<u>1°Anchor</u> LMIVQAT	YFW	STC	YFW		A	P	<u>1°Anchor</u> VLMAT	
deleterious	DEP		DERKH			RKH	DERKH			
A2.1 preferred 10-mer	AYFW	<u>1°Anchor</u> LMIVQAT	LVIM	G		G		FYWL VIM		<u>1°Anchor</u> VLMAT
deleterious	DEP		DE	RKHA	P		RKH	DERK H	RKH	

POSITION									
	1	2	3	4	5	6	7	8	9 or C-terminus
A3 preferred	RHK	1°Anchor LMVISAT FCGD	YFW	PRHKYFW	A	YFW		P	1°Anchor KYRHHFA
deleterious	DEP		DE						
A11 preferred	A	1°Anchor VTLMISA GNCDF	YFW	YFW	A	YFW	YFW	P	1°Anchor KRYH
deleterious	DEP						A	G	
A24 preferred 9-mer	YFWRHK	1°Anchor YFWM		STC			YFW	YFW	1°Anchor FLIW
deleterious	DEG		DE	G	QNP	DERHK	G	AQN	
A24 preferred 10-mer		1°Anchor YFWM		P	YFWP		P		1°Anchor FLIW
deleterious			GDE	QN	RHK	DE	A	QN	DEA

POSITION									
	1	2	3	4	5	6	7	8	9 or C-terminus 1°Anchor RK
A3101 preferred	RHK	1°Anchor MVTALIS	YFW	P		YFW	YFW	AP	
deleterious	DEP		DE		ADE	DE	DE	DE	
A3301 preferred		1°Anchor MVALFIS T	YFW				AYFW		1°Anchor RK
deleterious	GP		DE						
A6801 preferred	YFWSTC	1°Anchor AVTMSLI			YFWLIV M		YFW	P	1°Anchor RK
deleterious	GP		DEG		RHK			A	
B0702 preferred	RHKFWY	1°Anchor P	RHK		RHK	RHK	RHK	PA	1°Anchor LMFWYIV
deleterious	DEQNP		DEP	DE	DE	GDE	QN	DE	
B3501 preferred	FWYLIVM	1°Anchor P	FWY				FWY		1°Anchor LMFWYIV/A
deleterious	AGP				G	G			

POSITION									
	1	2	3	4	5	6	7	8	9 or C-terminus
B51	preferred	LIVMFY	<u>1°Anchor</u> P	FWY	STC	FWY	G	FWY	<u>1°Anchor</u> LIVFWYAM
	deleterious	AGPDERHKSTC			DE	G	DEQN	GDE	
B5301	preferred	LIVMFY	<u>1°Anchor</u> P	FWY	STC	FWY	LIVMFY	FWY	<u>1°Anchor</u> IMFWYALY
	deleterious	AGPQN				G	RHKQN	DE	
B5401	preferred	FWY	<u>1°Anchor</u> P	FWYLIVM	LIVM	FWYAP	ALIVM	FWYAP	<u>1°Anchor</u> ATIVLMFW Y
	deleterious	GPQNDE		GDESTC	RHKDE	DE	QNDGE	DE	

Italicized residues indicate less preferred or "tolerated" residues.
The information in Table II is specific for 9-mers unless otherwise specified.

TABLE III

MOTIFS	POSITION					
	1° anchor 1	2	3	4	5	1° anchor 6
DR4 preferred deleterious	FMYLIVW	M	T		I	VSTCPALIM
				W		R
DR1 preferred deleterious	MFLIVWY			PAMQ		VMATSPLIC
		C	CH	FD	CWD	GDE
DR7 preferred deleterious	MFLIVWY	M	W	A		IVMSACTPL
		C		G		GRD
DR Supermotif	MFLIVWY					VMSTACPLI
DR3 MOTIFS	1° anchor 1	2	3	1° anchor 4	5	1° anchor 6
motif a preferred	LIVMFY			D		
motif b preferred	LIVMFAY			DNQEST		KRH

Italicized residues indicate less preferred or "tolerated" residues.

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	25
A*0201	941.01	FLPSDYFPSV	5.0
A*0202	941.01	FLPSDYFPSV	4.3
A*0203	941.01	FLPSDYFPSV	10
A*0205	941.01	FLPSDYFPSV	4.3
A*0206	941.01	FLPSDYFPSV	3.7
A*0207	941.01	FLPSDYFPSV	23
A*6802	1141.02	FTQAGYPAL	40
A*0301	941.12	KVFPYALINK	11
A*1101	940.06	AVDLYHFLK	6.0
A*3101	941.12	KVFPYALINK	18
A*3301	1083.02	STLPETYVRR	29
A*6801	941.12	KVFPYALINK	8.0
A*2402	979.02	AYIDNYNKF	12
B*0702	1075.23	APRTLVL	5.5
B*3501	1021.05	FPFKYAAAF	7.2
B51	1021.05	FPFKYAAAF	5.5
B*5301	1021.05	FPFKYAAAF	9.3
B*5401	1021.05	FPFKYAAAF	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	YKTLAFDEEARR	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	EALHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2 β 1	507.02	GRTQDENPVVHFFKNIV TPRTPPP	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2 β 2	553.01	QYIKANSKFIGITE	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table VI

HLA-supertype	Allele-specific HLA-supertype members	
	Verified ^a	Predicted ^b
A1	A*0101, A*2501, A*2601, A*2602, A*3201	A*0102, A*2604, A*3601, A*4301, A*0001
A2	A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, A*6901	A*0208, A*0210, A*0211, A*0212, A*0213
A3	A*0301, A*1101, A*3101, A*3301, A*6001	A*0302, A*1102, A*2603, A*3302, A*3303, A*3401, A*3402, A*6601, A*6602, A*7401
A24	A*2301, A*2402, A*3001	A*2403, A*2404, A*3002, A*3003
B7	B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, B*7801	B*1511, B*4201, B*5901
B27	B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3001, B*3901, B*3902, B*7301	B*2701, B*2707, B*2708, B*3802, B*3903, B*3904, B*3905, B*4801, B*4802, B*1510, B*1518, B*1503
B44	D*1801, D*1802, D*3701, B*4402, D*4403, D*4404, D*4001, D*4002, D*4006	D*4101, D*4501, B*4701, B*4901, B*5001
B50	D*5701, D*5702, D*5801, D*5802, D*1516, D*1517	
D62	D*1501, D*1502, D*1513, D*5201	D*1301, D*1302, D*1504, D*1505, D*1506, D*1507, D*1515, D*1520, D*1521, D*1512, D*1514, D*1510

a. Verified alleles includes alleles whose specificity has been determined by pool sequencing analysis, peptide binding assays, or by analysis of the sequences of CTL epitopes.

b. Predicted alleles are alleles whose specificity is predicted on the basis of D and F pocket structure to overlap with the supertype specificity.

Table VII
HIV Δ01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0101	SEQ ID NO
ENV	KLWVTYYY	44	8	11	17		1
ENV	NLWVTYYY	44	8	35	56		2
ENV	DTEVINWV	75	8	19	30		3
ENV	VTEFNMMW	102	8	34	53		4
ENV	RIGPGQTF	357	8	11	17		5
ENV	GIGPGQTF	360	8	01	33		6
ENV	SIGSQQAF	360	8	01	33		7
ENV	KLREIRQF	405	8	01	25		8
ENV	STNGTETF	537	8	01	17		9
ENV	AVGIGAVF	595	8	11	17		10
ENV	IILLKLTW	650	8	13	20		11
ENV	IILLQLTW	650	8	34	53		12
ENV	IIMQLTVW	650	8	10	16		13
ENV	RVLAVERY	665	8	33	52		14
ENV	NVPWNSSW	693	8	13	20		15
ENV	EIWDMITW	716	8	13	20		16
ENV	DLALADKW	754	8	21	33		17
ENV	ELLELDKW	754	8	20	31		18
ENV	DITNWLWY	769	8	10	16		19
ENV	WLWYKIF	773	8	50	78		20
ENV	LIGLRIF	787	8	16	25		21
ENV	LIGLRVF	787	8	29	45		22
ENV	SIRLVNGF	842	8	13	20		23
ENV	SIRLVSGF	842	8	13	20		24
ENV	DLRNLCLF	856	8	17	27		25
ENV	DLRSLCLF	856	8	38	59		26
ENV	KSLCLFSY	858	8	35	55		27
ENV	ELLGRKGW	881	8	31	37		28
ENV	TVYGVGVVW	48	9	55	86		29
ENV	NYTFNFMW	101	9	34	53		30
ENV	DSSNSTGNY	218	9	01	20		31
ENV	ILKCNDRKF	271	9	12	19		32
ENV	RIGPGQTFY	357	9	11	17		33
ENV	GIGPGQTFY	360	9	01	33		34
ENV	SIGSQQAFY	360	9	01	33		35
ENV	DLEITHSF	428	9	21	33		36
ENV	IISFNCGGEF	434	9	36	56		37
ENV	IISFNCRGEF	434	9	16	25		38
ENV	RIKQINMW	488	9	30	47		39
ENV	RIKQIVNMW	488	9	12	19		40
ENV	GSENGTETF	538	9	02	18		41
ENV	GIGAVFLGF	598	9	11	18		42
ENV	MLGAMFLGF	599	9	04	36		43
ENV	TIGAMFLGF	599	9	03	27		44
ENV	LICTTAVPW	688	9	19	30		45
ENV	LICTTNVPW	688	9	17	27		46
ENV	LICTTVPW	688	9	12	19		47
ENV	ALDKWASLW	757	9	11	13		48

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0101	SEQ ID NO
ENV	GLIGLRIVF	786	9	29	45		51
ENV	IVNRVRQGY	799	9	38	59		52
ENV	RSIRLVNGF	841	9	12	19		53
ENV	RSIRLVSGF	841	9	13	20		54
ENV	VSGFLALAW	846	9	16	25		55
ENV	FSYIRLRDF	863	9	18	28		56
ENV	SLKGLRLGW	889	9	11	39		57
ENV	SLRGLQGW	889	9	05	18		58
ENV	RLGWEGLY	894	9	09	29		59
ENV	VTVYGVVPW	47	10	55	86		60
ENV	QMIHEDISLW	116	10	29	45		61
ENV	ITOACPKVSF	245	10	29	45		62
ENV	VSEFPIIHY	253	10	28	44		63
ENV	PHIYCAPAGF	260	10	27	42		64
ENV	PHIYCTPAGF	260	10	10	16		65
ENV	AILKNDUKKE	270	10	12	19		66
ENV	NYSMSRVAY	376	10	01	33		67
ENV	IISFNCGGIEFF	434	10	35	55		68
ENV	IISFNCRGIEFF	434	10	16	25		69
ENV	NTEINKTEIF	537	10	01	17		70
ENV	NTGNTETIF	537	10	01	17		71
ENV	KLICITAVPW	687	10	19	30		72
ENV	KLICITVVPW	687	10	17	27		73
ENV	KLICTTVVPW	687	10	12	19		74
ENV	TTNVPWNSS	691	10	11	17		75
ENV	SIVNRVRQGY	798	10	36	56		76
ENV	LVSGFLALAW	845	10	16	25		77
ENV	DLRNLCLFSY	856	10	16	25		78
ENV	DLRSLCLFSY	856	10	35	55		79
ENV	IVELLGRRGW	879	10	22	34		80
ENV	SSLKGLRLGW	886	10	10	16		81
ENV	WVTVYGVVPV	46	11	55	86		82
ENV	PWKIEATITL	54	11	22	34		83
ENV	TLFCASDAKA	64	11	40	63		84
ENV	VITQACPKVSF	244	11	14	22		85
ENV	KVSFEMPIHY	252	11	28	44		86
ENV	GTAGNSRAA	375	11	01	33		87
ENV	TIISFNCGGE	432	11	16	25		88
ENV	TIISFNCRGE	432	11	12	19		89
ENV	VMIISFNCGGE	432	11	13	20		90
ENV	IISFNCGGIEFF	434	11	35	55		91
ENV	IISFNCRGIEFF	434	11	16	25		92
ENV	NMWQEVGKA	494	11	15	23		93
ENV	DMRDNRWSEL	552	11	37	58		94
ENV	AVGIGAVFLGF	595	11	11	17		95
ENV	YLKDQQLLGI	672	11	27	42		96
ENV	YLRDQQLLGI	672	11	18	28		97
ENV	CTTNVPWNSS	690	11	11	17		98
ENV	WMWEEREIDN	723	11	10	16		99
ENV	LLALDKVASL	755	11	11	17		100

Table VII
HIV Δ01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0101	SEQ ID NO
ENV	LLELDKWASL	755	11	18	28		101
ENV	ALDKWASLW	757	11	10	16		102
ENV	ELDKWASLWN	757	11	16	25		103
ENV	ISNWLWYIKIF	770	11	11	17		104
ENV	ITNWLWYIKIF	770	11	12	19		105
ENV	ITNWLWYIKIF	770	11	14	22		106
ENV	LSIVNLVRQGY	797	11	34	53		107
ENV	KVRQGYSLSF	802	11	47	73		108
ENV	RLVSGFLALA	844	11	16	25		109
ENV	CLFSYIHLRDF	861	11	18	28		110
ENV	RIVELLORRG	878	11	22	34		111
ENV	GLRLGWIEGLK	892	11	09	29		112
ENV	RLGWIEGLKYL	894	11	07	23		113
GAG	ASRELERF	38	8	46	72		114
GAG	SSQVSONY	145	8	15	31		115
GAG	KVIEEKAF	178	8	24	38		116
GAG	KVIEEKAF	178	8	28	44		117
GAG	TLQHQIAW	263	8	12	19		118
GAG	TLQHQIGW	263	8	27	42		119
GAG	PIPVGDY	279	8	11	17		120
GAG	PIPVGEY	279	8	35	55		121
GAG	ASQEVKNW	333	8	11	17		122
GAG	ATQDVKNW	333	8	15	23		123
GAG	ATQEVKNW	333	8	18	28		124
GAG	IMMOKSNF	408	8	11	17		125
GAG	IMMQRGNF	408	8	27	42		126
GAG	CTEQQANF	459	8	55	87		127
GAG	ETIDKDLV	537	8	01	25		128
GAG	LTSLKSLF	549	8	13	20		129
GAG	LTSLRSLF	549	8	12	19		130
GAG	LSCGKLDAW	8	9	16	25		131
GAG	GSEELRSLV	73	9	12	19		132
GAG	NSQVSONY	144	9	14	31		133
GAG	ISPTLNW	168	9	36	56		134
GAG	LSPTLNW	168	9	17	27		135
GAG	FSPEVIMF	185	9	54	84		136
GAG	TINEEAWE	225	9	53	83		137
GAG	STLQEQIAW	262	9	12	19		138
GAG	STLQEQIGW	262	9	27	42		139
GAG	PVGDIYKRW	281	9	18	28		140
GAG	PVGEYKRW	281	9	40	63		141
GAG	GLNKIVRMV	293	9	60	94	0.0017	142
GAG	NIMMQRGNF	407	9	10	17		143
GAG	TIMMQRGNF	407	9	13	22		144
GAG	SSKGRPCNF	476	9	11	18		145
GAG	PTAPPAESF	495	9	20	31		146
GAG	PTAPPEESF	495	9	15	23		147
GAG	PTAPPAESF	507	9	02	67		148
GAG	PTAPPEESF	507	9	01	33		149
GAG	PLASKSLF	548	9	15	23		150

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0101	SEQ ID NO
GAG	PLTSLKSLF	548	9	12	19		151
GAG	PLTSLRSLF	548	9	12	19		152
GAG	VLSCGKLDAAW	7	10	15	23		153
GAG	RLRIGGKKKY	20	10	34	53		154
GAG	SLFNTVATLY	79	10	15	23		155
GAG	SLYNTVATLY	79	10	22	34		156
GAG	ALSPRTLNAW	167	10	29	45		157
GAG	ALSPRTLNAW	167	10	10	16		158
GAG	WVKVVEEKAF	176	10	24	38		159
GAG	WVKVVEEKAF	176	10	28	44		160
GAG	DTINEEAWEW	224	10	31	48		161
GAG	DTINEEAWEW	224	10	22	34		162
GAG	TSTLQEQIAW	261	10	12	19		163
GAG	TSTLQEQIGW	261	10	27	42		164
GAG	DIKQGPKEPF	308	10	19	30		165
GAG	DIKQGPKEPF	308	10	41	64		166
GAG	ATIMMQRGNF	406	10	11	28		167
GAG	PSIKGRPGNF	475	10	23	36		168
GAG	PSNKGRPGNF	475	10	14	22		169
GAG	PSKGRPGNF	475	10	11	17		170
GAG	SVLSGGKLLDA	6	11	15	23		171
GAG	IVWASRELERF	35	11	19	30		172
GAG	LVWASKELER	35	11	25	39		173
GAG	RSLYNTVATL	78	11	15	24		174
GAG	TSTLQEQIA	260	11	27	43		175
GAG	TSTLQEQIG	260	11	34	53		176
GAG	PIIVGIEYKRW	279	11	57	89		177
GAG	ILGLNKIVRMV	291	11	01	50		178
GAG	ASAQDQLKGG	392	11	01	50		179
GAG	ATAQDQLKGG	392	11	10	16		180
GAG	PTAPPAESFGF	495	11	14	22		181
GAG	PTAPPAESFRF	495	11	02	67		182
GAG	PTAPPAESFRF	507	11	01	33		183
GAG	PTAPPAESFRF	507	11	12	22		184
NEF	ATNADCAW	71	8	12	22		185
NEF	PMYKGA	105	8	12	19		186
NEF	DLDLWVY	185	8	20	31		187
NEF	EILDWVY	185	8	33	52		188
NEF	WVYHTQGF	191	8	13	20		189
NEF	WVYHTQGY	191	8	21	33		190
NEF	GIRYPLTF	213	8	13	20		191
NEF	GTRFPLTF	213	8	43	67		192
NEF	PLTEGWCF	219	8	10	16		193
NEF	WKSISVGVW	5	9	20	31		194
NEF	QVPLRPMTF	100	9	46	72	0.0008	195
NEF	QVPLRPMTY	100	9	13	20		196
NEF	WVYHTQGF	191	9	21	33		197
NEF	WVYHTQGYF	191	9	14	22		198
NEF	IITQGFDDW	194	9	25	39		199
NEF	IITQGFDDW	194	9				200

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
NEF	NTQGYFHDW	194	9	12	19		201
NEF	YTHGGRY	207	9	17	27		202
NEF	YTHGGRY	207	9	13	20		203
NEF	DLWVYITQGF	188	10	13	20		204
NEF	DLWVYITQGY	188	10	21	33		205
NEF	GIRYPLTFGW	213	10	13	20		206
NEF	GTRFPLTFGW	213	10	12	19		207
NEF	IMARELIHPEY	320	10	10	16		208
NEF	NTAATNAIDCA	68	11	12	19		209
NEF	PLRPMYKGA	102	11	12	19		210
NEF	DLWVYITQGF	188	11	13	20		211
NEF	DLWVYITQGY	188	11	21	33		212
NEF	IMARELIHPEY	320	11	10	16		213
POL	DINLGGKW	122	8	13	20		214
POL	EINLGGKW	122	8	12	19		215
POL	MIGGIGGF	133	8	62	97		216
POL	QIGCTLNF	179	8	41	64		217
POL	QLGCTLNF	179	8	16	25		218
POL	KIGPENPY	238	8	51	80		219
POL	RIGPENPY	238	8	11	17		220
POL	VLDVGDAY	297	8	60	94		221
POL	SVPLKDDF	306	8	18	28		222
POL	MTKLEHF	353	8	44	69		223
POL	QLPEKDSW	434	8	13	20		224
POL	VLPEKDSW	434	8	13	20		225
POL	KLVGKLNW	448	8	62	97		226
POL	ATESIVW	568	8	19	30		227
POL	ETWWTIDYW	591	8	10	16		228
POL	PIVGAETF	625	8	28	44		229
POL	IVGAETFY	626	8	28	44		230
POL	KTELQATY	668	8	12	19		231
POL	NIVTDSQY	686	8	62	97		232
POL	LIKKEKVV	717	8	35	55		233
POL	AVIIVASGY	828	8	59	92		234
POL	ETGQETAY	844	8	59	92		235
POL	ILKLGRW	853	8	34	53		236
POL	LLKLGRW	853	8	25	39		237
POL	ITDNGSNF	866	8	51	80		238
POL	TVKAACW	876	8	15	23		239
POL	AVKAACW	877	8	32	50		240
POL	TVKAACW	877	8	24	38		241
POL	QIKIQNF	968	8	12	19		242
POL	QITKIQNF	968	8	35	55		243
POL	KIQNFRVY	971	8	52	81		244
POL	PIRRELQVW	30	9	13	20		245
POL	FSFRQITLW	85	9	14	22		246
POL	KMIGIGGF	132	9	62	97		247
POL	ELNKRTQDF	268	9	57	89		248
POL	TVLDVGDAY	296	9	57	89		249
POL	VLDVGDAYF	297	9	60	94	0.0180	250

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	FSVPLDKDF	305	9	18	28		251
POL	PLDKFRKY	308	9	19	30		252
POL	ETPGIRYQY	327	9	52	81	0.0052	253
POL	SMTKILEPF	352	9	43	67		254
POL	ELREHLLKW	393	9	17	27		255
POL	FLRQHLLRW	393	9	15	23		256
POL	IVLPEKDSW	433	9	13	20		257
POL	KLNWASQIY	452	9	60	94	0.0070	258
POL	VIWGTKPKF	573	9	47	73		259
POL	KLPIQKETW	582	9	20	31		260
POL	RLPIQKETW	582	9	26	41		261
POL	WTDYWQATW	594	9	14	22		262
POL	WTEYWQATW	594	9	24	38		263
POL	ATWIPHEWF	600	9	52	81		264
POL	NTHPLVKLW	610	9	57	89		265
POL	PIVGAETPY	625	9	28	44	0.0007	266
POL	ETKLGKAGY	641	9	35	55	0.0010	267
POL	OLIKKEKVV	716	9	28	44	0.0007	268
POL	SSGIRKVLV	745	9	26	41		269
POL	QVDCSPGIW	805	9	57	89		270
POL	ETQETAYF	844	9	57	89		271
POL	FLKLAGRW	852	9	32	50		272
POL	FLKLAGRW	852	9	25	39		273
POL	STTVKAACW	875	9	15	23		274
POL	TTVKAACW	876	9	15	23		275
POL	KTAVQMAVF	925	9	57	89		276
POL	QMAVFIINF	929	9	60	94		277
POL	KIQNFRVYY	971	9	52	81	0.0056	278
POL	LTQIGCTLNF	177	10	41	64		279
POL	LTQIGCTLNF	177	10	15	23		280
POL	GMIKPKVKQ	201	10	51	80		281
POL	ISKIPENPY	236	10	42	66	0.0130	282
POL	ISKIPENPY	236	10	11	17		283
POL	AIKKKISTKW	251	10	57	89		284
POL	STKWRKLVDF	257	10	58	91		285
POL	ELNKRITQDFW	268	10	57	89		286
POL	VTVLDVGDAY	295	10	56	88	0.2000	287
POL	TVLDVGDAYF	296	10	57	89		288
POL	SSMTKILEPF	351	10	52	80	0.2500	289
POL	VIYQYMDL	368	10	51	80		290
POL	PIQLPEKDSW	432	10	13	20		291
POL	PIVLPEKDSW	432	10	13	20		292
POL	ILKEPIVIGVY	498	10	40	63	0.0017	293
POL	EIQKQGDQW	520	10	13	20		294
POL	EIQKQGDQW	520	10	15	23		295
POL	WTYQIQEPIF	529	10	42	66		296
POL	KIATESIVW	566	10	14	22		297
POL	IVIWGTKPKF	572	10	47	73		298
POL	PIKETWEAW	584	10	15	23		299
POL	PIKETWETW	584	10	27	42		300

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0101	SEQ ID NO
POL	ETWETWWTID	588	10	10	16		301
POL	ETWETWWTIE	588	10	10	16		302
POL	NTPLVKLWY	610	10	57	89	0.0041	303
POL	EVNIVTDSQY	684	10	59	92	0.0510	304
POL	VSAGIRKVLV	744	10	15	23		305
POL	VSSGIRKVLV	744	10	26	41		306
POL	LVAVIVASGY	826	10	53	83	0.0390	307
POL	TIITDNGSNF	864	10	14	22		308
POL	VIIITDNGSNF	864	10	24	38		309
POL	TSAAVKAAACW	874	10	27	42		310
POL	TSTVKAACW	874	10	14	22		311
POL	STTVKAACW	875	10	23	34		312
POL	GKQEFQIPY	886	10	22	34	0.0010	313
POL	GKQEFQIPY	886	10	11	17		314
POL	IKIQNFRVY	969	10	12	19		315
POL	ITKIQNFRVY	969	10	36	57	0.0010	316
POL	NSPTREELQV	28	11	12	19		317
POL	VSEFPQITLW	78	11	07	15		318
POL	GTYLNFQITF	79	11	01	17		319
POL	PSLSFPQITLW	79	11	02	33		320
POL	GTLNCPQITL	80	11	01	33		321
POL	PTFNFQITLW	80	11	01	33		322
POL	SSFESHQITLW	82	11	03	30		323
POL	VLEDINLPCKW	119	11	13	20		324
POL	VLEENLPCKW	119	11	12	19		325
POL	GIGGFIKVRQY	136	11	53	83		326
POL	LLTQIGCTLNF	176	11	21	33		327
POL	MLTQIGCTLNF	176	11	17	27		328
POL	MLTQIGCTLN	176	11	10	16		329
POL	KISKIGPENPY	235	11	41	64		330
POL	KISKIGPENPY	235	11	11	17		331
POL	DSTKWRKLVLD	256	11	58	91		332
POL	SVTVLDVGDV	294	11	56	88		333
POL	SVTVLDVGDV	295	11	56	88		334
POL	SVPLDKIDFRK	306	11	36	50		335
POL	SINNETPGIRY	323	11	32	50		336
POL	STNNETPGIRY	323	11	11	17		337
POL	QSSMTKILEPF	350	11	33	52		338
POL	IVIVQYMDLLY	367	11	42	66		339
POL	ELREILLKWG	393	11	14	22		340
POL	ELRQILLRWG	393	11	12	19		341
POL	WMGYELIPDK	418	11	60	94		342
POL	DIQKLVGKLN	445	11	62	97		343
POL	EILKEPIVIGVY	497	11	40	63		344
POL	ILKEPIVIGVY	498	11	38	59		345
POL	SIVIVGKTPKF	571	11	41	64		346
POL	PIQKETWEAW	584	11	15	23		347
POL	PIQKETWETW	584	11	27	42		348
POL	ETWETWWTID	588	11	10	16		349
POL	FVNTPLVLKL	608	11	54	86		350

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	LIKKEKVYLA	717	11	20	31		351
POL	LIKKEKVYLSW	717	11	13	20		352
POL	LVSAGIRKVLV	743	11	15	23		353
POL	LVSSGIRKVLV	743	11	26	41		354
POL	IISNWKAMAS	768	11	32	50		355
POL	ILVAVIIVASGY	825	11	53	83		356
POL	KVHIITDNGSNF	863	11	21	33		357
POL	FTSAAYKAAAC	873	11	27	42		358
POL	FTSTTVKAAAC	873	11	14	22		359
POL	TSAAYKAAACW	874	11	27	42		360
POL	TSTTVKAAACW	874	11	14	22		361
POL	ILKTAVQMAV	923	11	57	89		362
POL	AVQMAVFIIN	927	11	60	94		363
POL	QIKIQNFRVY	968	11	12	19		364
POL	QITKIQNFRVY	968	11	35	55		365
POL	IKIQNFRVY	969	11	12	19		366
POL	ITKIQNFRVY	969	11	36	57		367
POL	PIWKGPAKLL	985	11	35	55		368
POL	PLWKGPAKLL	985	11	18	28		369
REV	ILYQSNPY	23	8	27	42	0.0110	370
REV	AVRIKILY	17	9	13	20		371
REV	KILYQSNPY	22	9	26	41		372
REV	IKILYQSNPY	20	11	18	28		373
TAT	PVDPILEPW	3	9	20	31		374
TAT	PVDPILEPW	3	9	14	22		375
TAT	FLNKGIGISY	41	10	14	22		376
VIF	SLVKIIMY	23	8	44	69		377
VIF	RLVITYW	65	8	12	19		378
VIF	QLIILYYF	110	8	14	22		379
VIF	QLIIMYYF	110	8	14	22		380
VIF	ILYYFDCF	113	8	16	25		381
VIF	IMIYYFDCF	113	8	15	23		382
VIF	IVSPIRCEY	133	8	18	22		383
VIF	KSLVKIIMY	22	9	14	28		384
VIF	NSLVKIIIMY	22	9	24	38		385
VIF	GLITIGERDW	73	9	22	34		386
VIF	GLITIGERDW	73	9	12	19		387
VIF	SEWRLLRY	89	9	11	17		388
VIF	QVDRMKIRTW	12	10	12	19		389
VIF	QVDRMRINTW	12	10	10	16		390
VIF	QVDRMRIRTW	12	10	31	48		391
VIF	ILGIGVSEW	83	10	25	39		392
VIF	ILCQGVSEW	83	10	26	41		393
VIF	VSIEWRLRY	88	10	11	17		394
VIF	LIILYYFDCF	111	10	16	25		395
VIF	LIIMYYFDCF	111	10	15	23		396
VIF	SVKKTEDRW	174	10	13	20		397
VIF	GVSEWRLLRR	87	11	10	16		398
VIF	GLADLIIMH	106	11	11	17		399
VIF	QLIILYYFDCF	110	11	13	20		400

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
VIF	QLHIMIIYEDCF	110	11	14	22		401
VIF	PSVKLTEDR	173	11	13	20		402
VPR	KSEAVRIIF	27	8	15	23		403
VPR	WLIQLGQY	38	8	11	17		404
VPR	RILQQLLF	62	8	45	70		405
VPR	AVRIIFRIW	30	9	14	22		406
VPR	AVRIIFRIW	30	9	34	53		407
VPR	ELKNEAVRIIF	25	10	17	27		408
VPR	ELKSEAVRIIF	25	10	15	23		409
VPR	WLIQLGQIIF	38	10	20	31		410
VPR	HIYETYGDTW	45	10	17	27		411
VPR	HIYNTYGDTW	45	10	14	22		412
VPR	YIYETYGDTW	45	10	41	64		413
VPR	IRILQQLLF	60	10	35	55		414
VPR	IRILQQLLF	63	10	38	59		415
VPR	IRILQQLLF	59	11	34	53		416
VPR	RILQQLLFHIF	62	11	10	16		417
VPU	LIAIVVW	26	8	15	23		418
VPU	IVVWTFV	30	8	12	19		419
VPU	WTIVFIEY	34	8	11	17		420
VPU	EMGHIIAPW	89	8	14	22		421
VPU	AIVWVTFV	29	9	12	19		422
VPU	VVWVTFVIEY	31	10	01	50		423
VPU	GVEMGHIIAP	91	10	01	50		424
VPU	KVDYRIVIVAF	7	11	12	19		425
VPU	IVWVTFVIEY	30	11	01	50		426
VPU	RIKEIKDDSDY	64	11	01	50		427
VPU	RIRKIRDDSDY	64	11	01	50		428

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*b206	Δ^*6802	SIQ ID NO
ENV	LILGLVII	21	8	09	15						429
ENV	GLVICS	28	8	10	16						430
ENV	GMLMICS	28	8	12	19						431
ENV	QLYATVYA	34	8	01	50						432
ENV	WVTVYGV	46	8	58	91						433
ENV	TVYGVV	48	8	55	86						434
ENV	GVVWKEA	52	8	34	51						435
ENV	PVWKEATT	54	8	22	34						436
ENV	ATTLFCA	59	8	24	38						437
ENV	TLFCA	64	8	54	84						438
ENV	EVIINWAT	77	8	36	56						439
ENV	ATHACVPT	83	8	56	88						440
ENV	NVTENFNM	101	8	34	53						441
ENV	NMWRKNDMV	107	8	34	53						442
ENV	NMWRKNNMV	107	8	34	53						443
ENV	EQMIEDII	115	8	24	38						444
ENV	DQSLKPCV	126	8	50	78						445
ENV	SLKIPVYKL	128	8	55	86						446
ENV	KLTPLCVT	134	8	53	83						447
ENV	LTPLCVT	135	8	54	84						448
ENV	VTSTGNSA	161	8	01	20						449
ENV	ALFYKLDV	202	8	10	16						450
ENV	ALFYRLDV	202	8	12	19						451
ENV	NISWNNIT	217	8	01	33						452
ENV	LINCNTSA	237	8	17	27						453
ENV	NTSATIOA	241	8	14	22						454
ENV	NTSVITQA	241	8	13	20						455
ENV	ITQACPKV	245	8	37	58						456
ENV	PIPIIYCA	258	8	40	63						457
ENV	PIPIIYCT	258	8	18	28						458
ENV	PIIYCAPA	260	8	37	58						459
ENV	PIIYCTPA	260	8	18	28						460
ENV	CAPAGFAI	264	8	29	45						461
ENV	CTPAGFAI	264	8	10	16						462
ENV	GTGPKNV	281	8	17	27						463
ENV	NVSTVQCT	287	8	51	80						464
ENV	TVQCTIIGI	290	8	51	80						465
ENV	CTHIGIKPV	294	8	33	52						466
ENV	CTHIGIRPV	294	8	26	41						467
ENV	GIRPVST	297	8	26	41						468
ENV	GIRPVST	297	8	26	41						469
ENV	PVSTQLL	300	8	60	94						470
ENV	VVSTQLLL	301	8	60	94						471
ENV	QLLLNGSL	305	8	57	89						472
ENV	LLLLNGSL	306	8	55	86						473
ENV	SLAEEVV	311	8	14	22						474
ENV	LAREEVVI	312	8	13	20						475
ENV	IIRSENL	319	8	10	16						476
ENV	CTRPNNNT	345	8	29	45						477
ENV	NTRKSIRI	351	8	10	16						478

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	NTPSRV	376	8	01	33						479
ENV	TAGNSRA	376	8	01	33						480
ENV	IGDIRQA	377	8	30	49						481
ENV	MONGTNT	458	8	01	17						482
ENV	ITEGNITL	478	8	01	50						483
ENV	NITLPCRI	482	8	11	17						484
ENV	TITLPCRI	482	8	14	22						485
ENV	RIKQIINM	488	8	30	47						486
ENV	RIKQIVNM	488	8	12	19						487
ENV	IINMVQEV	492	8	17	27						488
ENV	WQEVGKAM	496	8	18	28						489
ENV	WQRVGQAM	496	8	11	17						490
ENV	EVGKAMYA	498	8	18	28						491
ENV	RVGQAMYA	498	8	10	16						492
ENV	KAMYAPPI	502	8	23	36						493
ENV	QAMYAPPI	502	8	14	22						494
ENV	KAMYAPPI	502	8	12	19						495
ENV	QIRCSSNI	512	8	11	17						496
ENV	NITGLILT	519	8	11	17						497
ENV	NITGLILT	519	8	35	55						498
ENV	ELYKYKVV	560	8	36	89						499
ENV	KVVKIEPL	565	8	25	39						500
ENV	KIEPLGVA	568	8	23	37						501
ENV	PTKAKRRV	576	8	22	34						502
ENV	VVEREKRA	588	8	32	50						503
ENV	VVQREKRA	588	8	17	27						504
ENV	VQREKRAV	589	8	17	27						505
ENV	RAVGIGAV	594	8	12	19						506
ENV	GALFLGFL	601	8	12	19						507
ENV	GAMFLGFL	601	8	13	20						508
ENV	GAVFLGFL	601	8	22	34						509
ENV	FLGFLGAA	604	8	48	75						510
ENV	FLGAAGST	608	8	55	86						511
ENV	AAGSTMGA	611	8	39	91						512
ENV	STMGAASI	614	8	39	61						513
ENV	TMGAASIT	615	8	39	61						514
ENV	GAASITLT	617	8	39	61						515
ENV	AASITLTV	618	8	36	56						516
ENV	SITLTVQA	620	8	32	50						517
ENV	LTVQARQL	623	8	38	59						518
ENV	TVQARQLL	624	8	36	56						519
ENV	ROLLSGIV	628	8	49	77						520
ENV	IVQQJNNL	634	8	26	41						521
ENV	IVQQJNNL	634	8	32	50						522
ENV	VQQQNNLL	635	8	26	41						523
ENV	VQQQNNLL	635	8	32	50						524
ENV	QNNLLRA	637	8	26	41						525
ENV	QSNLLRA	637	8	26	41						526
ENV	NLLRAIEA	640	8	51	80						527
ENV	AIEAQUIL	644	8	49	77						528

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
ENV	AQHLLKL	647	8	13	20						529
ENV	AQHLLQL	647	8	35	55						530
ENV	AQHMLQL	647	8	10	16						531
ENV	QHLLKLT	648	8	13	20						532
ENV	QHLLQLT	648	8	34	53						533
ENV	QHMLQLT	648	8	10	16						534
ENV	LQTVWGI	652	8	44	69						535
ENV	TVWGIKQL	655	8	59	92						536
ENV	QLQARVL	660	8	41	64						537
ENV	QLQARVLA	661	8	41	64						538
ENV	LQARVLAV	662	8	33	52						539
ENV	VLAVERYL	666	8	34	53						540
ENV	YKIDQQL	672	8	31	48	0.0001					541
ENV	YLRDQQL	672	8	18	28						542
ENV	KLICITAV	687	8	19	30						543
ENV	KLICITNV	687	8	17	27						544
ENV	KLICITTV	687	8	12	19						545
ENV	WMEVEREI	723	8	12	19						546
ENV	LLALDKWA	755	8	19	30						547
ENV	LLELDQWA	755	8	21	33						548
ENV	ALDKWASL	757	8	11	17						549
ENV	ELDKWASL	757	8	18	28						550
ENV	SLWNWFDI	763	8	17	27						551
ENV	ITKWLWYI	770	8	16	25						552
ENV	ITNWLWYI	770	8	19	30						553
ENV	YKIFIMI	776	8	43	67						554
ENV	FMIVGGL	780	8	44	69						555
ENV	IMIVGGLI	781	8	35	56						556
ENV	IVGCLIGL	783	8	42	66						557
ENV	IVGGLVGL	783	8	10	16						558
ENV	GLIGLRII	786	8	15	23						559
ENV	GLIGLRIV	786	8	32	50						560
ENV	GLRIIFAV	789	8	18	28						561
ENV	GLRIIFAV	789	8	29	45						562
ENV	IIFAVLSI	792	8	15	23						563
ENV	IVFAVLSI	792	8	20	31						564
ENV	VLSIVNRV	796	8	38	59						565
ENV	PLSFQTL	809	8	10	16						566
ENV	PLSFQTLT	809	8	13	20						567
ENV	GLDRPGGT	823	8	01	33						568
ENV	RLVNGFLA	844	8	13	20						569
ENV	RLVSGFLA	844	8	20	31						570
ENV	LVNGFLAL	845	8	14	22						571
ENV	LVSGFLAL	845	8	19	30						572
ENV	LALAWDDL	850	8	25	39						573
ENV	CLFSYIIRL	861	8	42	66						574
ENV	RLRDLILI	867	8	13	20	0.0001					575
ENV	IAARTVEL	874	8	12	19						576
ENV	AARTVELL	876	8	11	17						577
ENV	ELGLISSL	881	8	09	15						578

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	LQYWSQEL	907	8	16	25						579
ENV	QDELKNSA	911	8	12	19						580
ENV	SOELKNSA	911	8	12	19						581
ENV	SAVSLNA	917	8	11	17						582
ENV	AVSLLNAT	918	8	11	17						583
ENV	SLLNATAI	920	8	14	22						584
ENV	LLNATAIA	921	8	15	23						585
ENV	DTAIAVA	923	8	10	16						586
ENV	NATAIAVA	923	8	14	22						587
ENV	AIATAEET	926	8	32	50						588
ENV	VAEETDRI	929	8	19	30						589
ENV	VAEGTDRV	929	8	16	25						590
ENV	GTDRVIEV	932	8	11	17						591
ENV	ILLIIPRI	947	8	13	20						592
ENV	PIRIKQGL	951	8	12	19						593
ENV	ROGLERAL	955	8	35	55	0.0003					594
ENV	VIVYGVIV	47	9	55	86	0.0002					595
ENV	GVPWKAT	52	9	22	34	0.0002					596
ENV	PWKATTT	54	9	22	34	0.0002					597
ENV	EATTLFCA	58	9	24	38	0.0002					598
ENV	ITLFCASDA	61	9	52	81	0.0002					599
ENV	DAKAYDIEV	70	9	17	27	0.0002					600
ENV	DIEVINVWA	75	9	18	28	0.0001					601
ENV	NWATIACV	80	9	49	77	0.0002					602
ENV	WATIACVPT	82	9	56	88	0.0002					603
ENV	PTDPRQEL	89	9	25	39	0.0002					604
ENV	PTDPRQEV	89	9	21	33	0.0002					605
ENV	MVEQMIEDI	113	9	23	36	0.0002					606
ENV	QMIHDIUSL	116	9	29	45	0.0023					607
ENV	ISLWDQSL	121	9	38	59	0.0180					608
ENV	VSLWDQSL	121	9	10	16	0.0001					609
ENV	SLKPCVKLT	128	9	55	86	0.0002					610
ENV	CVKLTPLCV	132	9	55	86	0.0002					611
ENV	KLTLPLCVTL	134	9	52	81	0.0005					612
ENV	PLCVLLNCT	137	9	22	34	0.0005					613
ENV	IKNI'SFNI	181	9	13	20						614
ENV	ALFYRLDVV	202	9	11	17						615
ENV	VQNNHNSNT	218	9	01	20						616
ENV	RLNCNTSA	236	9	17	27						617
ENV	LINCHTSAI	237	9	15	23						618
ENV	AIQACPKV	244	9	13	20						619
ENV	VITQACPKV	244	9	15	23						620
ENV	KVSFERPI	252	9	30	47						621
ENV	CAPAGFAL	264	9	29	45	0.0001					622
ENV	STVQC'THGI	289	9	51	80	0.0001					623
ENV	CTHIGKPVV	294	9	32	50	0.0001					624
ENV	CTHIGRPVV	294	9	26	41	0.0001					625
ENV	PVSTQLLL	300	9	60	94	0.0001					626
ENV	TQLLNGSL	304	9	57	89	0.0001					627
ENV	QLLNGSLA	305	9	55	86	0.0001					628

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*0201	Λ^*0202	Λ^*0203	Λ^*0206	Λ^*6802	SEQ ID NO
ENV	SLAGEEVVI	311	9	13	20	0.0020					629
ENV	NAKTHVQL	329	9	14	22						630
ENV	ATGDHIGDI	369	9	12	19						631
ENV	DIIGDIKQA	372	9	12	19						632
ENV	ELIGDIRQA	372	9	09	15						633
ENV	GTAGHSSRA	375	9	01	33						634
ENV	NTSPRSRVA	376	9	01	33						635
ENV	TAGN'SSRAA	376	9	01	33						636
ENV	DIRQALICNI	380	9	15	23						637
ENV	DIRQALICNV	380	9	10	16						638
ENV	TLPCRIKQI	484	9	26	41						639
ENV	QINMWQEV	491	9	17	27						640
ENV	NMWQEVGKA	494	9	15	23	0.0026					641
ENV	QQAMYAPPI	501	9	14	22	0.0022					642
ENV	QQR'LSSNI	511	9	11	17						643
ENV	QIRC'SNIT	512	9	11	17	0.0001					644
ENV	NTETNKTTET	537	9	01	17						645
ENV	NTTGN'TTET	537	9	01	17						646
ENV	VVKU'PLGV	566	9	23	36						647
ENV	PLGVAPTKA	571	9	23	36	0.0001					648
ENV	PTKAKRRVV	576	9	22	34	0.0001					649
ENV	RVVEREKRA	587	9	32	50						650
ENV	RVVQREKRA	587	9	17	27	0.0001					651
ENV	VVERLEKRAV	588	9	25	39						652
ENV	VVQREKRAV	588	9	16	25						653
ENV	AVGIGAVFL	595	9	11	17						654
ENV	ALFLGFLGA	602	9	11	17						655
ENV	AMFLGFLGA	602	9	12	19	0.0050					656
ENV	AVFLGFLGA	602	9	19	30						657
ENV	FLGAAGSTM	608	9	55	86	0.0190					658
ENV	GAAGSTMGA	610	9	55	86	0.0009					659
ENV	AAGSTMGA	611	9	45	70	0.0001					660
ENV	STMGAASIT	614	9	39	61						661
ENV	TMGAASITL	615	9	39	61						662
ENV	GAASITLTV	617	9	36	56						663
ENV	TLTVQARQL	622	9	37	58						664
ENV	LTVQARQLL	623	9	36	56						665
ENV	QARQLLSGI	626	9	38	59						666
ENV	GIVQQNNL	633	9	26	41						667
ENV	GIVQQQSNL	633	9	32	50	0.0001					668
ENV	IVQQQNNL	634	9	26	41						669
ENV	IVQQQSNL	634	9	32	50	0.0001					670
ENV	QQQNNLLRA	636	9	25	39						671
ENV	QQQNNLLRA	636	9	26	41						672
ENV	QQNNLLRAI	637	9	26	41						673
ENV	QQNNLLRAI	637	9	26	41						674
ENV	RAIEAQIIL	643	9	45	70						675
ENV	ALAEQQIIL	644	9	48	75						676
ENV	EAQIILLKL	646	9	12	19						677
ENV	EAQIILLQL	646	9	35	56						678

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SFQ ID NO
ENV	AQIIILLKLT	647	9	13	20						679
ENV	AQIIILLQLT	647	9	34	53						680
ENV	AQIIIMQLT	647	9	10	16						681
ENV	QQIIIMQLTV	648	9	13	20						682
ENV	QQIIILQLTV	648	9	34	53						683
ENV	LLKLTVMGI	651	9	13	20						684
ENV	LLQLTVWGI	651	9	34	53	0.5100	0.0200	0.2300	0.1500	0.1620	685
ENV	MLQLTVWGI	651	9	10	16	0.2500					686
ENV	LTVWGIKQL	654	9	59	92	0.0001					687
ENV	GIKQLQARV	658	9	40	63	0.0001					688
ENV	KQLQARVLA	660	9	41	64						689
ENV	QLQARVLAV	661	9	33	52	0.0085					690
ENV	RLATERYL	665	9	33	52	0.0009					691
ENV	GIWGC'SGKL	680	9	48	75	0.0011					692
ENV	QOEKNEQDL	747	9	16	25						693
ENV	QOEKNEQEL	747	9	18	28						694
ENV	DLALDKWA	754	9	15	23	0.0002					695
ENV	ELLEDKWA	754	9	18	28						696
ENV	LALDKWASL	756	9	11	17						697
ENV	SLWNWFDIT	763	9	13	20						698
ENV	DLTNWLYI	769	9	10	16						699
ENV	WLWYKIFI	773	9	40	77	0.0360					700
ENV	YIKIFIMIV	776	9	39	61	0.0001					701
ENV	FIMIVGGI	780	9	35	55						702
ENV	MIVGSLIGL	782	9	36	56						703
ENV	LIGLRIIFA	787	9	16	25						704
ENV	LIGLRIIFA	787	9	21	33						705
ENV	GLRIIFAVL	789	9	17	27						706
ENV	GLRIIFAVL	789	9	28	44	0.0009					707
ENV	RIIFAVLSI	791	9	14	22						708
ENV	RIIFAVLSI	791	9	19	30	0.0002					709
ENV	IIFAVLSIV	792	9	15	23						710
ENV	IVFVLSIV	792	9	18	28						711
ENV	AVLSIVNRV	795	9	31	48	0.0012					712
ENV	RVRQGYSPL	802	9	55	86	0.0130					713
ENV	SIRLVNGFL	842	9	11	17	0.0005					714
ENV	SIRLVSGFL	842	9	13	20						715
ENV	RLVNGFLAL	844	9	12	19						716
ENV	RLVSGFLAL	844	9	19	30						717
ENV	LYSGFLALA	845	9	16	25						718
ENV	FLALAWDDL	849	9	25	39						719
ENV	LAWDDLRLS	852	9	20	31						720
ENV	LIAARTVEL	873	9	12	19						721
ENV	IAARTVELL	874	9	11	17						722
ENV	LLGRQWEA	882	9	10	16						723
ENV	GLRLGWEG	892	9	10	32						724
ENV	LLQYWSQEL	906	9	16	25						725
ENV	QOELKNSAI	911	9	12	19	0.0270					726
ENV	SOELKNSAV	911	9	10	16						727
ENV	ELKNSAINL	913	9	10	16						728

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 HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*0802	SEQ ID NO
ENV	ELKNSAISL	913	9	10	16						729
ENV	ELKNSAVSL	913	9	12	19						730
ENV	SAVSLLNAT	917	9	11	17	0.0001					731
ENV	AVSLLNAT	918	9	11	17						732
ENV	SLLNATAIA	920	9	14	22						733
ENV	LLNATAIAV	921	9	15	23						734
ENV	IAIAVAEGT	925	9	10	16						735
ENV	TAIAVAEGT	925	9	22	34						736
ENV	AVAEGTDRI	928	9	16	25	0.0008					737
ENV	AVAEGTDRV	928	9	14	22						738
ENV	VAEGTDRII	929	9	18	28						739
ENV	VAEGTDRVI	929	9	16	25	0.0001					740
ENV	AIHIIIPRI	946	9	12	19						741
ENV	RIQGLERA	953	9	34	53	0.0003					742
ENV	RQGLERALL	955	9	34	53						743
ENV	ILGLVICS	26	10	10	16						744
ENV	LLGLMLICS	26	10	10	16						745
ENV	QLYATVYAGV	34	10	01	50						746
ENV	KLWTVVYGV	44	10	11	17						747
ENV	NLWTVVYGV	44	10	34	54	0.0150					748
ENV	WTVVYGVYV	46	10	55	86	0.0160					749
ENV	GVFWKEATT	52	10	22	34	0.0009					750
ENV	PWKEATTTL	54	10	22	34	0.0001					751
ENV	KTLFCASDA	60	10	12	19	0.0003					752
ENV	ITTLFCASDA	60	10	24	38	0.0001					753
ENV	TLFCASIDAKA	64	10	46	72	0.0006					754
ENV	CASDAKAYDT	67	10	19	30	0.0001					755
ENV	KAYDTEVINV	72	10	17	27	0.0001					756
ENV	DTEVINRWAT	75	10	18	28	0.0013					757
ENV	EVINRWATIA	77	10	35	55	0.0001					758
ENV	PTDINIQEVV	89	10	13	20						759
ENV	NMVEQMIEDI	112	10	20	31	0.0001					760
ENV	MVEQMIEDII	113	10	23	36	0.0001					761
ENV	EQMIIEIISL	115	10	22	34						762
ENV	DIISLWDQSL	120	10	38	59	0.0001					763
ENV	DVISLWDQSL	120	10	10	16						764
ENV	DQSLKPCVKL	126	10	47	73						765
ENV	CVKLTPLCVT	132	10	53	83						766
ENV	STSNSSNST	159	10	01	50	0.0001					767
ENV	VTSTGNSAGT	161	10	01	20						768
ENV	EIKNCSFNT	181	10	12	19						769
ENV	SVQNNVNSNT	217	10	01	33						770
ENV	RLINCNTSAI	236	10	15	24						771
ENV	LINCNTSAIT	237	10	14	22						772
ENV	SAITQACPKV	243	10	13	20						773
ENV	SVITQACPKV	243	10	15	23						774
ENV	PIPIHYCAFA	258	10	36	56	0.0002					775
ENV	PIPIHYCTPA	258	10	18	28						776
ENV	GTGFCINVT	281	10	12	19						777
ENV	CTNVSTVQCT	285	10	13	20						778

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*0802	SI:Q ID NO
ENV	VQCTIIGIKIV	292	10	32	50						779
ENV	VQCTIIGIRIV	292	10	25	39						780
ENV	GIRPVSTQL	297	10	33	52						781
ENV	GIRPVSTQL	297	10	26	41	0.0002					782
ENV	STQLLNGSL	303	10	57	89	0.0001					783
ENV	TQLLLNGSL	304	10	55	86						784
ENV	RIIGVQTFYA	357	10	10	16						785
ENV	GIGVQTFYA	360	10	01	33						786
ENV	SIGSGQAFYV	360	10	01	33						787
ENV	YATGDIIGDI	368	10	11	17						788
ENV	GTAGNSSKAA	375	10	01	33						789
ENV	MQNGTNTIST	438	10	01	17						790
ENV	NANITPCRI	478	10	01	50						791
ENV	ITLPCRKIQI	483	10	25	39						792
ENV	TLPCRKIQI	484	10	15	23						793
ENV	TLPCRKIQIV	484	10	10	16						794
ENV	KQINNIWQIEV	490	10	17	27						795
ENV	NMWQIEVGKAM	494	10	15	23	0.0004					796
ENV	WQEVGKAMYA	496	10	18	28						797
ENV	WQRYGQAMYA	496	10	10	16						798
ENV	QQRCSNIT	511	10	11	17						799
ENV	EIFRPGGGDM	544	10	17	27	0.0001					800
ENV	ETFRPGGGDM	544	10	21	33	0.0001					801
ENV	DMRDNRWSEL	552	10	37	58						802
ENV	ELYKYKVVEI	560	10	13	21						803
ENV	ELYKYKVVKI	560	10	29	46						804
ENV	KVKIEPLGV	565	10	23	36						805
ENV	VVKIEPLGVA	566	10	23	36						806
ENV	KIEPLVAPT	568	10	23	37						807
ENV	VAPTKAKRV	574	10	17	27	0.0001					808
ENV	STRTHREKRA	586	10	01	50						809
ENV	RVVEREKRAV	587	10	25	39						810
ENV	RVVQREKRAV	587	10	16	25						811
ENV	RAVGIGAVFL	594	10	11	17						812
ENV	GIGAVFLGFL	598	10	11	18						813
ENV	MLGAMFLGFL	599	10	04	36						814
ENV	TIGAMFLGFL	599	10	03	27						815
ENV	GALFLGFLGA	601	10	11	17	0.0003					816
ENV	GAMFLGFLGA	601	10	12	19						817
ENV	GAFLGFLGA	601	10	19	30						818
ENV	AMFLGFLGAA	602	10	11	17						819
ENV	AMFLGFLGAA	602	10	12	19	0.5000					820
ENV	AVFLGFLGAA	602	10	19	30						821
ENV	GAAGSTMGA	610	10	42	66						822
ENV	STMGAASITL	614	10	39	61	0.0004					823
ENV	TMGAASITLT	615	10	39	61						824
ENV	AASITLTVQA	618	10	28	44						825
ENV	ITLTVQARQL	621	10	27	42						826
ENV	ITLTVQARQL	622	10	35	55						827
ENV	VQARQLLSGI	625	10	36	56						828

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SI:Q ID NO
ENV	QARQLLSGIV	626	10	38	59						829
ENV	GIVQQQNLL	633	10	26	41	0.0402					830
ENV	GIVQQSNLL	633	10	32	50						831
ENV	VQQQNLLRA	635	10	25	39						832
ENV	VQQSNLLRA	635	10	26	41						833
ENV	QQQNLLRAI	636	10	25	39						834
ENV	QQSNLLRAI	636	10	26	41						835
ENV	RAIEAQQIILL	643	10	44	69						836
ENV	EAQQIILLKLT	646	10	12	19						837
ENV	EAQQIILLQLT	646	10	34	54						838
ENV	AQQIILLKLT	647	10	13	20						839
ENV	AQQIILLQLTV	647	10	34	53						840
ENV	ILLKLT'VWGI	650	10	13	20						841
ENV	ILLQLTVWGI	650	10	34	53						842
ENV	KLT'VWGIKQL	653	10	13	20						843
ENV	QLTVWGIKQL	653	10	44	69	0.0015					844
ENV	'VWGIKQLQA	655	10	49	77	0.0150					845
ENV	GIKQLQARVL	658	10	40	63	0.0002					846
ENV	KQLQARVLAV	660	10	33	52						847
ENV	YKIDQQLLGI	672	10	27	42						848
ENV	YLRDXQLLGI	672	10	18	28						849
ENV	GIWGLSGKLI	680	10	48	75	0.0004					850
ENV	MTWMEWIERI	721	10	12	19						851
ENV	NOQKNEQDL	746	10	13	20						852
ENV	NOQKNEQEL	746	10	15	23						853
ENV	QKQKNEQDL	747	10	16	25						854
ENV	QKQKHEQEL	747	10	18	28						855
ENV	LLALDKWASL	755	10	11	17						856
ENV	LELDK'WASL	755	10	18	28	0.0024					857
ENV	WASLW'WFDI	761	10	17	27						858
ENV	ITKWLWYIKI	770	10	15	23						859
ENV	ITRWLWYIKI	770	10	14	22	0.0002					860
ENV	WLWYIKIFIM	773	10	43	67	0.0001					861
ENV	KIFIMVGGI	778	10	38	59	0.0003					862
ENV	IMIVCGILGI	781	10	34	54						863
ENV	IVGGILGLRI	783	10	42	66						864
ENV	GLIGLRIIFA	786	10	15	23						865
ENV	GLIGLRIVFA	786	10	21	33						866
ENV	LIGLRIFAV	787	10	16	25						867
ENV	LIGLRIVFAV	787	10	21	33						868
ENV	RIFAVLSIV	791	10	14	22						869
ENV	RIVFAVLSIV	791	10	17	27	0.0007					870
ENV	FAVLSIVNRV	794	10	31	48	0.0002					871
ENV	SIRLVSGFLA	842	10	12	19						872
ENV	RLVSGFLALA	844	10	16	25						873
ENV	ALAWIDLRSL	851	10	19	30						874
ENV	NLCLEFYIIRL	859	10	11	17						875
ENV	SLCLEFYIIRL	859	10	31	48						876
ENV	LIAARTVELL	873	10	11	17						877
ENV	ELLGRQWEA	881	10	10	16						878

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IIIY A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	LLCRRGWEL	882	10	09	15						879
ENV	RLCWEGKYL	894	10	09	29						880
ENV	NLLQYWSQEL	905	10	16	25	0.0059					881
ENV	ELKNSAVSLL	913	10	10	16						882
ENV	SAVSLINATA	917	10	11	17						883
ENV	AVSLLNATAI	918	10	11	17						884
ENV	SLLNATAIAV	920	10	14	22	0.0650	0.0074	0.0390	0.0640	0.0390	885
ENV	LLNATAIAVA	921	10	14	22	0.0740					886
ENV	ATAIAVAEGT	924	10	14	22						887
ENV	IAVAEGTDRI	927	10	16	25						888
ENV	IAVAEGTDRV	927	10	14	22	0.0001					889
ENV	AVAEGTDRII	928	10	15	23	0.0004					890
ENV	AVAEGTDRVI	928	10	14	22						891
ENV	RAIIHPRRI	945	10	12	19						892
ENV	HIIPRRIRQIL	949	10	13	21						893
ENV	NIPRRIRQGL	949	10	11	17						894
ENV	RIRQGLERAL	953	10	34	53						895
ENV	LILGLVICS	21	11	09	15	0.0001					896
ENV	KQLYATVYSGV	34	11	01	50						897
ENV	GVRVWKEATT	52	11	22	34						898
ENV	ATTLFCASDA	59	11	23	36						899
ENV	ITLFCASDAKA	61	11	44	69						900
ENV	NVWATIIACVPT	80	11	25	39						901
ENV	CVPTDIPNQEI	87	11	25	39						902
ENV	CVPTDIPNQEIV	87	11	21	33						903
ENV	ITDIPNQEIVL	89	11	12	19						904
ENV	NMWKNHNVIEQM	107	11	30	47						905
ENV	NMVEQMIIEHII	112	11	20	31						906
ENV	SLWDOSLKPCV	123	11	47	75						907
ENV	DQSLKPCVKLT	126	11	47	73						908
ENV	SLKPCVKLTPL	128	11	54	84						909
ENV	CVKLTPLCVTL	132	11	52	81						910
ENV	LTPLCVTLNLT	135	11	22	34						911
ENV	EIKNCSFNIT	181	11	11	17						912
ENV	RLNCHTSAT	236	11	14	22						913
ENV	QACPKVSEFI	248	11	30	47						914
ENV	PIIYCAPAGFA	260	11	27	42						915
ENV	PIIYCTPAGFA	260	11	10	16						916
ENV	GTGICKNVSTV	281	11	12	19						917
ENV	NVSTVQCTIIGI	287	11	51	80						918
ENV	TVQCTIIGIKPV	290	11	28	44						919
ENV	TVQCTIIGIRPV	290	11	22	34						920
ENV	VQCTHIGIKPVV	292	11	31	48						921
ENV	VQCTHIGIRPVV	292	11	25	39						922
ENV	CTHIGIKPVVST	294	11	32	50						923
ENV	CTHIGIRPVST	294	11	26	41						924
ENV	GIRPVVSTQLL	297	11	33	52						925
ENV	GIRPVVSTQLL	297	11	26	41						926
ENV	STQLLLNGSLA	303	11	55	86						927
ENV	LLNOSIAEEV	307	11	16	25						928

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SEQ ID NO
ENV	EINCTRPNNNT	342	11	10	16						929
ENV	RIGFGQTFYAT	357	11	10	16						930
ENV	GIGFGQTFYAT	360	11	01	33						931
ENV	SIGSQAFYVT	360	11	01	33						932
ENV	EMITNYTSDT	458	11	01	17						933
ENV	NITLPCRIKQI	482	11	11	17						934
ENV	TITLPCRIKQI	482	11	13	20						935
ENV	ITLPCRIKQI	483	11	15	23						936
ENV	IINMWQEVGKA	492	11	12	19						937
ENV	EVGKAMYAPPI	498	11	18	28						938
ENV	RVQQAMYAPPI	498	11	10	16						939
ENV	QIRCSSNITGL	512	11	11	17						940
ENV	KVVKIEPLQVA	565	11	23	36						941
ENV	GVAPTAKRRRV	573	11	17	27						942
ENV	VAPTAKRRRV	574	11	17	27						943
ENV	NHITPIREKRA	586	11	01	50						944
ENV	STRTIIREKRAV	586	11	01	50						945
ENV	VVEREKRAVGI	588	11	11	17						946
ENV	GALFLGFLGAA	601	11	601	17						947
ENV	GAMFLGFLGAA	601	11	12	19						948
ENV	GAVFLGFLGAA	601	11	19	30						949
ENV	FLGFLGAAAGST	604	11	48	75						950
ENV	FLGAAAGSTMGA	608	11	55	86						951
ENV	AAGSTMGAASI	611	11	34	53						952
ENV	STMGAASITLT	614	11	39	61						953
ENV	TMGAASITLT	615	11	36	56						954
ENV	GAASHILTVOA	617	11	28	44						955
ENV	SITLTVOARQL	620	11	27	42						956
ENV	ITLTVOARQL	621	11	27	42						957
ENV	TVQARQLLSGI	624	11	36	56						958
ENV	VQARQLLSGIV	625	11	36	56						959
ENV	IVQQQINLLRA	634	11	23	39						960
ENV	IVQQQINLLRA	634	11	26	41						961
ENV	VQQQINLLRAI	635	11	25	39						962
ENV	VQQQINLLRAI	635	11	26	41						963
ENV	QQNNLLRAIEA	637	11	26	41						964
ENV	QQNNLLRAIEA	637	11	23	36						965
ENV	LLRAIEAQHILL	641	11	45	70						966
ENV	AIEAQHILLKL	644	11	12	19						967
ENV	AIEAQHILLQL	644	11	35	55						968
ENV	EAQHIILLKLT	646	11	12	19						969
ENV	EAQHIILLKLT	646	11	34	54						970
ENV	LQTVWGKQL	652	11	44	69						971
ENV	LTVWGKQLQA	654	11	49	77						972
ENV	GIKQLQARVLA	658	11	40	63						973
ENV	QARVLAVERYL	663	11	33	52						974
ENV	AVERYLKDQQL	668	11	23	36						975
ENV	AVERYLKDQQL	668	11	11	17						976
ENV	LLGIWGCCKL	678	11	46	72						977
ENV	NMTWMEWEREI	720	11	12	19						978

Table VIII
 HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	NQKEKNEQDLL	746	11	13	20						979
ENV	NQKEKNEQELL	746	11	13	23						980
ENV	EQKEKNEQDLLA	747	11	16	25						981
ENV	EQDLLALDKWA	752	11	12	19						982
ENV	EQELLEDKWA	752	11	11	17						983
ENV	ELLELDKWASL	754	11	15	23						984
ENV	WASLWNVFDIT	761	11	13	20						985
ENV	WLWYIKIFIM	773	11	43	67						986
ENV	KIFIMIVGGLI	778	11	31	48						987
ENV	FIMIVGGLIGL	780	11	34	53						988
ENV	MIVGGLIGLRI	782	11	36	56						989
ENV	IVGGLIGLRII	783	11	12	19						990
ENV	IVGGLIGLRIV	783	11	30	47						991
ENV	GLIGLRIFAV	786	11	15	23						992
ENV	GLIGLRIFAV	786	11	21	33						993
ENV	LIGLRIFAVL	787	11	15	23						994
ENV	LIGLRIFAVL	787	11	20	31						995
ENV	GLRIIFAVLSI	789	11	14	22						996
ENV	GLRIIFAVLSI	789	11	19	30						997
ENV	RQGYSPLSFQT	804	11	45	70						998
ENV	SIRLVSQFLAL	842	11	11	17						999
ENV	LALAWDDLKSL	850	11	19	30						1000
ENV	LAWDDLKSLCL	852	11	20	31						1001
ENV	CLFSYIIRLRL	861	11	20	31						1002
ENV	ELLRGREGWEAL	881	11	09	15						1003
ENV	SOELKNSAVSL	911	11	10	16						1004
ENV	SAVSLNATAI	917	11	11	17						1005
ENV	AVSLNATAIA	918	11	11	17						1006
ENV	SLLNATAIAVA	920	11	13	20						1007
ENV	NATAIAVAEGT	923	11	13	20						1008
ENV	AIATAVAEGTDRI	926	11	16	25						1009
ENV	IAVAEGTDRI	927	11	14	22						1010
ENV	IAVAEGTDRI	927	11	15	23						1011
ENV	PIRIKQGLERKA	951	11	14	22						1012
ENV	RIKQGLERALL	953	11	11	17						1013
GAG	SVLSGGEL	6	8	33	52						1014
GAG	SVLSGGKL	6	8	28	44						1015
GAG	KLDKWEKI	12	8	18	28						1016
GAG	KLDKWEKI	12	8	10	16						1017
GAG	DAWEKIRL	14	8	10	16						1018
GAG	KLKHIWVA	31	8	17	27						1019
GAG	RLKILVWA	31	8	13	20						1020
GAG	IWVASREL	35	8	21	27						1021
GAG	LWVASREL	35	8	33	56						1022
GAG	FALNPGLL	46	8	22	34						1023
GAG	FAVNPGLL	46	8	22	34						1024
GAG	QLQFALQT	65	8	16	25						1025
GAG	QLQPSLQT	65	8	17	27						1026
GAG	LQTCSEEL	70	8	15	23						1027
GAG			8	17	27						1028

0.2700

Table VIII
HIV Δ92 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SEQ ID NO
GAG	GTEELRSL	73	8	12	19						1029
GAG	ELRSLYNT	76	8	17	27						1030
GAG	SLFNIVAT	79	8	16	25						1031
GAG	SLNIVAT	79	8	22	34						1032
GAG	TVATLYCV	83	8	41	64						1033
GAG	DVKIDTKEA	95	8	11	17						1034
GAG	EYKDTKEA	95	8	22	34						1035
GAG	AQQAADT	119	8	10	16						1036
GAG	AQQAADT	132	8	01	33						1037
GAG	KVSNYPI	148	8	15	27						1038
GAG	QVSNYPI	148	8	27	48						1039
GAG	VQNAQQQM	156	8	21	33						1040
GAG	VQNLQQQM	156	8	29	45						1041
GAG	QGMVHIQAI	161	8	28	44						1042
GAG	IQALSPRT	165	8	29	45						1043
GAG	IQALSPRT	165	8	11	17						1044
GAG	QALSPRTL	166	8	29	45						1045
GAG	QALSPRTL	166	8	11	17						1046
GAG	TLNAWVKV	172	8	61	95						1047
GAG	KAFSPVI	183	8	50	78						1048
GAG	EVIIMPFA	188	8	46	72						1049
GAG	EVIIMPFA	188	8	14	22						1050
GAG	VIIIMPFA	189	8	46	72						1051
GAG	VIIIMPFA	189	8	14	22						1052
GAG	FTALSEGA	193	8	15	23						1053
GAG	SALSEGAT	194	8	44	69						1054
GAG	TALSEGAT	194	8	15	23						1055
GAG	ATPQDLNM	200	8	12	19						1056
GAG	ATPQDLNT	200	8	42	66						1057
GAG	PQDLNMML	202	8	12	19						1058
GAG	PQDLNTML	202	8	43	67						1059
GAG	DLNMMLNI	204	8	12	19						1060
GAG	DLNTMLNT	204	8	44	69						1061
GAG	NIVGGIIQA	210	8	12	19						1062
GAG	NTVGGIIQA	210	8	47	73						1063
GAG	IVGGIIQAA	211	8	12	19						1064
GAG	TVGGIIQAA	211	8	47	73						1065
GAG	HQAAMQML	215	8	61	95						1066
GAG	AMQNLKDT	218	8	33	52						1067
GAG	AMQNLKET	218	8	26	41						1068
GAG	MQMLKDTI	219	8	33	52						1069
GAG	MQMLKETI	219	8	26	41						1070
GAG	DTINSEAA	224	8	33	52						1071
GAG	ETINSEAA	224	8	22	34						1072
GAG	EAAEWDR	229	8	39	61						1073
GAG	EAAEWDRV	229	8	15	23						1074
GAG	PVHAGPIA	238	8	19	30						1075
GAG	DIAGTTST	256	8	55	86						1076
GAG	IAGTTSTL	257	8	48	75						1077
GAG	STLQEQA	262	8	12	19						1078

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^{\circ}201$	$\Delta^{\circ}202$	$\Delta^{\circ}203$	$\Delta^{\circ}206$	$\Delta^{\circ}602$	SEQ ID NO
GAG	LQEQIAWM	264	8	14	22						1079
GAG	LQEQIGWM	264	8	29	45						1080
GAG	WMTNNPPI	270	8	20	31						1081
GAG	WMTSNPPI	270	8	16	25						1082
GAG	DIYKRWII	284	8	17	27						1083
GAG	EIYKRWII	284	8	39	61						1084
GAG	ILGLNKI	290	8	57	89						1085
GAG	ILGLNKIV	291	8	58	91						1086
GAG	GLNKIVIM	293	8	60	94						1087
GAG	IVRMYSPT	297	8	15	23						1088
GAG	IVRMYSPT	297	8	42	66						1089
GAG	RMYSPTSII	299	8	14	22						1090
GAG	RMYSPTSL	299	8	40	63						1091
GAG	YVDRFFKT	320	8	28	44						1092
GAG	YVDRFFKT	320	8	28	44						1093
GAG	YVDRFFKT	320	8	28	44						1094
GAG	YVDRFFKT	320	8	28	44						1095
GAG	YVDRFFKT	320	8	28	44						1096
GAG	YVDRFFKT	320	8	28	44						1097
GAG	YVDRFFKT	320	8	28	44						1098
GAG	YVDRFFKT	320	8	28	44						1099
GAG	YVDRFFKT	320	8	28	44						1100
GAG	YVDRFFKT	320	8	28	44						1101
GAG	YVDRFFKT	320	8	28	44						1102
GAG	YVDRFFKT	320	8	28	44						1103
GAG	YVDRFFKT	320	8	28	44						1104
GAG	YVDRFFKT	320	8	28	44						1105
GAG	YVDRFFKT	320	8	28	44						1106
GAG	YVDRFFKT	320	8	28	44						1107
GAG	YVDRFFKT	320	8	28	44						1108
GAG	YVDRFFKT	320	8	28	44						1109
GAG	YVDRFFKT	320	8	28	44						1110
GAG	YVDRFFKT	320	8	28	44						1111
GAG	YVDRFFKT	320	8	28	44						1112
GAG	YVDRFFKT	320	8	28	44						1113
GAG	YVDRFFKT	320	8	28	44						1114
GAG	YVDRFFKT	320	8	28	44						1115
GAG	YVDRFFKT	320	8	28	44						1116
GAG	YVDRFFKT	320	8	28	44						1117
GAG	YVDRFFKT	320	8	28	44						1118
GAG	YVDRFFKT	320	8	28	44						1119
GAG	YVDRFFKT	320	8	28	44						1120
GAG	YVDRFFKT	320	8	28	44						1121
GAG	YVDRFFKT	320	8	28	44						1122
GAG	YVDRFFKT	320	8	28	44						1123
GAG	YVDRFFKT	320	8	28	44						1124
GAG	YVDRFFKT	320	8	28	44						1125
GAG	YVDRFFKT	320	8	28	44						1126
GAG	YVDRFFKT	320	8	28	44						1127
GAG	YVDRFFKT	320	8	28	44						1128

Table VIII
 HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6R02	SEQ ID NO
GAG	PLSLKSL	548	8	15	23						1129
GAG	PLTSLKSL	548	8	12	19						1130
GAG	PLTSLRSL	548	8	12	19						1131
GAG	SLFGNDPL	554	8	12	19						1132
GAG	SLFGSDPL	554	8	11	17						1133
GAG	VLSGGIKLDA	7	9	15	23						1134
GAG	HLVWASREL	34	9	21	33						1135
GAG	HLVWASREL	34	9	36	56						1136
GAG	ALNPGILET	47	9	19	30						1137
GAG	AVNPGILET	47	9	14	22						1138
GAG	ETSEGICRQI	54	9	16	25						1139
GAG	ILGQIQPSL	62	9	11	17						1140
GAG	GQLQPSLOT	64	9	11	17						1141
GAG	LQPAIQTGT	66	9	14	22						1142
GAG	SLOTISEEL	69	9	14	22						1143
GAG	ELRSLYNTV	76	9	15	23						1144
GAG	SLFNTVATL	79	9	16	25	0.0037					1145
GAG	SLYNTVATL	79	9	22	34	0.0053				0.0004	1146
GAG	NTVATLYCV	82	9	41	64						1147
GAG	TYLCVHQI	86	9	12	19						1148
GAG	TYLCVHQRI	86	9	15	23						1149
GAG	IQRIEYKDT	91	9	10	16						1150
GAG	DKDTKEAL	95	9	11	17						1151
GAG	EVKDTKEAL	95	9	20	31						1152
GAG	DTKEALDKI	98	9	32	50						1153
GAG	DTKEALEKI	98	9	10	16						1154
GAG	EONKSKKKA	109	9	17	27						1155
GAG	KAQQAADT	118	9	10	16						1156
GAG	QVSNQYPI	146	9	22	44						1157
GAG	KVSNQYPIV	148	9	15	27						1158
GAG	QVSNQYPIV	148	9	27	48						1159
GAG	IVQNAQQQM	155	9	21	33	0.0001					1160
GAG	IVQNLQQQM	155	9	29	45						1161
GAG	VQNAQQQM	156	9	14	22						1162
GAG	VQNLQQQM	156	9	29	45						1163
GAG	QVQNAQQQM	159	9	12	19						1164
GAG	LQQQNVIIQA	159	9	21	33						1165
GAG	IQALSPRTL	165	9	29	45						1166
GAG	IQALSPRTL	165	9	11	17						1167
GAG	ALSPRTLNA	167	9	29	45						1168
GAG	ALSPRTLNA	167	9	10	16						1169
GAG	RTLNAWVKV	171	9	61	95	0.0012					1170
GAG	TLNAWVKVI	172	9	30	47	0.0032					1171
GAG	TLNAWVKV	172	9	31	48	0.0005					1172
GAG	WVKVIEKA	176	9	25	39						1173
GAG	WVKVIEKA	176	9	28	44						1174
GAG	EVIMFSAI	188	9	46	72	0.0001					1175
GAG	EVIMFSAI	188	9	14	22						1176
GAG	FTALSEGAT	191	9	15	23						1177
GAG	GATPQDLNM	199	9	12	19						1178

[illegible]

Table VIII
 HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	Nn. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6R02	SEQ ID NO
GAG	AATLEEMMT	364	9	16	25						1229
GAG	GASLEEMMT	364	9	10	16						1230
GAG	GATLEEMMT	364	9	28	44						1231
GAG	ATLEEMMTA	365	9	46	72						1232
GAG	EMMTACQGV	369	9	59	58	0.0006					1233
GAG	GVGGPGIKA	376	9	37	36						1234
GAG	GVGGPSIIKA	376	9	23	36						1235
GAG	KARVLAEM	383	9	57	89						1236
GAG	VLAEMSQV	386	9	16	25						1237
GAG	VLAEMSQV	386	9	33	52	0.1100					1238
GAG	LAEAMSVT	387	9	23	37						1239
GAG	AMSQVNSA	390	9	11	17						1240
GAG	CTERQANFL	459	9	55	87						1241
GAG	QANFLGKI	465	9	56	88						1242
GAG	FLQNIPEPT	486	9	10	16						1243
GAG	FLQNIPEPT	486	9	28	44	0.0110	0.0004	0.3100	0.0002	0.0130	1244
GAG	LQNIPEPTA	487	9	10	16						1245
GAG	LOSHPEPTA	487	9	28	44						1246
GAG	PAEPTAIPA	492	9	01	50						1247
GAG	KQEPIDKEL	531	9	12	19						1248
GAG	MDKELYPL	534	9	12	19						1249
GAG	KQEPIDKEL	535	9	01	25						1250
GAG	KQETIDKDL	535	9	01	25						1251
GAG	MDKELYPL	538	9	01	25						1252
GAG	TIDKILYPL	538	9	01	25						1253
GAG	RASVLSGGEL	4	10	11	17						1254
GAG	RASVLSGGKL	4	10	28	44						1255
GAG	SVLSGGKLDA	6	10	15	23						1256
GAG	KLDWWEKIRL	12	10	16	25						1257
GAG	KLDKWEKIRL	12	10	10	16						1258
GAG	WASRELERFA	37	10	44	69						1259
GAG	FALNPGLEET	46	10	18	28						1260
GAG	FAVNPGLLET	46	10	14	22						1261
GAG	ETSEGCROIL	54	10	14	22						1262
GAG	QILGQLQPSL	61	10	11	17						1263
GAG	QLQPALQTGT	65	10	14	22						1264
GAG	QTGSEELKSL	71	10	12	19						1265
GAG	ELSLYNTVA	76	10	15	23						1266
GAG	ATLYCVIIQRI	85	10	12	19						1267
GAG	ATLYCVIIQRI	85	10	15	23						1268
GAG	RIEVKDTKEA	93	10	13	20						1269
GAG	GAAATDSNI	123	10	01	50						1270
GAG	AAGTGNSQV	130	10	01	50						1271
GAG	SONYQNTIV	146	10	22	44						1272
GAG	SONYPIVQNA	150	10	22	34						1273
GAG	SONYPIVQNL	150	10	30	47						1274
GAG	PIVQNAQQQM	154	10	21	33						1275
GAG	PIVQNAQQQM	154	10	29	45						1276
GAG	IVQNAQQQMV	155	10	14	22						1277
GAG	IVQNLQQQMV	155	10	29	45						1278

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
GAG	NAQQQMVIQA	158	10	12	19						1279
GAG	NLQQQMVIQA	158	10	21	33						1280
GAG	LQQQMVIQA	159	10	15	23						1281
GAG	MVIQAISPRT	163	10	27	42						1282
GAG	QALSPRTLNA	166	10	29	45						1283
GAG	QALSPRTLNA	166	10	10	16						1284
GAG	RTLNAWVKV	171	10	30	47						1285
GAG	RTLNAWVKV	171	10	31	48						1286
GAG	KAESPEVPM	183	10	50	78	0.0003					1287
GAG	PMFSALSEGA	191	10	45	70						1288
GAG	PMFTALSEGA	191	10	15	23						1289
GAG	GATPQDLNMM	199	10	12	19						1290
GAG	GATPQDLNMM	199	10	42	66						1291
GAG	ATPQDLNMM	200	10	12	19						1292
GAG	ATPQDLNMM	200	10	42	66						1293
GAG	PQDLNMM	202	10	11	17						1294
GAG	PQDLNMM	202	10	43	67						1295
GAG	MLNIVGGIQA	208	10	12	19						1296
GAG	MLNIVGGIQA	208	10	47	73	0.0022					1297
GAG	NIVGGIQAAM	210	10	12	19						1298
GAG	NIVGGIQAAM	210	10	47	73						1299
GAG	QAAMQMLKDT	216	10	33	52						1300
GAG	QAAMQMLKET	216	10	26	41						1301
GAG	QAAMQMLKET	217	10	33	52						1302
GAG	QAAMQMLKET	217	10	26	41						1303
GAG	AAEQMLKET	221	10	32	50						1304
GAG	MLKDTINEEA	221	10	22	34						1305
GAG	MLKDTINEEA	221	10	34	53						1306
GAG	AAEQDRVIIPV	230	10	14	22						1307
GAG	AAEQDRVIIPV	230	10	22	34						1308
GAG	RLIIPVIAQPI	235	10	14	22						1309
GAG	RVIIIPVIAQPI	235	10	18	28						1310
GAG	IIAGPIAPGQM	240	10	17	27						1311
GAG	IIAGPIAPGQM	240	10	44	69						1312
GAG	QMRPIPGSDI	248	10	45	70						1313
GAG	QMRPIPGSDI	248	10	11	17						1314
GAG	TTSTLQEQIA	260	10	12	19						1315
GAG	STLQEQIAWM	262	10	27	42						1316
GAG	STLQEQIAWM	262	10	12	19						1317
GAG	TLQEQIAWMT	263	10	27	42						1318
GAG	TLQEQIAWMT	263	10	20	31	0.0510	0.0014	0.5900	0.0002	0.0180	1319
GAG	WMTNHPPIPV	270	10	16	25						1320
GAG	WMTNHPPIPV	270	10	01	50						1321
GAG	GANSIPVGD	276	10	17	27						1322
GAG	PVGDIIYKRWI	281	10	40	63						1323
GAG	PVGDIIYKRWI	281	10	57	89	0.0009					1324
GAG	WIIGLNKIV	289	10	57	89	0.0010					1325
GAG	ILGLNKIVRM	291	10	14	22						1326
GAG	IVRMYSPTS	297	10	40	63						1327
GAG	IVRMYSPTS	297	10	11	17						1328
GAG	QASQEVKNWM	332	10	11	17						1329

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*0802	SEQ ID NO
GAG	QATQDVKNWM	332	10	15	23						1329
GAG	QATQEVKNWM	332	10	18	28						1330
GAG	ATQDVKNWMT	333	10	15	23						1331
GAG	ATQEVKNWMT	333	10	18	28						1332
GAG	QVKNWMTDTL	336	10	12	19						1333
GAG	QVKNWMTETL	336	10	11	17						1334
GAG	EVKNWMTETL	336	10	25	39						1335
GAG	MTDTLLVQNA	341	10	22	34						1336
GAG	MTETLLVQNA	341	10	36	56						1337
GAG	VQNANPDCKT	347	10	45	70						1338
GAG	NANPDCKSIL	349	10	11	17						1339
GAG	NANPDCKTIL	349	10	45	70						1340
GAG	KTILKALGPA	355	10	16	25						1341
GAG	TILKALGPAA	356	10	16	25						1342
GAG	TILRALGPAA	356	10	13	20						1343
GAG	ILKALGPAAT	357	10	16	25						1344
GAG	PAATLEEMMT	363	10	16	25						1345
GAG	AAATLEEMMTA	364	10	16	25						1346
GAG	GATLEEMMTA	364	10	10	16						1347
GAG	RVLAIEAMSQA	385	10	28	44						1348
GAG	RVLAIEAMSOV	385	10	33	52	0.0058					1349
GAG	VLAIEAMSOVT	386	10	20	31						1350
GAG	EAMSOVTNSA	389	10	11	17						1351
GAG	AMSQVTSNAT	390	10	10	16						1352
GAG	QMKDCTERQA	455	10	49	77						1353
GAG	FLQNRPEPTA	486	10	10	16						1354
GAG	FLQSRPEPTA	486	10	28	44						1355
GAG	PAESFRFEET	511	10	02	67						1356
GAG	THSQKQEPH	522	10	09	45						1357
GAG	ETIDKDLVPL	537	10	01	25						1358
GAG	PIDKELYPLT	538	10	01	25	0.0013					1359
GAG	RTENSLYPL	538	10	01	25						1360
GAG	TIDKDLVPLA	538	10	01	25						1361
GAG	WASRELERFAL	37	11	22	34						1362
GAG	WASRELERFV	37	11	17	27						1363
GAG	ELERFALNPGL	42	11	14	22						1364
GAG	ELERFVNPGL	42	11	15	23						1365
GAG	LLTSEGCROI	52	11	16	25						1366
GAG	RQILGQLQPSL	60	11	11	17						1367
GAG	LQTGSEELKSL	70	11	11	17						1368
GAG	ELRSLYNTVAT	76	11	13	20						1369
GAG	VATLYCVIQQI	84	11	12	19						1370
GAG	VATLYCVIQRH	84	11	15	23						1371
GAG	RIEVKDTKEAL	93	11	12	19						1372
GAG	PVQNAQQGMV	154	11	14	22						1373
GAG	PVQNLQGMV	154	11	29	45						1374
GAG	NLQGMVVIQAI	158	11	15	23						1375
GAG	QMVIIQAISPR	162	11	27	42						1376
GAG	QMVIIQAISPR	163	11	27	42						1377
GAG	QMVIIQAISPR	163	11	27	42						1378

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SHQ ID NO
GAG	IIQASPRTLNA	165	11	29	45						1379
GAG	IIQALSPTLNA	165	11	10	16						1380
GAG	ALSPRTLNAWV	167	11	29	45						1381
GAG	ALSPRTLNAWV	167	11	10	16						1382
GAG	NAWVKVVEEKA	174	11	25	39						1383
GAG	NAWVKVVEEKA	174	11	27	42						1384
GAG	VIEKAFSEV	179	11	20	31						1385
GAG	VVEEKAFSEV	179	11	28	44						1386
GAG	PMFSALSEGAT	191	11	44	69						1387
GAG	PMFTALSEGAT	191	11	15	23						1388
GAG	ALSEGATPQDL	195	11	58	91						1389
GAG	GATPQDLNML	199	11	12	19						1390
GAG	GATPQDLNML	199	11	42	66						1391
GAG	PQDLNMLNIV	202	11	11	17						1392
GAG	PQDLNMLNIV	202	11	41	64						1393
GAG	MLNIVGGIIQA	207	11	12	19						1394
GAG	MLNIVGGIIQA	207	11	43	67						1395
GAG	MLNIVGGIIQA	208	11	12	19						1396
GAG	MLNIVGGIIQA	208	11	47	73						1397
GAG	IVGGIIQAAMQM	211	11	11	17						1398
GAG	TVGGIIQAAMQM	211	11	47	73						1399
GAG	IIQAAMQMLKDT	215	11	33	52						1400
GAG	IIQAAMQMLKDT	215	11	26	41						1401
GAG	QAAMQMLKDTI	216	11	33	52						1402
GAG	QAAMQMLKDTI	216	11	26	41						1403
GAG	QMLKDTINEEA	220	11	32	50						1404
GAG	QMLKDTINEEA	220	11	22	34						1405
GAG	MLKDTINEEA	221	11	32	50						1406
GAG	MLKDTINEEA	221	11	22	34						1407
GAG	EAAEWDRLIIPV	229	11	34	53						1408
GAG	EAAEWDRVIIPV	229	11	14	22						1409
GAG	RLIIPVIAAGPIA	235	11	15	23						1410
GAG	QMREIRGSDI	247	11	44	69						1411
GAG	QMREIRGSDIA	248	11	44	69						1412
GAG	GTTSLQEQIA	259	11	11	17						1413
GAG	GTTSLQEQIAMT	262	11	12	19						1414
GAG	STLQEQIGWMT	262	11	27	42						1415
GAG	QIGWMTNPPH	267	11	18	29						1416
GAG	QIGWMTNPPH	267	11	10	16						1417
GAG	PVGDIYKRWII	281	11	17	27						1418
GAG	PVGDIYKRWII	281	11	39	61						1419
GAG	DIYKRWIIIGL	284	11	17	27						1420
GAG	EIYKRWIIIGL	284	11	37	58						1421
GAG	IILGNKIVRM	290	11	56	88						1422
GAG	KIVRMYSPTSI	296	11	14	22						1423
GAG	KIVRMYSPTSI	296	11	39	61						1424
GAG	IVRMYSPTSIL	297	11	14	22						1425
GAG	IVRMYSPTSIL	297	11	40	63						1426
GAG	RMYSPTSILDI	299	11	13	20						1427
GAG	RMYSPTSILDI	299	11	38	59						1428

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6R02	SI:Q ID NO
GAG	YVDRFFKTLRA	320	11	27	42						1429
GAG	YVDRFFKTLRA	320	11	28	44						1430
GAG	TLRAEQASQEV	327	11	12	19						1431
GAG	TLRAEQATQDV	327	11	11	17						1432
GAG	TLRAEQATQEV	327	11	24	38						1433
GAG	EQASQEVKNWM	331	11	11	17						1434
GAG	EQATQDVKNWM	331	11	15	23						1435
GAG	EQATQEVKNWM	331	11	18	28						1436
GAG	QASQEVKNWMT	332	11	11	17						1437
GAG	QATQDVKNWMT	332	11	15	23						1438
GAG	QATQEVKNWMT	332	11	18	28						1439
GAG	QSEVKNWMTET	334	11	11	17						1440
GAG	TQDVKNWMTDT	334	11	11	17						1441
GAG	TQEVKNWMTET	334	11	14	22						1442
GAG	QVKNWMTDTLL	336	11	12	19						1443
GAG	DVKNWMTETLL	336	11	11	17						1444
GAG	EVKNWMTETLL	336	11	25	39						1445
GAG	WMTDTLLVQNA	340	11	22	34						1446
GAG	WMTETLLVQNA	340	11	35	55						1447
GAG	LVQNAVPDCKT	346	11	45	70						1448
GAG	VQNAVPDCKSI	347	11	10	16						1449
GAG	VQNAVPDCKTI	347	11	45	70						1450
GAG	KTILKALGPA	355	11	16	25						1451
GAG	KTILKALGPA	355	11	13	20						1452
GAG	TILKALGPAAT	356	11	16	25						1453
GAG	ILKALGPAATL	357	11	16	25						1454
GAG	ALGPAATLEEM	360	11	16	25						1455
GAG	ALGPAATLEEM	360	11	17	27						1456
GAG	PAATLEEMMTA	363	11	16	25						1457
GAG	COGVGGPGHIKA	374	11	36	56						1458
GAG	COGVGGPGSIKA	374	11	23	36						1459
GAG	GVGGPGSIKARV	376	11	36	56						1460
GAG	GVGGPGSIKARV	376	11	19	30						1461
GAG	RVLAEMSQVT	385	11	20	31						1462
GAG	FAMSOVTNSAT	389	11	10	16						1463
GAG	SAQQDLKGGYT	393	11	01	50						1464
GAG	TAQQDLKGGYT	393	11	01	50						1465
GAG	IQMKDCTERQA	454	11	49	77						1466
GAG	PAEPTAPPAEI	492	11	01	50						1467
GAG	PAESFRFEET	511	11	02	67						1468
GAG	SQKQEPIDKEL	529	11	09	15						1469
GAG	ETIDKIDLYPLA	537	11	01	25						1470
GAG	RTENSLYPPLT	538	11	01	25						1471
GAG	SLKSLFGNDPL	551	11	12	19						1472
NEF	RAQAEPAA	32	8	01	17						1473
NEF	AAAEPA	33	8	01	17						1474
NEF	PAADGVGA	41	8	15	23						1475
NEF	PAADGVGA	41	8	21	33						1476
NEF	AADGVGAV	42	8	11	18						1477
NEF	AAEGVGAA	42	8	10	16						1478

Table VIII
 HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SI:Q ID NO
NEF	ALEGVGAV	42	8	17	28						1479
NEF	DLEKIGAI	57	8	14	22						1480
NEF	GAITSSNT	62	8	32	50						1481
NEF	GALTSSNT	62	8	10	16						1482
NEF	AITSSNTA	63	8	27	42						1483
NEF	ITSSNTAA	64	8	15	23						1484
NEF	AATNADCA	70	8	12	22						1485
NEF	EAQEEVEV	82	8	16	25						1486
NEF	PVRQVPL	95	8	48	75						1487
NEF	POVPLRIM	99	8	56	88						1488
NEF	QVPLRPMT	100	8	57	89	0.0001					1489
NEF	ALDLSHFL	111	8	11	17						1490
NEF	AVDLSHFL	111	8	15	23						1491
NEF	FLKEKGGL	117	8	56	88						1492
NEF	SQKRQDIL	177	8	12	19						1493
NEF	QTEPAAVGV	32	9	01	17						1494
NEF	RAEPAADGV	32	9	01	17						1495
NEF	RAQAEPAAA	32	9	01	17						1496
NEF	RTEPAAVGV	32	9	01	17						1497
NEF	QAEPAAEV	33	9	01	17						1498
NEF	QAPTAAGV	33	9	01	17						1499
NEF	QAEPAAGV	34	9	01	33						1500
NEF	PAADGVGV	41	9	11	17						1501
NEF	PAEGVGAV	41	9	12	19						1502
NEF	GVGAASQDL	45	9	11	17						1503
NEF	GVGAASQDL	45	9	21	33						1504
NEF	GVGAVSRDL	45	9	17	17						1505
NEF	DLEKIIGAIT	57	9	14	22						1506
NEF	GAITSSNTA	62	9	27	42						1507
NEF	AITSSNTAA	63	9	14	22						1508
NEF	ITSSNTAAT	64	9	13	20						1509
NEF	TAATNADCA	69	9	12	19						1510
NEF	ATNALCAWL	71	9	12	22						1511
NEF	NACCAWLEA	73	9	17	27						1512
NEF	QVPLRPMT	99	9	56	88						1513
NEF	PLRPMTYKA	102	9	21	33						1514
NEF	MTYKGAIDL	106	9	12	19						1515
NEF	GAFDLSFFL	110	9	10	16						1516
NEF	RQDILDWV	182	9	20	31						1517
NEF	RQDILDWV	182	9	35	55						1518
NEF	ILDWVYIIT	186	9	34	53						1519
NEF	ILDWVYNT	186	9	19	30						1520
NEF	LTFGWCFKL	221	9	39	61	0.1400	0.1300	0.0022	0.0180	7.2000	1521
NEF	LVPVDPREV	229	9	11	17						1522
NEF	KQAEPAEGV	32	10	01	17						1523
NEF	RQAPTAAGV	32	10	01	17						1524
NEF	AQAEPAAGV	33	10	01	17						1525
NEF	GAITSSNTAA	62	10	14	22						1526
NEF	AITSSNTAAT	63	10	13	20						1527
NEF	NTAATNADCA	68	10	12	19						1528

Table VIII
IIIY A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6R02	SEQ ID NO
NEF	AATNADCAWL	70	10	12	22						1529
NEF	WLEAQEELEV	79	10	15	24						1530
NEF	EVGFVRPQV	91	10	40	63						1531
NEF	PLRPMYKAA	102	10	20	31						1532
NEF	PLRPMYKGA	102	10	25	39						1533
NEF	PMTYKGAIDL	105	10	12	19						1534
NEF	LYSKKRQEI	174	10	18	28						1535
NEF	SQKRQDIDL	177	10	12	19						1536
NEF	DILDLVYIIT	185	10	12	19						1537
NEF	EILDLVYIIT	185	10	22	34						1538
NEF	EILDLVYIIT	185	10	11	17						1539
NEF	WQNYTPGPGI	204	10	18	29						1540
NEF	WQNYTPGPGT	204	10	21	33						1541
NEF	WQNYTPGPGV	204	10	11	17						1542
NEF	PLTFGWCFKL	219	10	39	61	0.0350	0.0058	0.0021	0.0010	0.8400	1543
NEF	LTFGWCFKL	221	10	35	55	0.0170	0.0880	0.0540	0.0640	6.5000	1544
NEF	KLVPDPRV	228	10	11	17						1545
NEF	LLIIPMSQIOM	257	10	10	16						1546
NEF	LLIIPMSQIOM	257	10	12	19						1547
NEF	QTEPAAVGVGA	32	11	01	17						1548
NEF	RAEPAAAGVGA	32	11	01	17						1549
NEF	RAEPAAAGVGA	32	11	01	17						1550
NEF	RTEPAAVGVGA	32	11	01	17						1551
NEF	QAEPAAGVGA	33	11	01	17						1552
NEF	QAPTAAGVGA	33	11	01	17						1553
NEF	QAEPAAGVGA	34	11	01	33						1554
NEF	AVSRDLEKIGA	48	11	11	17						1555
NEF	GAITSNTAAT	62	11	13	20						1556
NEF	ITSSNTAATNA	64	11	12	19						1557
NEF	TAATNADCAWL	69	11	12	22						1558
NEF	ATNADCAWLEA	71	11	12	22						1559
NEF	AQEEEGVGFV	83	11	17	27						1560
NEF	PVRQVPLRPM	95	11	47	73						1561
NEF	QVPLRPMYKA	100	11	20	31						1562
NEF	FLKEKGIGLGL	117	11	26	41						1563
NEF	FLKEKGIGLGL	117	11	29	45						1564
NEF	GLYSKKRQEI	173	11	18	28						1565
NEF	LYSKKRQEI	174	11	18	28						1566
NEF	YTPGNGIRYPL	207	11	16	25						1567
NEF	YTPGNGIRYPL	207	11	13	20						1568
NEF	PLTFGWCFKL	219	11	35	55						1569
NEF	CLLIIPMSQIOM	256	11	10	16						1570
POL	LAFQJGEA	6	8	12	19						1571
POL	LAFQJGEA	6	8	12	19						1572
POL	LAFQJGEA	6	8	16	25						1573
POL	QTRANSPT	21	8	28	45						1574
POL	PTRELQV	30	8	14	22						1575
POL	QTRANSPT	35	8	01	33						1576
POL	PTRELQV	36	8	01	33						1577
POL	GADRQGV	70	8	01	20						1578

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	GTLCNQI	80	8	01	33						1579
POL	PTFNFOI	80	8	01	33						1580
POL	ITLWQRIL	90	8	47	73						1581
POL	TLWQRILV	91	8	49	77						1582
POL	WQRPLVTI	93	8	21	33						1583
POL	WQRPLVTV	93	8	19	30						1584
POL	TIKIGQI	99	8	17	27						1585
POL	TVKIGGQL	99	8	11	17						1586
POL	GQIEALL	104	8	10	16						1587
POL	GQIEALL	104	8	34	53						1588
POL	LIEALLDT	106	8	10	16						1589
POL	EALLDTGA	108	8	61	95						1590
POL	DTGADDTV	112	8	63	98						1591
POL	TVLFDINL	118	8	13	20						1592
POL	TVLEENL	118	8	15	23						1593
POL	GIGGFIK	136	8	64	100						1594
POL	KVRQYDIQI	142	8	41	64						1595
POL	ROYDQILI	144	8	20	31						1596
POL	ROYDQIPI	144	8	13	20						1597
POL	EICGHKAI	152	8	19	30						1598
POL	EICGKKAI	152	8	24	38						1599
POL	KAGIVLV	157	8	48	75						1600
POL	GTVLVGIT	160	8	60	94						1601
POL	VLVGITPV	162	8	53	83						1602
POL	NIIGHNLL	170	8	26	41						1603
POL	NIIGHNML	170	8	31	48						1604
POL	IIGHNLLT	171	8	26	41						1605
POL	IIGHNMLT	171	8	30	47						1606
POL	LLTQIGCT	176	8	21	33						1607
POL	MLTQIGCT	176	8	18	28						1608
POL	MLTQLOCT	176	8	10	16						1609
POL	LTQIGCTL	177	8	42	66						1610
POL	LTQLGCTL	177	8	15	23						1611
POL	PISMETV	187	8	57	89						1612
POL	PVKLKPGM	195	8	56	88						1613
POL	KVKQWPLT	207	8	49	77						1614
POL	LTEEKIKA	213	8	56	88						1615
POL	KIKALTEI	217	8	28	44						1616
POL	KIKALVEI	217	8	15	23						1617
POL	KALTEICT	219	8	12	19						1618
POL	KALVEICT	219	8	15	24						1619
POL	LVEICTEM	221	8	15	24						1620
POL	EMEKEGKI	229	8	42	66						1621
POL	AIKKKDDST	251	8	59	92						1622
POL	STKWRKLV	257	8	59	92						1623
POL	KLVDREL	262	8	63	98						1624
POL	RTQDFWEV	272	8	55	86						1625
POL	QLGPHIPA	280	8	56	89						1626
POL	GIPHIPAGL	282	8	56	89						1627
POL	GLKKKKSV	288	8	52	81						1628

Table VIII
 HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SI:Q 113 NO
POL	TVLDVGDGDA	296	8	58	91						1629
POL	DAYFSVPL	302	8	55	86						1630
POL	TAFTIPSI	317	8	37	58						1631
POL	TAFTIPST	317	8	13	20						1632
POL	GIRYQYNY	330	8	52	81						1633
POL	PAIFQSSM	346	8	42	66						1634
POL	AIFFQSSMT	347	8	39	61						1635
POL	FQSSWTKI	349	8	38	59						1636
POL	KQNDIVI	362	8	14	22						1637
POL	DIVYQYM	366	8	18	28						1638
POL	EIVYQYM	366	8	24	38						1639
POL	DLYVGSDL	375	8	63	98						1640
POL	YVGSDEI	377	8	58	91						1641
POL	ILLKRWGFT	397	8	22	34						1642
POL	ILLRWGFT	397	8	25	39						1643
POL	LLKRWGFTT	398	8	23	36						1644
POL	LLRWGFTT	398	8	24	38						1645
POL	IQKEPPEL	410	8	62	97						1646
POL	FLWMGYEL	416	8	64	100						1647
POL	ELIPDKWT	422	8	60	94						1648
POL	WTVQPIQL	428	8	28	44						1649
POL	WTVQPIVL	428	8	13	20						1650
POL	TVNDIQKL	442	8	62	97						1651
POL	IQKLVGKL	446	8	62	97						1652
POL	LVGKLNWA	449	8	61	95						1653
POL	KLNWASQI	452	8	61	95						1654
POL	QIYAGIKV	458	8	27	43						1655
POL	QIYPIKIV	458	8	27	43						1656
POL	KVKOLCKL	464	8	29	45						1657
POL	KVRQLCKL	464	8	19	30						1658
POL	KLRGAKA	470	8	25	40						1659
POL	KLRGTGA	470	8	24	38						1660
POL	LLRGAKAL	471	8	30	47						1661
POL	LLRGTKAL	471	8	24	38						1662
POL	GAKALTDI	474	8	25	39						1663
POL	GTKALTEV	474	8	19	30						1664
POL	ALTDIVPL	477	8	21	33						1665
POL	ALTEVIPL	477	8	16	25						1666
POL	LTDIVPLT	478	8	23	36						1667
POL	LTEVIPLT	478	8	16	25						1668
POL	IVPLTEEA	481	8	13	20						1669
POL	VIPLTEEA	481	8	11	17						1670
POL	PLTEEAEL	483	8	30	47						1671
POL	ELAENREI	491	8	57	89						1672
POL	LAENREIL	492	8	57	89						1673
POL	KQGQDQWT	523	8	15	23						1674
POL	KQGQGWWT	523	8	25	39						1675
POL	YQEPFKNL	534	8	43	67						1676
POL	NLKTGKYA	540	8	58	92						1677
POL	KTGKYAKM	542	8	19	30						1678

Table VIII

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Lambda^{\circ}0201$	$\Lambda^{\circ}0202$	$\Lambda^{\circ}0203$	$\Lambda^{\circ}0206$	$\Lambda^{\circ}6802$	SFQ ID NO
POL	KTGKYARM	542	8	13	21						1679
POL	RTATINDV	550	8	11	17						1680
POL	IITNDVKQL	553	8	49	77						1681
POL	DKVQLTEA	556	8	33	52						1682
POL	LTEAVOKI	560	8	34	53						1683
POL	EAVQKIAT	562	8	11	17						1684
POL	KIATESIV	566	8	14	22						1685
POL	IATESIVI	567	8	14	22						1686
POL	SIVIWGKT	571	8	42	66						1687
POL	KLHQKET	582	8	20	31						1688
POL	RLHQKET	582	8	26	41						1689
POL	IQKETWEA	585	8	15	23						1690
POL	IQKETWET	585	8	27	42						1691
POL	ETWEAWWT	588	8	11	17						1692
POL	ETWETWWT	588	8	22	34						1693
POL	WTDEYWQAT	594	8	15	23						1694
POL	WTDEYWQAT	594	8	24	38						1695
POL	WIPEWEFV	602	8	52	84						1696
POL	FVNTPLPV	608	8	54	86						1697
POL	NTPLPLVKL	610	8	57	89						1698
POL	LVKLWYQL	614	8	58	91						1699
POL	KLWYQLET	616	8	12	19						1700
POL	YQLEKDPH	619	8	14	22						1701
POL	YQLEKEPH	619	8	31	48						1702
POL	YQLETEPI	619	8	11	17						1703
POL	QLEKEPHV	620	8	16	25						1704
POL	ETFYVDGA	630	8	55	86						1705
POL	AANRETKL	637	8	30	47						1706
POL	KLKGAGYV	643	8	36	56						1707
POL	RQKVVSILT	655	8	19	30						1708
POL	KVVSILTET	657	8	11	17						1709
POL	VVSLTDIT	658	8	10	16						1710
POL	VVSLTETT	658	8	11	17						1711
POL	TTNQKTEL	664	8	55	86						1712
POL	NQKTELHA	666	8	12	19						1713
POL	NQKTELQA	666	8	42	66						1714
POL	ELQAIHLA	670	8	16	25						1715
POL	ELQAIYLA	670	8	12	19						1716
POL	LQAIHLAL	671	8	16	25						1717
POL	LQAIYLLAL	671	8	12	19						1718
POL	LALQDSGL	676	8	27	42						1719
POL	LQDSGLEV	678	8	27	42						1720
POL	LQDSQSEV	678	8	25	39						1721
POL	GLEVNIIVT	682	8	26	41						1722
POL	IVTDSQYA	687	8	61	95						1723
POL	VTDQSYAL	688	8	59	92						1724
POL	SQYALGHI	691	8	59	92						1725
POL	YALGHIQA	693	8	58	91						1726
POL	NQIEQLI	711	8	24	38						1727
POL	SQIEQLI	711	8	20	31						1728

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SEQ ID NO
POL	QLIKKEKV	716	8	28	44						1729
POL	WVPATIKGI	727	8	63	98						1730
POL	GIGGNEQV	733	8	59	92						1731
POL	QVDKLVSA	739	8	16	25						1732
POL	SAGIRKVL	745	8	15	23						1733
POL	GIRKVLFL	747	8	51	80						1734
POL	KVLFLDGI	750	8	50	78						1735
POL	FLDGIDKA	753	8	55	86						1736
POL	AMASDFNL	773	8	45	70						1737
POL	PIVAKEIV	782	8	26	41						1738
POL	PVVAKEIV	782	8	28	44						1739
POL	IVAKEIVA	783	8	26	41						1740
POL	VVAKEIVA	783	8	31	48						1741
POL	COLKGEAM	795	8	53	83						1742
POL	QVIX:SPGI	805	8	57	89						1743
POL	GIWQLDCT	811	8	59	92						1744
POL	WQLDCTIIL	813	8	61	95						1745
POL	CTHILEGKI	817	8	35	55						1746
POL	CTHILEGKV	817	8	26	41						1747
POL	IILEGKIIL	819	8	31	48						1748
POL	IILEGKVIL	819	8	23	36						1749
POL	IILVAVIIV	824	8	30	47						1750
POL	VILVAVIIV	824	8	24	38						1751
POL	ILVAVIIVA	825	8	54	84						1752
POL	VASGVILEA	831	8	52	81						1753
POL	PAETGQET	842	8	58	91						1754
POL	GOETAYFI	846	8	31	48						1755
POL	GOETAYFL	846	8	26	41						1756
POL	TAYTILKL	849	8	32	50						1757
POL	TAYFLLKL	849	8	27	42						1758
POL	KLGRWIV	855	8	59	92						1759
POL	FTSAAVKA	873	8	28	44						1760
POL	FTSTTVKA	873	8	14	22						1761
POL	AACW:WAGI	880	8	32	50						1762
POL	GIKCFEFGI	886	8	22	34						1763
POL	GIQCFEFGI	886	8	11	17						1764
POL	SQGVVESM	899	8	53	83						1765
POL	DQAEILKT	919	8	46	72						1766
POL	EQAEILKT	919	8	13	20						1767
POL	QAEILKTA	920	8	59	92						1768
POL	IILKTAVQM	923	8	57	89						1769
POL	KTAVQMAV	925	8	57	89						1770
POL	AVQMAVEI	927	8	60	94						1771
POL	RIDIIAT	951	8	29	45						1772
POL	RIVDIIAT	951	8	12	19						1773
POL	IASDIQT	955	8	15	23						1774
POL	IATDIQT	955	8	41	64						1775
POL	LQKQIKI	965	8	13	20						1776
POL	LQKQITKI	965	8	36	56						1777
POL	LLWKGEKA	993	8	62	97						1778

Table VII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SEQ ID NO
POL	VIQINSID	1003	8	37	58						1779
POL	VIQINSEI	1003	8	12	19						1780
POL	KVVIIRKA	1011	8	52	81						1781
POL	KVVIIRKV	1011	8	11	17						1782
POL	QMAIGDCV	1027	8	44	69						1783
POL	MAGIDCVV	1028	8	44	69						1784
POL	NLAFFQGEA	5	9	10	16						1785
POL	NLAFFQGEA	5	9	16	25						1786
POL	EQTRANSPT	20	9	26	41						1787
POL	SQTRANSPT	34	9	01	33						1788
POL	QTRANSPTT	35	9	01	33						1789
POL	EAGADROGT	64	9	10	16						1790
POL	GQRQGVSL	69	9	01	17						1791
POL	GTTLNFQI	79	9	01	17						1792
POL	ASLSLPQI	80	9	01	33						1793
POL	GTLNCTQIT	80	9	01	33						1794
POL	PTFNFPQIT	80	9	01	33						1795
POL	QTLWQRLP	89	9	47	73						1796
POL	ITLWQRLPV	90	9	47	73						1797
POL	TLWQRLPV	91	9	39	61	0.0185	0.0002	0.0040	0.0002	0.0140	1798
POL	VTKIGGQI	98	9	17	27						1799
POL	VTVKIGGQI	98	9	11	17						1800
POL	KIGGQIKIA	101	9	23	36						1801
POL	QLIEALLDT	105	9	10	16						1802
POL	QLKEALLDT	105	9	34	53						1803
POL	LLDTGADDT	110	9	63	98						1804
POL	DTGADDTVL	112	9	61	95						1805
POL	DTVLEDINL	117	9	13	20						1806
POL	ITVLEIENL	117	9	14	22						1807
POL	MIGGIGGH	133	9	62	97	0.0025					1808
POL	KVRQYDQIL	142	9	21	33	0.0001					1809
POL	LIEICGIIKA	150	9	10	16						1810
POL	LIEICGKKA	150	9	13	20						1811
POL	TVLVGPTPV	161	9	53	83						1812
POL	LVGPTPVNI	163	9	54	84	0.0047	0.0280	0.5200	0.0013	0.5900	1813
POL	PVNIIGRNL	168	9	26	41	0.0110					1814
POL	PVNIIGRNM	168	9	24	38	0.0001					1815
POL	NIIGRNLIT	170	9	26	41						1816
POL	NIIGRNLIT	170	9	30	47						1817
POL	NLLTQIGCT	175	9	21	33						1818
POL	NMLTQIGCT	175	9	18	28						1819
POL	NMLTQIGCT	175	9	10	16						1820
POL	LLTQIGCTL	176	9	21	33	0.0002					1821
POL	MLTQIGCTL	176	9	18	28						1822
POL	MLTQIGCTL	176	9	10	16						1823
POL	TLNFPISPI	183	9	61	97						1824
POL	PIETVPVKL	190	9	53	83	0.0660	0.0029	9.1000	0.0019	0.7000	1825
POL	PLTEEKIKAL	212	9	54	84	0.0001					1826
POL	LTEEKIKAL	213	9	56	88						1827
POL	ALVEICTEM	220	9	15	23	0.0230	0.0230	0.0710	0.0140	0.0140	1828

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*0802	SI:Q ID NO
POL	FAIKKKDST	250	9	59	92						1829
POL	TQDFWEVOL	273	9	55	86						1830
POL	VQLGIPHPA	279	9	54	84						1831
POL	GLKKKKSVT	288	9	49	77						1832
POL	VTVLIVGDA	295	9	57	89						1833
POL	DVGDAYFSV	299	9	54	84	0.0005					1834
POL	YTAFTIPSI	316	9	37	58	0.1910	0.7100	1.1000	0.5300	2.4000	1835
POL	YTAFTIPST	316	9	13	20						1836
POL	TIPSINNET	320	9	37	58						1837
POL	TIPSTNET	320	9	14	22						1838
POL	SINNETPGI	323	9	32	50						1839
POL	STNNETIGI	323	9	11	17						1840
POL	GIRYQYNVL	330	9	52	81	0.0001					1841
POL	PQGWKGSFA	339	9	59	92						1842
POL	PAIFCSSMT	346	9	39	61						1843
POL	FQSSMTKIL	349	9	38	59						1844
POL	VYQYMDL	368	9	51	80	0.0004					1845
POL	YQYMDLLV	370	9	61	95						1846
POL	DLEIGHIRA	381	9	28	44						1847
POL	DLFICQIRT	381	9	21	33						1848
POL	EIGQIRAKI	383	9	26	41						1849
POL	EIGQIRTKI	383	9	21	33						1850
POL	KIEELREHL	390	9	19	30						1851
POL	KIEELRQIL	390	9	17	27	0.0001					1852
POL	HLLKVGFTT	397	9	22	34						1853
POL	HLLRWGFTT	397	9	24	38						1854
POL	ELHDPKWT	422	9	60	94	0.0001					1855
POL	QLPEKDSWT	434	9	13	20						1856
POL	VLPEKDSWT	434	9	13	20						1857
POL	WTVNDIQKL	441	9	62	97	0.0001					1858
POL	TVNDIQKLV	442	9	61	95	0.0001					1859
POL	DIQKLVGKL	445	9	62	97	0.0001					1860
POL	KLVGGLNWA	448	9	61	95	0.0001					1861
POL	WASQIVAGI	455	9	27	42	0.0840	0.3400	1.7000	0.0930	0.0130	1862
POL	WASQIVPGI	455	9	29	45	0.0020					1863
POL	SQIYAGIKV	457	9	27	42						1864
POL	SQIYIGIKV	457	9	27	42						1865
POL	YAGIK:VKQL	460	9	18	28						1866
POL	KVKQLCKLL	464	9	28	44						1867
POL	KVRQ:CKLL	464	9	19	30						1868
POL	QLCKILRGA	467	9	25	39						1869
POL	QLCKILRGT	467	9	21	33						1870
POL	KLLRGAKAL	470	9	25	40	0.0069					1871
POL	KLLRGTKAL	470	9	24	38						1872
POL	LLRGAKALT	471	9	30	47						1873
POL	LLRGTKALT	471	9	24	38						1874
POL	GAKALDIV	474	9	24	38						1875
POL	GKALTEVI	474	9	11	17						1876
POL	KALTDIVPL	476	9	21	33						1877
POL	KALTEVIPL	476	9	16	25						1878

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SI:Q ID NO
POL	ALTDIVPLT	477	9	21	33						1879
POL	ALTEVPLT	477	9	16	25						1880
POL	DIVPLTEEA	480	9	13	20						1881
POL	EVPLTEEA	480	9	11	17						1882
POL	LTTEAELEL	484	9	37	58						1883
POL	ELAEAREIL	491	9	57	89						1884
POL	ILKEPVIQV	498	9	41	64	0.0001					1885
POL	GDQWYIQI	525	9	13	20	0.0055					1886
POL	GQWYIQI	525	9	25	39						1887
POL	YAKMRTAIT	546	9	10	16						1888
POL	YAKMRTAIT	546	9	13	20						1889
POL	ITNDYKQLT	553	9	43	67						1890
POL	DKQLTEAV	556	9	33	52						1891
POL	OLTEAVQKI	559	9	34	53	0.0001					1892
POL	LTEAYQKIA	560	9	26	41	0.0007					1893
POL	VQKIATISI	564	9	14	22						1894
POL	KIATESIVI	566	9	14	22						1895
POL	KTPKFRLLP	577	9	17	27						1896
POL	KTPKFRLLP	577	9	29	45						1897
POL	PIQKETWEA	584	9	15	23						1898
POL	PIQKETWET	584	9	27	42						1899
POL	PLVKLWYQL	613	9	54	84	0.0002					1900
POL	YQLEKEPIV	619	9	16	25						1901
POL	IVGAETFYV	626	9	28	44	0.0099					1902
POL	ETFYVDGAA	630	9	51	80						1903
POL	GAANRETKL	636	9	30	47						1904
POL	KLGRAGYVT	643	9	36	56						1905
POL	VTDGRQKV	650	9	30	47	0.0012					1906
POL	KVSLTETT	657	9	11	17						1907
POL	LYDTTNQKT	661	9	19	30						1908
POL	LYDTTNQKT	661	9	25	39						1909
POL	DTTNQKT	663	9	26	41						1910
POL	ETTNQKT	663	9	29	45						1911
POL	NQKTELHAI	666	9	12	19						1912
POL	NQKTELQAI	666	9	42	66						1913
POL	KTELQAIIL	668	9	15	23						1914
POL	KTELQAIYL	668	9	12	19						1915
POL	ELQAIILAL	670	9	16	25	0.0001					1916
POL	ELQAIYLAL	670	9	12	19						1917
POL	IILALQDSGL	675	9	15	23						1918
POL	ALQDSGLEV	677	9	27	42	0.0005					1919
POL	ALQDSGSEV	677	9	25	39	0.0083					1920
POL	NIVTDSQYA	686	9	61	95						1921
POL	IVTDSQYAL	687	9	59	92	0.0024					1922
POL	LVNQIIEQL	709	9	19	30						1923
POL	LVNQIIEQL	709	9	19	30						1924
POL	EQLKKEKV	715	9	28	44						1925
POL	LIKKEKYYL	717	9	35	55						1926
POL	KVYLAWVPA	722	9	20	32	0.0001					1927
POL	KVYLSWVPA	722	9	23	37						1928

Table VIII
 LUV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*0802	SEQ ID NO
POL	EQVDKLYSA	738	9	16	25						1929
POL	LVSAGIRKV	743	9	15	23	0.0001					1930
POL	LVSSGIRKV	743	9	26	41						1931
POL	RAMASDFNL	772	9	41	64	0.0230	0.0370	0.0004	0.0710	0.0130	1932
POL	PIVAKELVA	782	9	25	39						1933
POL	PVYAKEIVA	782	9	28	44						1934
POL	VASCDKRCQL	789	9	43	67						1935
POL	GOVDCSPGI	804	9	57	89						1936
POL	CTHLEGGKII	817	9	35	55						1937
POL	CTHLEGGKVI	817	9	26	41						1938
POL	IILEGKILV	819	9	31	48	0.0010					1939
POL	IILEGKIVLV	819	9	23	36	0.0006					1940
POL	KILVAVHV	823	9	30	47	0.0007					1941
POL	KVILVAVIIV	823	9	23	36	0.0001					1942
POL	ILVAVIIVA	824	9	30	47						1943
POL	VILVAVIIVA	824	9	23	36						1944
POL	AVIVASGYI	828	9	53	83						1945
POL	IIVASGYIEA	830	9	52	81						1946
POL	YIEAEVIPA	835	9	53	83						1947
POL	EAEVIPAET	837	9	62	98						1948
POL	PAETQGETA	842	9	58	91						1949
POL	GOETAYFIL	846	9	31	48						1950
POL	GOETAYFLL	846	9	26	41						1951
POL	ETAYFILKL	848	9	31	48						1952
POL	ETAYFLLKL	848	9	27	42						1953
POL	TAYFILKLA	849	9	32	50						1954
POL	TAYFILKLA	849	9	27	42						1955
POL	LAGRWIVKT	856	9	14	22						1956
POL	LAGRWIPKV	856	9	30	47						1957
POL	ITDNGSNFT	866	9	49	77						1958
POL	FTSAAVKAA	873	9	27	42						1959
POL	FTSTTVKAA	873	9	14	22						1960
POL	AVKAAACWVA	877	9	32	50						1961
POL	TVKAAACWVA	877	9	23	36						1962
POL	KAACVWAGI	879	9	31	49	0.0180	0.0040	0.1200	0.0230	0.0150	1963
POL	VVESMKNEL	902	9	48	75						1964
POL	SMNKLKLI	905	9	53	83	0.0001					1965
POL	ELKKIIGQV	909	9	57	89						1966
POL	IIGQVRDQA	913	9	44	69						1967
POL	IIGQVREQA	913	9	13	20						1968
POL	QVRDQAEHL	916	9	48	75	0.0001					1969
POL	QVREQAEHL	916	9	13	20						1970
POL	DQAEIILKTA	919	9	46	72						1971
POL	QAEIILKTA	919	9	13	20						1972
POL	QAEIILKTAV	920	9	59	92						1973
POL	ILKTAVQMA	923	9	57	89	0.0033					1974
POL	TAVQMAVFI	926	9	59	92						1975
POL	SAGERIIDI	947	9	41	64						1976
POL	SAGERIVDI	947	9	14	22						1977
POL	IIDIASDI	952	9	12	19						1978

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*4802	SEQ ID NO
POL	IIDIIATDI	952	9	29	45						1979
POL	IVDIATDI	952	9	12	19						1980
POL	DIIASDIQT	954	9	15	23						1981
POL	DIATDIQT	954	9	40	63						1982
POL	ATDIQTKEL	957	9	35	55						1983
POL	QTKELQKQH	961	9	46	72						1984
POL	ELQKQIKI	964	9	13	21						1985
POL	ELQKQIKI	964	9	34	54						1986
POL	IKIQNFRV	969	9	12	19						1987
POL	ITKIQNFRV	969	9	36	57						1988
POL	PIWKGPAPKL	985	9	36	56						1989
POL	PLWKGPAPKL	985	9	19	30						1990
POL	LLWKGEVGA	992	9	60	94	0.0002					1991
POL	VVIQJNSDI	1002	9	62	97	0.0230					1992
POL	VVIQJNSDI	1002	9	37	58	0.0001					1993
POL	VVIQJNSDI	1002	9	12	19						1994
POL	IQDNSDIKV	1004	9	38	59						1995
POL	IQDNSDIKV	1004	9	12	19						1996
POL	VVPRIKAKI	1012	9	51	80						1997
POL	VVPRIKAKI	1012	9	11	17						1998
POL	IKDYGIKQM	1020	9	11	17						1999
POL	IKDYGIKQM	1020	9	50	78						2000
POL	KQAGIDDCV	1026	9	44	69						2001
POL	QKAGIDDCV	1027	9	44	69	0.0001					2002
POL	KAREFSEQT	12	10	16	16						2003
POL	RANSPTREL	26	10	16	25						2004
POL	RANSPTREL	26	10	10	16						2005
POL	STNSPTREL	32	10	01	33						2006
POL	SQTRANSPTT	34	10	01	33						2007
POL	RANSPTREL	35	10	01	33						2008
POL	RANSPTREL	37	10	01	50						2009
POL	GAISLSLPI	79	10	01	17						2010
POL	GTILNFPQT	80	10	01	17						2011
POL	AISSLNPIIT	80	10	01	33						2012
POL	GTILNCPQIIL	80	10	01	33						2013
POL	PTENFPQIIL	80	10	01	33						2014
POL	QITLWQRPPL	88	10	47	73						2015
POL	QITLWQRPPL	89	10	47	73						2016
POL	ITLWQRPPLV	90	10	37	58						2017
POL	TLWQRPPLVTI	91	10	21	33						2018
POL	TLWQRPPLVTI	91	10	18	28						2019
POL	WQRPPLVTIKI	93	10	14	22						2020
POL	WQRPPLVTIKI	93	10	12	19						2021
POL	LVTIKIGGQL	97	10	13	20						2022
POL	KIGGQLKEAL	101	10	23	36	0.0002					2023
POL	GQIEALLDT	104	10	10	16						2024
POL	GQIEALLDT	104	10	34	53						2025
POL	LIEALLDTGA	106	10	10	16						2026
POL	ALLDTGADDT	109	10	10	95						2027
POL	LLDTGADDTV	110	10	63	98	0.0005					2028

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	Site ID NO
POL	GADDTVLEDI	114	10	15	23						2029
POL	GADDTVLEEI	114	10	18	28						2030
POL	GADDTVLEEM	114	10	11	17						2031
POL	NLTKKWKPKM	124	10	35	55						2032
POL	KMIGGIGGFI	132	10	62	97						2033
POL	FKVRQYDQI	140	10	41	64	0.0290	0.0790	2.1000	0.0048	0.0120	2034
POL	KVRQYDQILI	142	10	20	31						2035
POL	KVRQYDQIPI	142	10	13	20						2036
POL	RQYDQILIEI	144	10	20	31						2037
POL	RQYDQIMIEI	144	10	12	19						2038
POL	ILIEICGKKA	149	10	13	20						2039
POL	LIEICGIIKAI	150	10	10	16						2040
POL	LIEICGKKAI	150	10	13	20						2041
POL	EICGIIKAIGT	152	10	19	30						2042
POL	EICGKKAIGT	152	10	24	38						2043
POL	AGTVLVGPT	158	10	52	81						2044
POL	GTVLVGPTIV	160	10	53	83						2045
POL	VLVGPTIVNI	162	10	53	83	0.0025					2046
POL	LVGPTIVNII	163	10	52	81	0.0015					2047
POL	PVNIIGRNLL	168	10	26	41	0.0002					2048
POL	PVNIIGRNML	168	10	24	38						2049
POL	IIGRNLLTQI	171	10	21	33						2050
POL	IIGRNMLTQI	171	10	18	28	0.0007					2051
POL	IIGRNMLTQL	171	10	11	17						2052
POL	NLLTQIGCTL	175	10	21	33						2053
POL	NMLTQIGCTL	175	10	18	28						2054
POL	NMLTQLGCTL	175	10	10	16						2055
POL	QIGCTLNFI	179	10	41	64	0.0025					2056
POL	QLGCTLNFI	179	10	16	25						2057
POL	CTLNFPSP	182	10	60	94	0.0340	0.1800	0.3300	0.4400	0.4000	2058
POL	PISPIETVPV	187	10	56	88	0.0002					2059
POL	TPVVKLKPGM	193	10	54	84						2060
POL	KQWPLTEIKI	209	10	56	88						2061
POL	PLTEEKIKAL	212	10	54	84						2062
POL	LTEEKIKALT	213	10	37	58						2063
POL	LTEEKIKALV	213	10	15	23						2064
POL	KIKALTEICT	217	10	12	19						2065
POL	KIKALVEICT	217	10	15	23						2066
POL	KALVEICTEM	219	10	15	24						2067
POL	CTEMEKEGKI	225	10	27	42						2068
POL	KIGPENPYNT	238	10	50	78						2069
POL	RIGPENPYNT	238	10	10	16						2070
POL	RTQDFWEVQL	272	10	53	83						2071
POL	EVQLGIIPIA	278	10	54	84						2072
POL	QLGIPIIAGL	280	10	56	89						2073
POL	PAGLKKKKS	286	10	50	78	0.0002					2074
POL	GLKKKKS	288	10	57	89	0.0002					2075
POL	SVTVLDVGD	294	10	49	77						2076
POL	PLDKDERKYT	308	10	19	30						2077
POL	FTISINNET	319	10	37	58						2078

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SI:Q ID NO
POL	FTPTSTNNIET	319	10	13	20						2079
POL	POGWKGSFAI	319	10	59	92						2080
POL	AFQSSMTKI	347	10	36	56						2081
POL	IVYQYMDDL	367	10	42	66						2082
POL	DLYVGSDEI	375	10	58	91	0.0007					2083
POL	GQIRAKIEEL	385	10	25	39	0.0001					2084
POL	GQIRTKIEEL	385	10	20	31						2085
POL	KIEELREILL	390	10	19	30						2086
POL	KIEELRQIILL	390	10	17	27	0.0002					2087
POL	KQILLRWGFT	395	10	12	19						2088
POL	IQKEPFLWM	410	10	62	97						2089
POL	IQLEKDSWT	433	10	13	20						2090
POL	IVLPEKDSWT	433	10	13	20						2091
POL	QLPEKDSWT	434	10	13	20						2092
POL	VLPEKDSWT	434	10	13	20						2093
POL	WTVNHIQKLV	441	10	61	95	0.0056					2094
POL	KLWASQIYA	452	10	27	42	0.0001					2095
POL	GKVKQLCKL	462	10	28	44	0.0230			0.0006	0.0130	2096
POL	GKVRQLCKL	462	10	18	28						2097
POL	KQLCKLLRGA	466	10	12	19						2098
POL	KQLCKLLRGT	466	10	14	22						2099
POL	QQLCKLLRGA	466	10	13	21						2100
POL	KLROAKALT	470	10	25	40						2101
POL	KLRGTKALT	470	10	24	38						2102
POL	KALTDIVPLT	476	10	21	33						2103
POL	KALTEVIPLT	476	10	16	25						2104
POL	IVPLTEAEEL	481	10	13	20						2105
POL	VIPLTEAEEL	481	10	11	17						2106
POL	PLTEAELEEL	483	10	30	47						2107
POL	LTEAELEELA	484	10	36	56						2108
POL	ELELAENREI	489	10	53	83						2109
POL	FILKEPVIIGV	497	10	41	64	0.0007					2110
POL	GVYYDIPSKDL	508	10	38	59						2111
POL	IQKQGQDQWT	521	10	12	19						2112
POL	IQKQGQDQWT	521	10	15	23						2113
POL	QYQIEPFKNL	532	10	40	63						2114
POL	YQEPFNKLT	534	10	43	67	0.0002					2115
POL	NLKTGXYAKM	540	10	18	29						2116
POL	NLKTGXYAKM	540	10	13	21						2117
POL	KTGKYAKMRT	542	10	10	16						2118
POL	RMRGAIITNDV	548	10	12	19						2119
POL	GAITNDVKQL	551	10	19	30						2120
POL	SAIITNDVKQL	551	10	16	25						2121
POL	TAITNDVKQL	551	10	11	17						2122
POL	KQLTEAVQKI	558	10	32	51						2123
POL	QLTEAVQKIA	559	10	26	41						2124
POL	LTEAVQKIAT	560	10	11	17						2125
POL	AVQKIATESI	563	10	10	16						2126
POL	VQKIATESIV	564	10	14	22						2127
POL	ETWWTIDYWQA	591	10	10	16						2128

Table VIII
IIIIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*0201	Λ^*0202	Λ^*0203	Λ^*0206	Λ^*6802	SEQ ID NO
POL	WTDYWQATWI	594	10	14	22						2129
POL	WTEYWQATWI	594	10	24	38						2130
POL	ATWIEWFEV	600	10	51	80	0.0013					2131
POL	WIPEWFEVNT	602	10	50	81						2132
POL	FVNTPLVLK	608	10	54	86	0.0002					2133
POL	LVKLWYQLIET	614	10	11	17						2134
POL	QLEKEPIVGA	620	10	16	25						2135
POL	PIVGAETFYV	625	10	28	44	0.0002					2136
POL	GAETFYVDGA	628	10	48	75						2137
POL	YVDGAANRET	633	10	45	70						2138
POL	ETKLGKAGYV	641	10	35	55						2139
POL	YVTDGRQKV	649	10	29	45						2140
POL	VTDGRGRQKV	650	10	28	44	0.0002					2141
POL	RQKVYSLTET	655	10	10	16						2142
POL	SLTDTTNQKT	660	10	11	17						2143
POL	SLTETTNQKT	660	10	19	30						2144
POL	TTNQKVELIA	664	10	12	19						2145
POL	TTNQKVELQA	664	10	42	66						2146
POL	KTELQAIILA	668	10	15	23						2147
POL	KTELQAIYLA	668	10	12	19						2148
POL	LALQDSGLEV	676	10	27	42						2149
POL	LALQDSGSEV	676	10	25	39	0.0006					2150
POL	LQDSGLEVNI	678	10	27	42						2151
POL	LQDSGSEVNI	678	10	25	39	0.0004					2152
POL	NIVTDSQYAL	686	10	59	92						2153
POL	VTDQSYALGI	688	10	58	91						2154
POL	SOYALGHQA	691	10	58	91						2155
POL	AQIDKSESEL	700	10	36	56						2156
POL	ELVNQIEQL	708	10	18	28						2157
POL	ELVSNQIEQL	708	10	19	30						2158
POL	LVNQHIEQLT	709	10	19	30						2159
POL	LVSNQIEQLT	709	10	19	30						2160
POL	QLIKKEKVYL	716	10	28	44	0.0006					2161
POL	LIKKEKVYLA	717	10	20	31						2162
POL	LAWVPAIKGI	725	10	22	34						2163
POL	QVDKLVSAGI	739	10	15	23						2164
POL	QVDKLVSSGI	739	10	29	45						2165
POL	KLVSAQIRKV	742	10	15	23	0.0074					2166
POL	KLVSSGIRKV	742	10	26	41						2167
POL	LVSAQIRKVL	743	10	15	23	0.0002					2168
POL	LVSSGIRKVL	743	10	26	41						2169
POL	SAGIRKVLFL	745	10	15	23	0.0007					2170
POL	VLFLDGDKA	751	10	51	80						2171
POL	MASDFNLPTI	774	10	22	34						2172
POL	MASDFNLPIV	774	10	25	39	0.0800	0.1900	0.1800	0.1100	2.2000	2173
POL	NLPPIVAKET	779	10	26	41						2174
POL	NLPPIVAKET	779	10	27	42	0.0007					2175
POL	IVASQDKCQL	788	10	43	67	0.0006					2176
POL	GIWQLDCTHL	811	10	59	92	0.0003					2177
POL	CTIILEGRKIL	817	10	31	48						2178

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	CTILLECKVIL	817	10	23	36						2179
POL	ILEGKILVA	819	10	31	48						2180
POL	ILEGKILVA	819	10	23	36						2181
POL	KILVAVIIVA	823	10	30	47						2182
POL	KVLVAVIIVA	823	10	22	34						2183
POL	VAVIVASGYI	827	10	51	83						2184
POL	VASGYIAEV	831	10	52	81						2185
POL	VIPAETGQET	840	10	58	91						2186
POL	ETGQETAYFI	844	10	31	48						2187
POL	ETGQETAYFL	844	10	26	41						2188
POL	ETAYFLLKLA	848	10	31	48						2189
POL	ETAYFLLKLA	848	10	27	42						2190
POL	ILKLAGRWPFV	853	10	34	53						2191
POL	LLKLAGRWPFV	853	10	25	39	0.0004					2192
POL	KLGRWIPYKT	855	10	14	22						2193
POL	KLGRWIPYKV	855	10	30	47						2194
POL	LGRWIPYKTI	856	10	13	20						2195
POL	LGRWIPYKVI	856	10	22	34						2196
POL	AAVKAACVWA	876	10	28	44						2197
POL	TTVKAACVWA	876	10	14	22						2198
POL	WAGIKQIEFGI	884	10	21	33						2199
POL	WAGIKQIEFGI	884	10	11	17						2200
POL	PQSQGVVISM	897	10	53	83						2201
POL	GVVISMINKEL	901	10	48	75						2202
POL	SMNKKELKII	905	10	53	83						2203
POL	KIIGQVRDQA	912	10	43	67						2204
POL	KIIGQVREQA	912	10	13	20						2205
POL	GVVREQAEIIL	915	10	44	69						2206
POL	GVVREQAEIIL	915	10	13	20						2207
POL	DQAEIILKTAV	919	10	46	72						2208
POL	EQAEIILKTAV	919	10	13	20						2209
POL	ILKTVOMAVFI	923	10	57	89						2210
POL	KTVOMAVFI	925	10	56	88	0.0005					2211
POL	SAGERIIDIH	947	10	41	64	0.0002					2212
POL	SAGERIIDIH	947	10	14	22						2213
POL	RIDIHSDI	951	10	12	19						2214
POL	RIDIHSDI	951	10	29	45						2215
POL	IASDIQTKEL	956	10	12	19						2216
POL	IATDIQTKEL	956	10	14	22						2217
POL	IQTKELQKQI	960	10	35	55						2218
POL	QTKELQKQII	961	10	44	69						2219
POL	QTKELQKQIT	961	10	10	16						2220
POL	QIKIQNFRV	968	10	32	50						2221
POL	QIKIQNFRV	968	10	12	19	0.0002					2222
POL	PIWKGPAPKLL	985	10	35	55						2223
POL	PLWKGPAPKLL	985	10	18	28						2224
POL	KLWKGEQAV	992	10	60	94	0.0016					2225
POL	LLWKGEQAVV	993	10	61	95	0.0360					2226
POL	AVVIQDNSDI	1000	10	37	58						2227

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SI:Q ID NO
POL	AVVIQDSEI	1000	10	12	19						2229
POL	VIQDSDIKV	1003	10	37	58	0.0013					2230
POL	VIQDSEIKV	1003	10	12	19						2231
POL	IQDSDIKV	1004	10	38	59						2232
POL	IQDSEIKV	1004	10	12	19						2233
POL	EIKVVRKA	1009	10	39	61						2234
POL	EIKVVRKA	1009	10	43	20						2235
POL	KVPRKAKI	1011	10	51	80						2236
POL	KVPRKAKI	1011	10	11	17						2237
POL	VVPRKAKI	1012	10	50	78						2238
POL	VVPRKAKI	1012	10	11	17						2239
POL	KIKDYCKQM	1019	10	11	17						2240
POL	KIKDYCKQM	1019	10	50	78						2241
POL	IKDYCKQMA	1020	10	11	17						2242
POL	IKDYCKQMA	1020	10	49	77						2243
POL	KQAGDUCVA	1026	10	44	69						2244
POL	GAISLSLPQIT	79	11	01	17						2245
POL	AISSLPQITL	80	11	01	33						2246
POL	PQITLWQRLV	88	11	47	73						2247
POL	QITLWQRLV	89	11	37	58						2248
POL	ITLWQRLV	90	11	19	30						2249
POL	ITLWQRLV	90	11	18	28						2250
POL	PLYIKGGQL	96	11	13	20						2251
POL	TIKIGGQLKEA	99	11	17	27						2252
POL	KIGGQLKEALL	101	11	23	36						2253
POL	OLIEALLDTGA	105	11	10	16						2254
POL	QLKEALLDTGA	105	11	34	53						2255
POL	EALLDTGADDT	108	11	60	94						2256
POL	ALLDTGADDT	109	11	61	95						2257
POL	LLDTGADDTVL	110	11	61	95						2258
POL	NLGRWKPKMI	124	11	35	55						2259
POL	MIGGGGFKV	133	11	62	97						2260
POL	FIKVRQYDQIL	140	11	21	33						2261
POL	QILIECKKA	148	11	13	20						2262
POL	ILIECKKKA	149	11	13	20						2263
POL	EICGIIKAGTV	152	11	19	30						2264
POL	EICGIIKAGTV	152	11	23	36						2265
POL	KAIGTVLVGPT	157	11	48	75						2266
POL	TVLVGPTPVNI	161	11	53	83						2267
POL	VLVGPITPVNI	162	11	51	80						2268
POL	PTPVNIICRNL	166	11	26	41						2269
POL	PTPVNIICRNL	166	11	24	38						2270
POL	PVNIICRNL	168	11	26	41						2271
POL	PVNIICRNL	168	11	23	36						2272
POL	NIICRNL	170	11	21	33						2273
POL	NIICRNL	170	11	18	28						2274
POL	NIICRNL	170	11	11	17						2275
POL	NIICRNL	170	11	41	64						2276
POL	NIICRNL	178	11	15	23						2277
POL	NIICRNL	183	11	54	86						2278

Table VIII

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^{\circ}\Delta G_{01}$	$\Delta^{\circ}\Delta G_{02}$	$\Delta^{\circ}\Delta G_{03}$	$\Delta^{\circ}\Delta G_{06}$	$\Delta^{\circ}\Delta G_{02}$	Site Q ID NO
POL	ETVIVKLRPGM	192	11	51	80						2279
POL	KLKFGMDGPKV	197	11	47	73						2280
POL	PLTEEKIKALT	212	11	35	55						2281
POL	PLTEEKIKALV	212	15	23	23						2282
POL	EMEKIKGKISKI	229	11	32	50						2283
POL	PIFAIKKKDST	248	11	22	34						2284
POL	PIFAIKKKDST	248	11	37	58						2285
POL	LVDRELNKRT	263	11	60	94						2286
POL	TQDFWEVQLGI	273	11	55	86						2287
POL	VQLGIHIPAGL	279	11	54	84						2288
POL	PAGLKKKSVT	286	11	47	73						2289
POL	GLKKKKSIVL	288	11	49	77						2290
POL	VLDVGDYFSV	297	11	53	83	0.0150					2291
POL	DVGDAYFSVPL	299	11	54	84						2292
POL	FLDKIDFKYTA	308	11	19	30						2293
POL	ETPGIRYOYV	327	11	51	80						2294
POL	VLPQGWKGSIA	337	11	58	92						2295
POL	PAIFQSSMTKI	346	11	36	56						2296
POL	AIFQSSMTKIL	347	11	36	56						2297
POL	DIVIQYMDIDL	366	11	36	58						2298
POL	EIVIQYMDIDL	366	11	24	38						2299
POL	VYQYMDIDLYV	368	11	51	80						2300
POL	YMDDLYVGSIDL	372	11	61	95						2301
POL	DLEIGQIRAKI	381	11	26	41						2302
POL	DLEIGQIRTKI	381	11	20	31						2303
POL	RAKIEFLREHL	388	11	13	20						2304
POL	RTKIEFLRQIIL	388	11	14	22						2305
POL	RQIILRWGFTT	395	11	12	19						2306
POL	PIQLPEKDSWT	432	11	13	20						2307
POL	PVLPPEKDSWT	432	11	13	20						2308
POL	IQLPEKDSWT	433	11	13	20						2309
POL	IVLPEKDSWT	433	11	13	20						2310
POL	IQKLVGKLNWA	446	11	61	95						2311
POL	LVGKLNWASQI	449	11	60	94						2312
POL	WASQIYAGIKV	455	11	26	41						2313
POL	WASQIYAGIKV	455	11	27	42						2314
POL	QIYAGIKVKQL	458	11	18	29						2315
POL	QIYFGIKVKQL	458	11	11	17						2316
POL	QIYFGIKVRQL	458	11	14	22						2317
POL	GIKVKQLCKLL	462	11	27	42						2318
POL	GIKVRQLCKLL	462	11	18	28						2319
POL	QLCKLLRGAKA	467	11	24	38						2320
POL	QLCKLLRGTKA	467	11	21	33						2321
POL	LLRGAKALTDI	471	11	22	34						2322
POL	LLRGTKALTEV	471	11	18	28						2323
POL	GAKALTDIVPL	474	11	17	27						2324
POL	GTKALTEVIPL	474	11	11	17						2325
POL	LTDIVPLTEEA	478	11	13	20						2326
POL	LTDIVPLTEEA	478	11	11	17						2327

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*4802	SEQ ID NO
POL	EVPLTEEAEL	480	11	11	17						2329
POL	PLTEEAELFA	483	11	29	45						2330
POL	ELELAENREIL	489	11	53	83						2331
POL	GVYYDTSKDLI	508	11	31	48						2332
POL	EQKQGGQQT	520	11	12	19						2333
POL	EQKQGGQQT	520	11	15	23						2334
POL	KQGGQQT	523	11	13	20						2335
POL	KQGGQQT	523	11	25	39						2336
POL	YQYQEPFKNL	531	11	40	63						2337
POL	KTGKYAKMRTA	542	11	10	16						2338
POL	KTGKYARMGA	542	11	13	21						2339
POL	GAITNDVKQLT	551	11	18	28						2340
POL	SAITNDVKQLT	551	11	12	19						2341
POL	TAITNDVKQLT	551	11	10	16						2342
POL	ITNDVKQLTEA	553	11	32	50						2343
POL	KQLTEAVQKIA	558	11	24	38						2344
POL	QLTEAVQKIAT	559	11	11	17						2345
POL	EAVQKIATESI	562	11	10	16						2346
POL	AVQKIATESIV	563	11	10	16						2347
POL	VQKIATESIVI	564	11	14	22						2348
POL	ATESIVIWCKT	568	11	16	25						2349
POL	VIWCKTIPFKL	573	11	17	27						2350
POL	VIWCKTIPFKL	573	11	29	45						2351
POL	RLPIKETWET	582	11	18	28						2352
POL	IQKETWEAWWT	585	11	11	17						2353
POL	IQKETWETWWT	585	11	21	33						2354
POL	ETWTDYWQAT	591	11	10	16						2355
POL	QATWIFWFEV	599	11	51	81						2356
POL	KLWYQLEKDPH	616	11	14	22						2357
POL	KLWYQLEKEPH	616	11	31	48						2358
POL	KLWYQLETEPI	616	11	11	17						2359
POL	YQLEKEPHVGA	619	11	16	25						2360
POL	GAETFYVDGAA	628	11	44	69						2361
POL	AANRETKLGKA	637	11	30	47						2362
POL	ETKLGKAGYVT	641	11	35	55						2363
POL	YVTDGRGRQVV	649	11	27	42						2364
POL	RQKVSLTETT	655	11	10	16						2365
POL	LTDTNQKTEL	661	11	19	30						2366
POL	LTETNQKTEL	661	11	25	39						2367
POL	DTTNQKTELQA	663	11	25	39						2368
POL	ETTNQKTELIA	663	11	11	17						2369
POL	ETTNQKTELQA	663	11	17	27						2370
POL	TTNQKTELIAI	664	11	12	19						2371
POL	TTNQKTELQAI	664	11	42	66						2372
POL	NQKTELQAIIL	666	11	15	23						2373
POL	NQKTELQAIYL	666	11	12	19						2374
POL	KTELQAIILAL	668	11	15	23						2375
POL	KTELQAIYLAL	668	11	12	19						2376
POL	AIILALQDSGL	673	11	15	23						2377
POL	ILALQDSGLEV	675	11	15	23						2378

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^{\circ}0701$	$\Delta^{\circ}0202$	$\Delta^{\circ}0203$	$\Delta^{\circ}0206$	$\Delta^{\circ}6R02$	SI:Q ID NO
POL	ALQDSGLEVNI	677	11	27	42						2379
POL	ALQDSGSEVNI	677	11	25	39						2380
POL	LQDSGLEVNIV	678	11	27	42						2381
POL	LQDSGSEVNIV	678	11	25	39						2382
POL	EVNIVDSQYA	684	11	59	92						2383
POL	IVTDSQYALGI	687	11	58	91						2384
POL	VTDQSYALGII	688	11	58	91						2385
POL	QAQIDKSESEL	699	11	36	56						2386
POL	QAQIDKSESELY	700	11	36	56						2387
POL	ELVNQIEQLI	708	11	18	28						2388
POL	ELVSCIEQLI	708	11	19	30						2389
POL	IEQLIKKEKV	713	11	28	44						2390
POL	EQLIKKEKVYL	715	11	28	44						2391
POL	QLIKKEKVYLA	716	11	19	30						2392
POL	YLAWVPAIKGI	724	11	22	34						2393
POL	YLSWVPAIKGI	724	11	37	58						2394
POL	GIGNIOVDKL	733	11	58	91						2395
POL	EQVDKLVSAIG	738	11	15	23						2396
POL	EQVDKLVSSGI	738	11	29	45						2397
POL	KLVSAGIRKVL	742	11	15	23						2398
POL	KLVSAGIRKVL	742	11	26	41						2399
POL	GIRKVLFLDIGI	747	11	49	77						2400
POL	KVFLFLDIGDKA	750	11	18	28						2401
POL	AMASDFNLPII	773	11	18	28						2402
POL	AMASDFNLPIV	773	11	25	39						2403
POL	MASDFNLPIIV	774	11	20	31						2404
POL	MASDFNLPIPV	774	11	25	39						2405
POL	NLPPIVAKIIV	779	11	26	41						2406
POL	NLPPIVAKIIV	779	11	27	42						2407
POL	ELVASCDCQL	787	11	43	67						2408
POL	QLKGEAMIGQV	796	11	53	83						2409
POL	QVDCSGIWIQL	805	11	56	88						2410
POL	QLDCTHILEGKI	814	11	33	52						2411
POL	QLDCTHILEGKI	814	11	26	41						2412
POL	CTHILEGKIIV	817	11	31	48						2413
POL	CTHILEGKIIV	817	11	23	36						2414
POL	IIEGKIIVLAV	819	11	31	48						2415
POL	IIEGKIIVLAV	819	11	23	36						2416
POL	LVAVHVASGYI	826	11	47	73						2417
POL	AVIIVASGYIEA	828	11	52	81						2418
POL	HVASGYIEAEV	830	11	52	81						2419
POL	VASGYIEAEVI	831	11	52	81						2420
POL	YIEAEVIPAET	835	11	53	83						2421
POL	EVIPAETQET	839	11	58	91						2422
POL	VIPAETQETA	840	11	58	91						2423
POL	ETQETAYFIL	844	11	31	48						2424
POL	ETQETAYFLL	844	11	26	41						2425
POL	GOETAYFILKL	846	11	31	48						2426
POL	GOETAYFILKL	846	11	26	41						2427
POL	FILKLAGRPV	852	11	32	50						2428

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*0201	A*0202	A*0203	A*0206	A*0202	SEQ ID NO
POL	FLKLAGRPV	852	11	25	39						2429
POL	KLGRWPVKTI	853	11	13	20						2430
POL	KLGRWPVKVI	855	11	22	34						2431
POL	THHDNGSNFT	864	11	13	20						2432
POL	VHHDNGSNFT	864	11	23	36						2433
POL	IITDNGSNFTSA	866	11	33	52						2434
POL	IITDNGSNFTST	866	11	11	17						2435
POL	SAAYKAAACWVA	875	11	28	44						2436
POL	STTVKAAACWVA	875	11	14	22						2437
POL	AVKAAACWVAGI	877	11	10	16						2438
POL	TVKAAACWVAGI	877	11	20	31						2439
POL	GIPYNQSQGV	892	11	63	98						2440
POL	QVRDQAEILKT	916	11	43	67						2441
POL	QVREQAEILKT	916	11	13	20						2442
POL	QAEILKTAQOM	920	11	57	89						2443
POL	PHNFKKKGKI	933	11	58	91						2444
POL	GIGGYSAGERI	942	11	57	89						2445
POL	SAGERIDIIA	947	11	40	63						2446
POL	SAGERIVDIIA	947	11	14	22						2447
POL	IIIIASDIQT	952	11	12	19						2448
POL	IIIIATDIQT	952	11	27	42						2449
POL	IIIIATDIQT	952	11	12	19						2450
POL	IIASDIQTKEL	955	11	14	22						2451
POL	IIASDIQTKEL	955	11	34	53						2452
POL	DIQTKELQKQI	959	11	44	69						2453
POL	IOTKELOKQI	960	11	10	16						2454
POL	IOTKELOKQIT	960	11	30	47						2455
POL	KQIKIQNFRV	967	11	12	19						2456
POL	KQIKIQNFRV	967	11	34	54						2457
POL	RVYRDSRDP	976	11	34	53						2458
POL	RVYRDSRDP	976	11	14	22						2459
POL	PAKLLWKGECA	990	11	59	92						2460
POL	LLWKGECAVVI	992	11	59	92						2461
POL	LLWKGECAVVI	993	11	59	92						2462
POL	GAVVIQNSDI	999	11	37	58						2463
POL	GAVVIQNSDI	999	11	12	19						2464
POL	VVIQDHSIKV	1002	11	37	58						2465
POL	VVIQDHSIKV	1002	11	12	19						2466
POL	VVIQDHSIKV	1003	11	37	58						2467
POL	VVIQDHSIKV	1003	11	12	19						2468
POL	KVPRRAKAKII	1011	11	50	78						2469
POL	KVPRRAKAKII	1011	11	11	17						2470
POL	KIIDYQKQMA	1019	11	11	17						2471
POL	KIIDYQKQMA	1019	11	49	77						2472
REV	LLKTVRLI	12	8	11	17						2473
REV	AVRIKIL	17	8	13	20						2474
REV	RQRQHISI	52	8	11	17						2475
REV	QLPIERL	78	8	14	22						2476
REV	QLPLERL	78	8	37	58						2477
REV	QTSQTQGV	94	8	21	33						2478

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
REV	GTOOSQGT	97	8	10	16						2479
REV	POGTETGV	101	8	05	18						2480
REV	SQGTETGV	101	8	05	18						2481
REV	LVESPAVL	114	8	11	17						2482
REV	SISERILST	58	9	10	16						2483
REV	CLGRPAEPV	67	9	10	16						2484
REV	PAEPVPLQL	71	9	21	33						2485
REV	SAEPVPLQL	71	9	12	19						2486
REV	PVPLQLPPI	74	9	11	17						2487
REV	PVPLQLPIL	74	9	35	55						2488
REV	LQLPIPERL	77	9	11	17						2489
REV	LQLPIPERL	77	9	36	56						2490
REV	QLPIPERLT	78	9	18	28						2491
REV	TQGVGSFQI	98	9	11	18						2492
REV	RARQRQHIS	50	10	10	16						2493
REV	PLQLPIPERL	76	10	11	17						2494
REV	PLQLPIPERL	76	10	34	53						2495
REV	LQLPIPERLT	77	10	17	27						2496
REV	QLPIPERLT	78	10	18	28						2497
REV	GTQGVGSFQI	97	10	11	18						2498
REV	PLQLPIPERLT	76	11	15	23						2499
REV	QLPIPERLT	77	11	17	27						2500
REV	GTSGTQSQSGT	94	11	10	16	0.0001					2501
TAT	SQPKTACT	19	8	13	20						2502
TAT	FLNKGLGI	41	8	14	22						2503
TAT	SQPKTACT	19	8	13	20						2504
TAT	KVERETET	80	8	12	19						2505
TAT	PTGPKSKKKV	88	11	12	19						2506
VIF	QVMIVWQV	6	8	43	67						2507
VIF	IVWQYDRM	9	8	59	92						2508
VIF	WQVDRMKI	11	8	13	20						2509
VIF	WQVDRMRI	11	8	48	75						2510
VIF	KIRTWNSL	17	8	12	19						2511
VIF	RIRTWNSL	17	8	15	23						2512
VIF	LVKIIIMYI	24	8	15	23						2513
VIF	LVKIIIMYV	24	8	19	30						2514
VIF	IIMYVSKKA	28	8	21	33						2515
VIF	KISSEVII	50	8	13	20						2516
VIF	KYSSEVIII	50	8	15	23						2517
VIF	RISSEVIII	50	8	20	31						2518
VIF	PLGDARLV	58	8	15	23						2519
VIF	PLGEARLV	58	8	11	17						2520
VIF	VIKTYWGL	67	8	19	30						2521
VIF	VITYWGL	67	8	10	16						2522
VIF	VVRTYWGL	67	8	22	34						2523
VIF	VVTYWGL	67	8	10	16						2524
VIF	TTYWGLHT	69	8	11	17						2525
VIF	HLGHGVSI	83	8	24	38						2526
VIF	HLGQGVSI	83	8	25	39						2527
VIF	HLGQGVSI	83	8	26	41						2528

Table VIII
 HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*0402	SEQ ID NO
VIF	GVSIEWRL	87	8	18	28						2529
VIF	STQIDPDL	100	8	12	19						2530
VIF	STQVDPGL	100	8	11	17						2531
VIF	TQIDPDLA	101	8	12	19						2532
VIF	TQVDPDLA	101	8	11	17						2533
VIF	TQVDPGLA	101	8	16	25						2534
VIF	LADQLIHL	107	8	25	39						2535
VIF	LADQLIIM	107	8	17	27						2536
VIF	SAIRKAIL	123	8	35	55						2537
VIF	SAIRNAIL	123	8	12	19						2538
VIF	YQAGINKV	140	8	38	59						2539
VIF	KVGSLOYL	146	8	52	81						2540
VIF	SLOYLALA	149	8	12	19						2541
VIF	SLOYLALT	149	8	31	48						2542
VIF	LQYLALAA	150	8	12	19						2543
VIF	LQYLALKA	150	8	11	17						2544
VIF	LQYLALTA	150	8	34	53						2545
VIF	YLALTA	152	8	28	44						2546
VIF	ALIKPKKI	157	8	10	16						2547
VIF	PLPSVRKL	168	8	21	33						2548
VIF	PLPSVRKL	168	8	14	22						2549
VIF	WQVMVWQV	5	9	43	67						2550
VIF	MIVWQVDRM	8	9	46	72						2551
VIF	QVDRWKRT	12	9	12	19						2552
VIF	QVDRMRINT	12	9	10	16						2553
VIF	QVDRMRINT	12	9	31	48						2554
VIF	KIRTWNSLV	17	9	12	19						2555
VIF	RIRTWNSLV	17	9	15	23						2556
VIF	RIRTWNSLV	17	9	15	23						2557
VIF	SLVKIIMYI	23	9	19	30						2558
VIF	SLVKIIMYV	23	9	21	33						2559
VIF	EVHIFLGDA	54	9	24	38						2560
VIF	EVHIFLGEA	54	9	25	39						2561
VIF	IIPLEGARL	56	9	13	20						2562
VIF	IIPLEGARL	56	9	20	31						2563
VIF	PLQEARLVI	58	9	10	16						2564
VIF	LVIKTYWGL	66	9	10	16						2565
VIF	LVITYWGL	66	9	22	34						2566
VIF	ITTYWGLIT	68	9	16	25						2567
VIF	IITGERDWIIL	75	9	21	33						2568
VIF	QTERDWIIL	75	9	12	19						2569
VIF	STQIDPDLA	100	9	12	19						2570
VIF	STQVDPGLA	100	9	11	17						2571
VIF	DLADQLIHL	106	9	18	28						2572
VIF	GLADQLIIM	106	9	15	23						2573
VIF	KVGSLOYLA	146	9	52	81						2574
VIF	SLOYLALAA	149	9	12	19						2575
VIF	SLOYLALKA	149	9	11	17						2576
VIF	SLOYLALTA	149	9	31	48						2577
VIF	LQYLALAA	150	9	12	19						2578

0.0031

Table VIII
IIIY Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
VIF	LQYLALAL	150	9	11	17						2579
VIF	LQYLALAL	150	9	33	52						2580
VIF	KIKPLPSV	164	9	19	30						2581
VIF	KIKPLPSV	164	9	12	19						2582
VIF	PLPSVKLT	168	9	13	20						2583
VIF	VMVWQVDRM	7	10	44	69						2584
VIF	IVWQVDRMKI	9	10	12	19						2585
VIF	IVWQVDRMKI	9	10	47	73						2586
VIF	WQVDRMKIRT	11	10	12	19						2587
VIF	WQVDRMKIRT	11	10	10	16						2588
VIF	WQVDRMKIRT	11	10	31	48						2589
VIF	RMKIRTWNSL	15	10	12	19						2590
VIF	RMKIRTWNSL	15	10	15	23						2591
VIF	RMKIRTWNSL	15	10	15	23						2592
VIF	KISSEVIHPL	50	10	14	22						2593
VIF	KYSSEVIHPL	50	10	19	30						2594
VIF	RISSEVIHPL	50	10	13	20						2595
VIF	HIPLGDARLV	56	10	10	16						2596
VIF	HIPLGEARLV	56	10	19	30						2597
VIF	RLVITYWGL	65	10	12	19						2598
VIF	VITYWGLIT	67	10	16	25						2599
VIF	LOTGERDWIL	74	10	12	19						2600
VIF	QIDPDLADQL	102	10	10	16						2601
VIF	QIDPDLADQL	102	10	14	22						2602
VIF	IVSPRCEYQA	133	10	11	17						2603
VIF	QAGIINKVGS	141	10	38	59						2604
VIF	KVGSLOYLAL	146	10	51	80						2605
VIF	SLQYLALAL	149	10	12	19						2606
VIF	SLQYLALAL	149	10	11	17						2607
VIF	SLQYLALAL	149	10	31	48						2608
VIF	LQYLALALI	150	10	28	44						2609
VIF	KTKGIIRGSIT	188	10	16	25						2610
VIF	QVMVWQVDRM	6	11	43	67						2611
VIF	MIVWQVDRMIRI	8	11	43	67						2612
VIF	RMKIRTWNSLV	15	11	12	19						2613
VIF	RMKIRTWNSLV	15	11	15	23						2614
VIF	RMKIRTWNSLV	15	11	15	23						2615
VIF	RTWNSLVKIIIM	19	11	14	22						2616
VIF	RTWNSLVKIIIM	19	11	24	38						2617
VIF	EVHPLGDARL	54	11	20	31						2618
VIF	EVHPLGEARL	54	11	20	31						2619
VIF	HIPLGEARLYI	56	11	10	16						2620
VIF	LVITYWGLIT	66	11	16	25						2621
VIF	GLITGERDWIL	73	11	21	33						2622
VIF	GLITGERDWIL	73	11	12	19						2623
VIF	TQIDPDLADQL	101	11	10	16						2624
VIF	TQVDPGLADQL	101	11	13	20						2625
VIF	QIDPDLADQL	102	11	10	16						2626
VIF	QVDFGLADQL	102	11	14	22						2627
VIF	YQAGIINKVGS	140	11	38	59						2628

0.0008

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SHQ ID NO
VIF	KVGSQYLALA	146	11	12	19						2629
VIF	KVGSQYLALT	146	11	28	44						2630
VIF	SLQYLALALT	149	11	27	42						2631
VIF	LKPKKIKITL	158	11	10	16						2632
VIF	KTGHIKGSITM	188	11	15	23						2633
VPR	ALELEEL	19	8	10	16						2634
VPR	TLELEEL	19	8	44	69						2635
VPR	AVRIIFRI	30	8	14	22						2636
VPR	ETYGDTWA	48	8	16	25						2637
VPR	ETYGDTWT	48	8	11	17						2638
VPR	DTWAGVEA	52	8	16	25						2639
VPR	DTWEGVEA	52	8	23	36						2640
VPR	WAGVEAI	54	8	16	25						2641
VPR	GVEAIIRI	56	8	34	53						2642
VPR	IRILQQL	60	8	42	66						2643
VPR	ILQCLLF	63	8	37	58						2644
VPR	LLFIIFRI	67	8	44	69						2645
VPR	LLFVIIFRI	67	8	12	19						2646
VPR	CQHSIRIGI	77	8	45	70						2647
VPR	WALELEEL	18	9	09	15	0.0035					2648
VPR	WLELELEEL	18	9	42	69						2649
VPR	LLEELKNEA	22	9	17	27						2650
VPR	LLEELKSEA	22	9	16	25						2651
VPR	EAVRIIFRI	29	9	14	22	0.0001					2652
VPR	WLJGLQIII	38	9	20	31						2653
VPR	IIYETYGDT	45	9	17	27						2654
VPR	IIYNTYGDT	45	9	14	22						2655
VPR	YIVETYGDT	45	9	14	22						2656
VPR	DTWAGVEAI	52	9	16	25						2657
VPR	DTWEGVEAI	52	9	20	31						2658
VPR	GVEAIIRIL	56	9	34	53						2659
VPR	IRILQQL	59	9	39	61	0.0150	0.1900	0.2400	0.0960	0.0730	2660
VPR	IRILQQLL	60	9	42	66	0.0004	0.0028	0.0800	0.1000	0.0220	2661
VPR	RIQQLLF	62	9	36	56	0.2640	0.0002	0.0004	0.0023	0.0840	2662
VPR	QLLFVIIFRI	66	9	44	69	0.0530					2663
VPR	RIGCQHSIRI	66	9	10	16						2664
VPR	RIGCFIISRI	74	9	47	73						2665
VPR	CQHSIRIGI	77	9	12	19						2666
VPR	CQHSIRIGIT	77	9	16	25						2667
VPR	QRRARNGA	90	9	14	22						2668
VPR	QRRPYNEWT	10	9	13	20						2669
VPR	ELLEEKNEA	21	10	29	45						2670
VPR	ELLEEKSEA	21	10	16	25						2671
VPR	LLEELKNEAV	22	10	16	25						2672
VPR	LLEELKSEAV	22	10	17	27						2673
VPR	AVRIIFRIWL	30	10	14	22						2674
VPR	AVRIIFRPWL	30	10	14	22	0.0002					2675
VPR	ETYGDTWAGV	48	10	34	53						2676
VPR	ETYGDTWTGV	48	10	16	25	0.0009					2677
VPR			10	11	17						2678

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VPR	NTYGDTEGV	48	10	16	25						2679
VPR	DTWAGVEAI	52	10	16	25						2680
VPR	DTWEGVEAI	52	10	19	30						2681
VPR	WAGVEAIRI	54	10	15	23						2682
VPR	EAIRILQQL	58	10	33	52						2683
VPR	AIRILQQL	59	10	39	61						2684
VPR	QQLFIIRI	65	10	44	69						2685
VPR	QQLFVIIRI	65	10	10	16	0.0014					2686
VPR	POREPNEWTI	10	11	29	45						2687
VPR	ELLEELKNEAV	21	11	16	25						2688
VPR	ELLEELKSEAV	21	11	16	25						2689
VPR	EAVRIIPRIWL	29	11	14	22						2690
VPR	EAVRIIPRIWL	29	11	34	53						2691
VPR	GQIHYTYGDT	43	11	17	27						2692
VPR	GQIHYTYGDT	43	11	13	20						2693
VPR	GQIHYTYGDT	43	11	13	20						2694
VPR	WAGVEAIRIL	54	11	15	23						2695
VPR	EAIRILQQL	58	11	33	52						2696
VPR	IRILQQLFI	60	11	33	52						2697
VPR	LQQLFIIRI	64	11	44	69						2698
VPR	LQQLFVIIRI	64	11	10	16						2699
VPR	RIGCQISIRIGI	74	11	45	70						2700
VPR	RIGCQISIRIGI	74	11	11	17						2701
VPR	#LPGRGRNGA	85	11	01	50						2702
VPU	LAKVDYRI	5	8	01	25						2703
VPU	LAKVDYRL	5	8	01	25						2704
VPU	KVDYRIVI	7	8	01	33						2705
VPU	KVDYRLGV	7	8	01	33						2706
VPU	RIDYRLGV	7	8	01	33						2707
VPU	ILAIVALV	12	8	12	19						2708
VPU	LAIVALVV	13	8	12	20						2709
VPU	AIVALVVA	14	8	12	19						2710
VPU	IIAIVVWT	27	8	23	36						2711
VPU	IIAIVVWT	28	8	23	36						2712
VPU	AIVVWTIV	29	8	29	45						2713
VPU	VVWTIVFI	31	8	15	23						2714
VPU	KILRQRKI	45	8	15	23						2715
VPU	RQRKIDRL	48	8	20	31						2716
VPU	DQEELSAL	79	8	13	22						2717
VPU	GVEMGHIIIA	91	8	01	50						2718
VPU	LAKVDYRIV	5	9	01	25						2719
VPU	KVDYRIVIV	7	9	01	33						2720
VPU	IIAIVALVV	12	9	11	17						2721
VPU	LAIVALVVA	13	9	09	15						2722
VPU	IIAIVVWTI	27	9	23	36						2723
VPU	IIAIVVWTIV	28	9	20	31						2724
VPU	IVVWTIVFI	30	9	15	23						2725
VPU	IVFIEYRKI	36	9	12	19						2726
VPU	RQRKIDRLI	48	9	17	27						2727
VPU	KIDRLIDRI	52	9	14	22						2728

Table VIII
 IIIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*0802	SEQ ID NO
VPU	LIDRIRERA	58	9	12	19						2729
VPU	DQHELSALV	79	9	11	18						2730
VPU	VTLLSSSKL	94	9	01	50						2731
VPU	LAKVDYRIVI	5	10	01	25						2732
VPU	LAKVDYRLGV	5	10	01	25						2733
VPU	KVDYRIVIVA	7	10	01	33						2734
VPU	KVDYRLGVGA	7	10	01	33						2735
VPU	RIDYRLGVGA	7	10	01	33						2736
VPU	HAIVVWTIV	27	10	20	31						2737
VPU	AIIVVWTVFI	29	10	14	22						2738
VPU	ILRQKIDRL	46	10	15	23						2739
VPU	LVTLSSSKL	91	10	01	50						2740
VPU	LAKVDYRIVIV	5	11	01	25						2741
VPU	KVDYRLGVGAL	7	11	01	33						2742
VPU	RIDYRLGVGAL	7	11	01	33						2743
VPU	KILRQKIDRL	45	11	15	23						2744
VPU	ILRQKIDRLI	46	11	13	20						2745

Table IX
HIV Δ03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^0001	Δ^0101	Δ^0301	Δ^03101	Δ^03301	Δ^06801	SEQ ID NO
ENV	SLWDQSLK	123	8	47	75							2746
ENV	QSLKPCVK	127	8	48	75							2747
ENV	AITQACPK	244	8	14	22							2748
ENV	TITQACPK	244	8	11	17							2749
ENV	VITQACPK	244	8	17	27							2750
ENV	PAGIAILK	266	8	38	59							2751
ENV	PAGYAILK	266	8	15	23							2752
ENV	AILKCNDK	270	8	20	31							2753
ENV	ILKCNDKK	271	8	12	19							2754
ENV	SVEINCTR	340	8	13	20							2755
ENV	GTAGNSSR	375	8	01	33							2756
ENV	TTHSFNCR	432	8	12	19							2757
ENV	ITLPCRIK	483	8	26	41							2758
ENV	NMWQEVGK	494	8	15	37							2759
ENV	ITGLLLTR	520	8	37	58							2760
ENV	ISELYKYK	558	8	54	84							2761
ENV	PLGVAPTK	571	8	26	41							2762
ENV	PLGVAPTR	571	8	19	16							2763
ENV	GVAPTKAK	573	8	19	30							2764
ENV	VAPTKAKR	574	8	19	30							2765
ENV	VISTRTIIR	584	8	01	50							2766
ENV	STRTHREK	586	8	01	50							2767
ENV	RVVQREKR	587	8	32	50							2768
ENV	ITLTQAR	621	8	17	27	0.0003	0.0001					2769
ENV	EAQGHLLK	646	8	32	50							2770
ENV	KLTVWGIK	653	8	12	19							2771
ENV	QLTVWGIK	653	8	13	20							2772
ENV	GKQLQAR	658	8	44	69							2773
ENV	LAVERYLK	667	8	49	77							2774
ENV	LAVERYLR	667	8	26	41							2775
ENV	GIWGCSGK	680	8	11	17							2776
ENV	MTWMEWEIR	721	8	52	81							2777
ENV	ESQNQKEK	743	8	12	19							2778
ENV	AVLSIVNR	795	8	27	42							2779
ENV	LSIVIRVIR	797	8	31	48							2780
ENV	ALAWIDDLR	851	8	38	59							2781
ENV	RIVELLOR	878	8	25	39							2782
ENV	IVELLGRR	879	8	22	34							2783
ENV	RLGWEGLK	894	8	22	34							2784
ENV	AVAEGTDR	928	8	10	32							2785
ENV	RAILIIIPR	945	8	48	81							2786
ENV	AILIIIPR	946	8	31	48							2787
ENV	RIRQGLER	953	8	13	20							2788
ENV	TLFCASDAK	953	8	44	69							2789
ENV	VTENFNMAWK	64	9	52	81	0.0930	0.5300	0.0017	0.0013	0.0020		2790
ENV	ISLWDQSLK	102	9	31	48	0.0048	0.0890	0.0017	0.0013	0.0021		2791
ENV	SAITQACPK	243	9	47	73							2792
ENV	SAITQACPK	243	9	14	22							2793
ENV	SVITQACPK	243	9	10	16							2794
ENV	SVITQACPK	243	9	17	27							2795

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3101	A*6801	SEQ ID NO
ENV	FAIKCNDK	269	9	14	22	0.0002	0.0002	0.0004	0.0015	0.0027	2796
ENV	AILKCNDDK	270	9	12	19						2797
ENV	TVQCTIIGIK	290	9	28	44	0.0021	0.0460	0.0042	0.0017	0.0190	2798
ENV	TVQCTIIGIR	290	9	23	36	0.0008	0.0008	0.0080	0.0030	0.0120	2799
ENV	LAEDEVIR	312	9	12	19	0.0002	0.0002	0.0004	0.0007	0.0002	2800
ENV	CTRPNNTR	345	9	28	44						2801
ENV	ITTIISFNCR	431	9	11	17						2802
ENV	NANITPCR	478	9	01	50						2803
ENV	NITLPCR	482	9	01	17						2804
ENV	NITLPCR	482	9	14	22						2805
ENV	NITLPCR	519	9	35	55	0.0004	0.0001				2806
ENV	STNGTETR	537	9	01	17						2807
ENV	ELYKYKVK	560	9	32	51						2808
ENV	GVPTKAKR	573	9	19	30						2809
ENV	KAKRVRQR	574	9	17	27	0.0002	0.0002	0.0004	0.0006	0.0002	2810
ENV	IINIIPIR	579	9	13	20	0.0002	0.0002	0.0000	0.0005	0.0002	2811
ENV	ISTRTHREK	584	9	01	50						2812
ENV	NITTHIREK	585	9	01	50						2813
ENV	STRTHIREK	586	9	01	50						2814
ENV	STRTHIREK	586	9	01	50						2815
ENV	STRTHIREK	586	9	01	50						2816
ENV	STRTHIREK	586	9	01	50						2817
ENV	STRTHIREK	586	9	01	50						2818
ENV	STRTHIREK	586	9	01	50						2819
ENV	STRTHIREK	586	9	01	50						2820
ENV	STRTHIREK	586	9	01	50						2821
ENV	STRTHIREK	586	9	01	50						2822
ENV	STRTHIREK	586	9	01	50						2823
ENV	STRTHIREK	586	9	01	50						2824
ENV	STRTHIREK	586	9	01	50						2825
ENV	STRTHIREK	586	9	01	50						2826
ENV	STRTHIREK	586	9	01	50						2827
ENV	STRTHIREK	586	9	01	50						2828
ENV	STRTHIREK	586	9	01	50						2829
ENV	STRTHIREK	586	9	01	50						2830
ENV	STRTHIREK	586	9	01	50						2831
ENV	STRTHIREK	586	9	01	50						2832
ENV	STRTHIREK	586	9	01	50						2833
ENV	STRTHIREK	586	9	01	50						2834
ENV	STRTHIREK	586	9	01	50						2835
ENV	STRTHIREK	586	9	01	50						2836
ENV	STRTHIREK	586	9	01	50						2837
ENV	STRTHIREK	586	9	01	50						2838
ENV	STRTHIREK	586	9	01	50						2839
ENV	STRTHIREK	586	9	01	50						2840
ENV	STRTHIREK	586	9	01	50						2841
ENV	STRTHIREK	586	9	01	50						2842
ENV	STRTHIREK	586	9	01	50						2843
ENV	STRTHIREK	586	9	01	50						2844
ENV	STRTHIREK	586	9	01	50						2845

Table IX
HIV Δ03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*3301	Δ^*4801	SEQ ID NO
ENV	SLAEIEVIR	311	10	12	19						2846
ENV	CTRNINTRK	345	10	22	34						2847
ENV	ATGDIIGDIR	369	10	12	19						2848
ENV	EITTHSFNCR	430	10	11	17						2849
ENV	IIMMWQEVGK	492	10	12	19						2850
ENV	GSENGTETFR	538	10	02	18						2851
ENV	PLGVAPTKAK	571	10	19	30						2852
ENV	GVAPTKAKRR	573	10	17	27						2853
ENV	VISTRITIREK	584	10	01	50						2854
ENV	ISRTIUREKR	585	10	01	50						2855
ENV	NIITPIUREKR	586	10	01	50						2856
ENV	ASITLVQAR	619	10	28	44						2857
ENV	IVQQNNLLR	634	10	25	39	0.0024	0.0190	0.0130	0.0072	0.0035	2858
ENV	IVQQSNLLR	634	10	26	41						2859
ENV	AIEAQOILLK	644	10	12	19						2860
ENV	LLKLTWGIK	651	10	13	20						2861
ENV	LLQLTVWGIK	651	10	34	53	0.0055	0.0110				2862
ENV	MLQLTVWGIK	651	10	10	16						2863
ENV	RVLAVERYLK	665	10	18	28						2864
ENV	RVLAVERYLK	665	10	10	16						2865
ENV	LLGIWQCSGK	678	10	50	78	0.1200	0.0120	0.0017	0.0020	0.0001	2866
ENV	MIVGLIGLGR	782	10	36	56						2867
ENV	AVLSINRVR	795	10	31	48						2868
ENV	FLALAWDLR	849	10	25	39						2869
ENV	RLCLFSYIIR	858	10	31	48						2870
ENV	GLRLGWEGLK	892	10	10	32						2871
ENV	LLQYWSQELK	906	10	12	19						2872
ENV	ALAVAEQDTR	926	10	31	48						2873
ENV	ALIHPRIR	946	10	12	19						2874
ENV	PTRIKQGLER	951	10	12	19						2875
ENV	VTVYGVVPVWK	47	11	41	64	0.0600	4.1000				2876
ENV	KTLTFCASDAK	60	11	12	19						2877
ENV	TTTLFCASDAK	60	11	22	34						2878
ENV	DIISLWQOSLK	120	11	38	59						2879
ENV	NTSAITQACPK	241	11	14	22						2880
ENV	NTSVITQACPK	241	11	13	20						2881
ENV	VSTVQCTHIGIK	288	11	28	44						2882
ENV	VSTVQCTHIGIR	288	11	23	36						2883
ENV	GSLAEIEVIR	310	11	12	19						2884
ENV	YATGDHIGDIR	368	11	11	17						2885
ENV	KLREIQFENK	405	11	01	25						2886
ENV	HTEGNITLQCR	478	11	01	50						2887
ENV	NANITPCRIK	478	11	01	50						2888
ENV	QINMWQEVGK	491	11	12	19						2889
ENV	SSNITGLLTR	516	11	19	30						2890
ENV	NETNKTETFR	537	11	01	17						2891
ENV	NTGNTTETFR	537	11	15	23						2892
ENV	EIFRPGGDMR	544	11	20	31						2893
ENV	ETERPGGDMR	544	11	20	31						2894
ENV	RSELYKYKVK	558	11	29	45						2895

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*3301	Δ^*6801	SEQ ID NO
ENV	KIEPLGYAFTK	568	11	15	24						2896
ENV	PLGVAITKAKR	571	11	19	30						2897
ENV	PTKAKRRVQQR	576	11	13	20						2898
ENV	KAKRRVVQRIK	579	11	13	20						2899
ENV	IINHTPIREK	584	11	01	50						2900
ENV	VISTRTHREKR	584	11	01	50						2901
ENV	AASITLTQAR	618	11	28	44						2902
ENV	GIVQQJNNLLR	633	11	25	39						2903
ENV	GIVQQSNLLR	633	11	26	41						2904
ENV	ILLKLTWGIK	650	11	13	20						2905
ENV	ILLQLTYWGIK	650	11	34	53						2906
ENV	TVWGIKLOQAR	655	11	48	75						2907
ENV	QLOARVLAVR	661	11	33	52						2908
ENV	QLLGWGCSSGK	677	11	50	78						2909
ENV	NYPWNKSWSNK	693	11	10	16						2910
ENV	LIEESQOQIEK	740	11	20	31						2911
ENV	IMIVGILIGLR	781	11	34	54						2912
ENV	IIFAVLSIVNR	792	11	14	22						2913
ENV	IFPAVISIVNR	792	11	17	27						2914
ENV	FAVLSIVNRVR	794	11	31	48						2915
ENV	GIEECGERDR	829	11	12	19						2916
ENV	NLCFSYIIRLR	859	11	11	17						2917
ENV	SLCLFSYIIRLR	859	11	31	48						2918
ENV	LLGRRCWEALK	882	11	09	15						2919
ENV	NLLQYWSQELK	905	11	12	19						2920
ENV	IAIAVAEGTDK	925	11	10	16						2921
ENV	TAIAVAEGTDR	925	11	21	33						2922
ENV	RAIIIPRRIR	945	11	12	19						2923
GAG	GARASILR	2	8	10	16						2924
GAG	ASVLSQOK	5	8	29	45						2925
GAG	RLRINGKK	20	8	49	77						2926
GAG	WASRELER	37	8	48	75						2927
GAG	QTGSEELR	71	8	12	19						2928
GAG	TYLCVTHQK	86	8	12	19						2929
GAG	TYLCVTHQR	86	8	15	23						2930
GAG	RIEVKDTK	93	8	13	20						2931
GAG	DTKEALDK	98	8	36	56		0.0001				2932
GAG	DTKEALEK	98	8	12	19						2933
GAG	KIEEQNK	105	8	23	36						2934
GAG	PAADREK	123	8	01	50						2935
GAG	RTLNAWK	171	8	63	98						2936
GAG	WVKVIEK	176	8	29	45		0.0410				2937
GAG	WVKVVEEK	176	8	31	48						2938
GAG	QAAMOMLK	216	8	61	95		0.0003				2939
GAG	PIATGQMR	243	8	19	30						2940
GAG	PIPTGQMR	243	8	17	27						2941
GAG	PVAPGQMR	243	8	10	16						2942
GAG	PVGDYKR	281	8	18	28						2943
GAG	PVGEIYKR	281	8	40	63						2944
GAG	WIIILGLNK	289	8	57	89		0.0003			0.0001	2945

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*3301	Δ^*6801	SEQ ID NO
GAG	PTSILDIR	303	8	12	19						2946
GAG	PVSILDIR	303	8	16	25						2947
GAG	PVSILDIR	303	8	25	39						2948
GAG	GVGGIPSHK	376	8	37	58		0.0018				2949
GAG	GVGGIPSHK	376	8	23	36						2950
GAG	ASAOQDLK	392	8	01	50						2951
GAG	ATAQQLDK	392	8	01	50						2952
GAG	AAAIMMQK	400	8	04	19						2953
GAG	AAAIMMQK	405	8	01	25						2954
GAG	SATIMMQK	405	8	01	25						2955
GAG	YTAVFMQR	405	8	02	50						2956
GAG	MMQKSNFK	409	8	10	16						2957
GAG	MMQKGNFK	409	8	10	16						2958
GAG	MMQKGNFR	409	8	23	36						2959
GAG	QMKDICTER	455	8	49	77						2960
GAG	RASVLSGK	4	9	29	45						2961
GAG	KLDLWIKIR	12	9	16	25						2962
GAG	KLDLWIKIR	12	9	10	16						2963
GAG	DAWEKIRLR	14	9	17	27						2964
GAG	KIRLRPGGK	18	9	44	69						2965
GAG	RLRPGGKKK	20	9	34	53						2966
GAG	LLETSECCR	52	9	17	27						2967
GAG	ATLYCVIIQK	85	9	12	19	0.0150	0.7100				2968
GAG	ATLYCVIIQK	85	9	15	23	0.1800	0.0670	1.0000	2.1000	0.8400	2969
GAG	MVIGAIQSPR	163	9	27	42	0.0002	0.0012	0.0006	0.0005	0.0003	2970
GAG	PIPVGEIYK	279	9	35	55	0.0008	0.0001	0.0032	0.0100	0.0004	2971
GAG	ILGLNKIVR	291	9	58	91						2972
GAG	ILDIKQGPYK	306	9	19	30						2973
GAG	ILDIKQGPYK	306	9	42	66	0.0420	0.0048	0.0106	0.0006	0.0002	2974
GAG	NSATIMMQK	404	9	01	33						2975
GAG	IMMQKSNFK	408	9	10	16						2976
GAG	IMMQKGNFR	408	9	20	31						2977
GAG	IVKCFNCGK	422	9	13	20						2978
GAG	IVKCFNCGK	422	9	11	17						2979
GAG	IVKCFNCGK	422	9	11	17						2980
GAG	IARNCRAPR	434	9	18	29		0.0003	0.0330	0.0500	0.0039	2981
GAG	IARNCRAPR	434	9	13	21						2982
GAG	LIARNCRAPR	434	9	20	32						2983
GAG	KIWPSTIKGR	472	9	22	35		0.0005	0.4400	0.0087	0.0001	2984
GAG	KIWPSTIKGR	472	9	13	21						2985
GAG	KIWPSTIKGR	472	9	10	16						2986
GAG	KIWPSTIKGR	472	9	15	23						2987
GAG	TAPPIESFR	508	9	02	67						2988
GAG	TAPPIESFR	508	9	01	33						2989
GAG	KIRLRPGGKK	18	10	44	69	1.9000	0.0010	0.0008	0.0005	0.0001	2990
GAG	KLKIIIVWASR	31	10	13	20						2991
GAG	KLKIIIVWASR	31	10	17	27						2992
GAG	IVWASRELER	35	10	20	31	0.0099	0.0066				2993
GAG	IVWASRELER	35	10	26	41						2994
GAG	GLLETSECCR	51	10	16	25						2995

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
GAG	VATLYCVIHK	84	10	12	19						2996
GAG	VATLYCVIQR	84	10	15	23						2997
GAG	KIEERQNSK	105	10	15	23						2998
GAG	QMVIIQAISPR	162	10	27	42	0.0260	0.0010	0.0740	0.1000	0.0430	2999
GAG	NAWVKVIEK	174	10	29	45						3000
GAG	NAWVKVVEEK	174	10	30	47	0.0004	0.0002				3001
GAG	IATGQMREPR	244	10	19	30						3002
GAG	PIPVGEIYKR	279	10	34	53	0.0003	0.0001	0.0009	0.0010	0.0005	3003
GAG	IILGLNKIVR	290	10	57	89	0.0003	0.0006	0.0110	0.0260	0.0073	3004
GAG	YSPTSLDIR	301	10	12	19						3005
GAG	YSPVSILDIK	301	10	16	25						3006
GAG	YSPVSILDIR	301	10	24	38						3007
GAG	SILDIKQIPK	305	10	18	28						3008
GAG	SILDIKQIPK	305	10	40	63	0.3100	0.7100	0.0017	0.0020	0.0060	3009
GAG	YVIDRFKTLR	320	10	27	42						3010
GAG	YVIDRFKTLR	320	10	28	44	0.0003	0.0006				3011
GAG	RAEQASQEVK	329	10	12	19						3012
GAG	RAEQATQDVK	329	10	15	23						3013
GAG	RAEQATQEVK	329	10	27	42						3014
GAG	LVONANPICK	346	10	59	92	0.0002	0.0110				3015
GAG	GVGKIPGIKAR	376	10	37	58	0.0003	0.0001				3016
GAG	GVGKIPGIKAR	376	10	22	34						3017
GAG	TIMMQRGNFR	407	10	12	21						3018
GAG	KTVKTCFCGK	421	10	08	16						3019
GAG	IIIAKNCRAPR	433	10	18	28						3020
GAG	IIIAKNCRAPR	433	10	13	20						3021
GAG	IIIAKNCRAPR	433	10	20	31						3022
GAG	IAKNCRAPRK	434	10	16	25						3023
GAG	IAKNCRAPRK	434	10	13	21						3024
GAG	LAKNCRAPRK	434	10	20	32						3025
GAG	RAPRKICQWK	439	10	51	80						3026
GAG	FLGKIWPSHK	469	10	23	36						3027
GAG	FLGKIWPSNK	469	10	13	20	0.0200	0.0013				3028
GAG	FLGKIWPSK	469	10	10	16						3029
GAG	GTRPGINYQK	480	10	01	50						3030
GAG	GTRPGINYQK	480	10	01	50						3031
GAG	PTAPPEESFR	495	10	15	23						3032
GAG	PTAPPEESFR	507	10	02	67						3033
GAG	PTAPPEESFR	507	10	01	33						3034
GAG	ITSLPKQEQK	526	10	01	50						3035
GAG	PSQKQEPIDK	528	10	11	18						3036
GAG	GARASVLSGGK	2	11	29	46						3037
GAG	LSGGKLDWEK	8	11	15	23						3038
GAG	KLDWEKILRL	12	11	16	25						3039
GAG	KLDWEKILRL	12	11	10	16						3040
GAG	KIRLRPGKKK	18	11	30	47						3041
GAG	RLRPGKKKKYK	20	11	12	19						3042
GAG	RLRPGKKKKYK	20	11	19	30						3043
GAG	HIVWASRELER	34	11	20	31						3044
GAG	HLVWASRELER	34	11	26	41						3045

Table IX
HIV Δ03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	Δ*1101	Δ*3101	Δ*3301	Δ*6801	SEQ ID NO
GAG	TVATLYCVIIQK	83	11	12	19						3046
GAG	TVATLYCVIIQR	83	11	14	22						3047
GAG	EVKDTKEALDK	95	11	13	20						3048
GAG	ALDKIEEQNK	102	11	17	23						3049
GAG	KIEEQNKSKK	105	11	15	23						3050
GAG	PAADKXKIDSK	123	11	01	50						3051
GAG	ISPRTLNAWVK	168	11	36	56						3052
GAG	LSPRTLNAWVK	168	11	17	17						3053
GAG	TINIEAAEWDIR	225	11	53	83						3054
GAG	IIAGPIAFQMR	240	11	18	28						3055
GAG	IIAGPIPPQMR	240	11	17	27						3056
GAG	PIAPGQMRPR	243	11	19	30						3057
GAG	PIPPGQMRPR	243	11	17	27						3058
GAG	WILGLNKIVR	289	11	57	89						3059
GAG	TSILDIRQGP	304	11	12	19						3060
GAG	VSILDIRQGP	304	11	16	25						3061
GAG	VSILDIRQGP	304	11	25	39						3062
GAG	DIKQIPKEIFR	308	11	19	30						3063
GAG	DIRQIPKEIFR	308	11	41	64						3064
GAG	LLVQNANPDK	345	11	58	91						3065
GAG	NANPDKTILK	349	11	27	42						3066
GAG	NANPDKTILK	349	11	18	28						3067
GAG	AAIMMQIKSNFK	406	11	06	15						3068
GAG	ATIMMQIKGNFR	406	11	11	28						3069
GAG	MMQIGHFRNQR	409	11	15	23						3070
GAG	IIAKNCRAPRK	433	11	16	25						3071
GAG	IIAKNCRAPRK	433	11	13	20						3072
GAG	IIAKNCRAPRK	433	11	20	31						3073
GAG	IIAKNCRAPRK	434	11	14	22						3074
GAG	IIAKNCRAPRK	434	11	13	21						3075
GAG	LARNCRAPRK	434	11	19	30						3076
GAG	CTERQANFLGK	459	11	52	83						3077
GAG	EITSLPKQEQK	525	11	01	50						3078
NEF	AVSQDLDK	48	8	10	16						3079
NEF	AVSRDLEK	48	8	11	17						3080
NEF	PLRPMTYK	102	8	10	16						3081
NEF	PLRPMTYK	102	8	49	77		0.0003				3082
NEF	LSFLLKEK	114	8	22	34						3083
NEF	LSIIFLKEK	114	8	27	42						3084
NEF	GLIYSKKR	173	8	23	36						3085
NEF	YTPGPGIR	207	8	20	31						3086
NEF	YTPGPGIR	207	8	21	33						3087
NEF	YTPGPGIR	207	8	12	19						3088
NEF	LTFGWCCK	221	8	39	61						3089
NEF	KLVPVDR	228	8	11	17						3090
NEF	ELIPEFYK	324	8	14	22						3091
NEF	ELHPEYK	324	8	22	34						3092
NEF	GAVSQDLDK	47	9	10	16						3093
NEF	GAVSQDLK	47	9	11	17						3094
NEF	PVRQVPLR	95	9	48	75	0.0002	0.0009	0.0004	0.0006	0.0001	3095

Table IX
HIV Δ03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ°0301	Δ°1101	Δ°3101	Δ°3301	Δ°6801	SEQ ID NO
NEF	AVDLSIFLK	111	9	14	22	0.0740	1.1000	0.0009	0.0008	0.0025	3096
NEF	DLSPFLKEK	113	9	22	34						3097
NEF	DLSPFLKEK	113	9	27	42						3098
NEF	GLDGLIYSK	125	9	16	25						3099
NEF	GLEGLIYSK	125	9	10	16						3100
NEF	PLTFGWCFK	219	9	39	61						3101
NEF	AADGVGVSR	42	10	09	15						3102
NEF	QVPLRIMTFK	100	10	10	16						3103
NEF	QVPLRIMTYK	100	10	46	72						3104
NEF	GAFDLSFFLK	110	10	10	16						3105
NEF	GLDGLIYSK	125	10	14	22		0.6300	0.0098	0.0130	0.0600	3106
NEF	GVGAVSQDLCK	45	11	10	16						3107
NEF	GVGAVSRDLCK	45	11	11	17						3108
NEF	AVDLSIFLKEX	111	11	13	20						3109
NEF	GLDGLIYSKKR	125	11	14	22						3110
NEF	MARELIPEYYK	321	11	10	16						3111
POL	RANSPTR	26	8	16	25						3112
POL	RANSPTR	26	8	17	27						3113
POL	STNSPTSR	32	8	01	33						3114
POL	RANSPSSR	35	8	01	33						3115
POL	RANSPTR	37	8	01	50						3116
POL	ILHICGK	149	8	14	22						3117
POL	LIEICGK	150	8	10	16						3118
POL	LIEICGKK	150	8	14	22						3119
POL	PIETVPVK	190	8	53	83						3120
POL	ETVPVKLK	192	8	53	83						3121
POL	QMDGPKVK	201	8	51	80	0.0049	0.0001				3122
POL	PLTEEKIK	212	8	55	86	0.0007	0.0004				3123
POL	EICTEMEK	223	8	27	42						3124
POL	NTPIFAIK	246	8	24	38						3125
POL	NTPVFAIK	246	8	37	58		0.0003				3126
POL	PIFAIKKK	248	8	25	39						3127
POL	PVFAIKKK	248	8	37	58		0.0001				3128
POL	PAGLKKKK	286	8	52	81						3129
POL	PLDKDFRK	308	8	19	30						3130
POL	NVLPQGWK	336	8	63	100		0.0012				3131
POL	KLEFPRK	355	8	23	36						3132
POL	DLKIQIR	381	8	52	81						3133
POL	EIQHIRAK	383	8	27	42						3134
POL	EIQHIRT	383	8	22	34						3135
POL	RAKIEELR	388	8	26	41						3136
POL	RTKIEELR	388	8	22	34						3137
POL	ELREHLIK	393	8	17	27						3138
POL	ELRQHLLR	393	8	15	23						3139
POL	WTVNDIQK	441	8	62	97		0.0001				3140
POL	DIQKLVGK	445	8	62	97						3141
POL	ELELAENR	489	8	53	83						3142
POL	GVYYDFSK	508	8	43	67						3143
POL	DLIAEIQK	516	8	28	44						3144
POL	QIQEPFK	532	8	41	64	0.0010	0.0013				3145

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*3301	Δ^*6801	SEQ ID NO
POL	GAITNDVK	551	8	19	30						3146
POL	SAITNDVK	551	8	16	25						3147
POL	TAITNDVK	551	8	11	17						3148
POL	QLTEAVOK	559	8	37	58						3149
POL	QLTEVQVK	559	8	11	17						3150
POL	ESIVIVGK	570	8	50	79						3151
POL	VIWGTKPK	573	8	48	75						3152
POL	KLWYQLEK	616	8	46	72						3153
POL	YVDGAANR	633	8	50	78	0.0003	0.0001				3154
POL	GAANRETK	636	8	45	70						3155
POL	KAGYVTDK	646	8	42	66						3156
POL	VTDRGRQK	650	8	40	63	0.0090	0.0065				3157
POL	LTDTTNQK	661	8	19	30						3158
POL	LTETTNQK	661	8	30	47						3159
POL	IIQAQPDK	697	8	40	63						3160
POL	IIQAQPDK	697	8	16	25						3161
POL	IIQELIK	712	8	37	58						3162
POL	IIQELIK	713	8	37	58						3163
POL	LAWVPATK	725	8	22	34						3164
POL	LSWVPATK	725	8	37	58						3165
POL	KLVSAGIR	742	8	16	25						3166
POL	KLYSSGIR	742	8	29	45						3167
POL	LVSSGIRK	743	8	16	25	0.0091	0.0054				3168
POL	LVSSGIRK	743	8	27	42						3169
POL	KAQEEIEK	759	8	27	43						3170
POL	KAQEEIEK	759	8	16	25						3171
POL	NLPPVAVK	779	8	26	41						3172
POL	NLPPVAVK	779	8	27	42						3173
POL	EIVASCDK	787	8	45	70						3174
POL	ETAYFILK	848	8	31	48						3175
POL	ETAYFLK	848	8	27	42	0.0037	0.0430				3176
POL	FLKLAKR	852	8	32	50						3177
POL	FLKLAKR	852	8	25	39						3178
POL	LAGRWPK	856	8	50	78						3179
POL	GVVESMNK	901	8	49	77						3180
POL	ESMNKELK	904	8	53	83						3181
POL	SMNKLK	905	8	53	83						3182
POL	AVFIINFK	931	8	62	97	0.0280	0.0380				3183
POL	FIINFKRK	933	8	58	91						3184
POL	IASDQTK	956	8	14	22						3185
POL	IATDIQTK	956	8	36	56						3186
POL	ELQKQIK	964	8	13	21						3187
POL	ELQKQIK	964	8	35	56						3188
POL	IKIQNFR	969	8	12	19						3189
POL	IKIQNFR	969	8	36	57						3190
POL	RYYYRUSK	976	8	58	91						3191
POL	DSRDIWK	981	8	35	55						3192
POL	DSRDIWK	981	8	14	22						3193
POL	PIWKGPAK	985	8	36	56						3194
POL	PLWKGPAK	985	8	19	30						3195

Table IX
 HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*3301	Δ^*6801	SEQ ID NO
POL	DIKVVPRR	1009	8	48	75						3196
POL	EIKVVPRR	1009	8	16	25						3197
POL	VVPRKAK	1012	8	52	81	0.0027	0.0001				3198
POL	VVPRKVK	1012	8	11	17						3199
POL	KIKDYGK	1019	8	11	17						3200
POL	KIKDYGK	1019	8	50	78						3201
POL	LAFQGGAR	6	9	12	19						3202
POL	LAFQGGAR	6	9	16	25						3203
POL	QTRANSPT	21	9	15	24						3204
POL	NSTNSPTSR	31	9	01	33						3205
POL	PTSRELQVR	36	9	01	33						3206
POL	PSSRELQVR	39	9	01	50						3207
POL	TIKIGGQLK	99	9	17	27	0.2700	0.0330	0.0062	0.0008	0.1100	3208
POL	DINLPGKWK	122	9	13	20						3209
POL	EINLPGKWK	122	9	12	19						3210
POL	NLNGKWKPK	124	9	36	56						3211
POL	GIGGFIKVK	136	9	11	17						3212
POL	GIGGFIKVK	136	9	53	83	0.0008	0.0005	0.0062	0.0120	0.0001	3213
POL	QILHICGK	148	9	14	22						3214
POL	ILHICGKK	149	9	14	22						3215
POL	PTVNIJGR	166	9	54	84	0.0008	0.0001	0.0007	0.0120	0.0002	3216
POL	CTEMIEKKG	225	9	28	44	0.0002	0.0001	0.0006	0.0006	0.0002	3217
POL	NTPIFAIK	246	9	24	38						3218
POL	NTVFAIKK	246	9	37	58	0.0330	0.0600	0.0006	0.0006	1.7000	3219
POL	AIKKKDSIK	251	9	57	87	0.0017	0.0006	0.0006	0.0005	0.0001	3220
POL	LYDFRELNK	263	9	62	99	0.0110	0.0300	0.0006	0.0006	0.0002	3221
POL	GIPIIPAGLK	282	9	56	89	0.2300	0.0650	0.0007	0.0005	0.0110	3222
POL	SVPLIKDPR	306	9	18	28						3223
POL	AIFQSSMTK	347	9	36	56	1.1000	0.9600	0.0076	0.0005	0.0230	3224
POL	MTKILEPR	353	9	43	67	0.0008	0.0160	0.2200	0.4200	0.3100	3225
POL	TPDKKLIQK	404	9	57	89	0.0002	0.0042	0.0021	0.0029	0.0053	3226
POL	ASQIYAGIK	456	9	27	43	0.0013	0.3400	0.0005	0.0018	0.0001	3227
POL	ASQIYPPGK	456	9	28	44						3228
POL	QIYAGIKVK	458	9	20	32						3229
POL	QIYGIKVK	458	9	12	19						3230
POL	QIYGIKVR	458	9	14	22						3231
POL	GKIVLQCK	462	9	28	44						3232
POL	GKIVLQCK	462	9	19	30						3233
POL	LAENREIK	492	9	54	84	0.0002	0.0003	0.0004	0.0006	0.0001	3234
POL	NLKTGKYAK	540	9	28	44						3235
POL	NLKTGKYAR	540	9	29	46						3236
POL	KTGKYAKMR	542	9	19	30	0.0008	0.0001	0.0130	0.4400	0.0033	3237
POL	KTGKYARMR	542	9	13	21						3238
POL	RSATINDVK	550	9	10	16						3239
POL	IVIWGKTPK	572	9	48	75	0.0850	0.3700	0.9900	0.3000	0.0330	3240
POL	FVNTIPLVK	608	9	54	86	0.0120	0.0660	0.0009	0.0009	0.0380	3241
POL	YVTDIGRQK	649	9	39	61	0.0011	0.0010	0.0006	0.0006	0.0039	3242
POL	SLTDITNQK	660	9	11	17						3243
POL	SLTETTNQK	660	9	21	33						3244
POL	GIHQAPDK	696	9	40	63	0.0009	0.0400	0.0006	0.0005	0.0003	3245

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	GIQAQPR	696	9	16	25	0.0091	0.1600	0.0006	0.0005	0.0120	3246
POL	QIEQLJK	712	9	37	58	0.0770	0.0570	0.0550	0.8800	4.0000	3247
POL	YLAWPAIK	724	9	22	34	0.1300	0.0770	0.0017	0.0020	0.0001	3248
POL	YLSWPAIK	724	9	37	58	0.0380	0.0320	0.0006	0.0006	0.0004	3249
POL	KLVSSGIRK	742	9	16	25	0.0027	0.0140	0.0020	0.0009	0.0001	3250
POL	KLVSAGIRK	742	9	27	42	2.7000	0.0690	0.2100	0.0006	0.0002	3251
POL	VLFLXGIRK	751	9	51	80	0.0130	0.0470	0.0023	0.0041	0.0014	3252
POL	ASCDKQK	790	9	43	67	0.0170	0.3000	0.0480	0.0560	3.2000	3253
POL	KLGRWPVK	855	9	50	78	0.1700	1.8000	3.5000	0.2700	1.9000	3254
POL	AACWVAGIK	880	9	21	33	0.0250	0.0080	0.0007	0.0005	0.0002	3255
POL	ESMKNELK	904	9	53	83	0.0009	0.0006	0.0006	0.0018	0.0001	3256
POL	MAVFIHFK	930	9	60	94	0.0021	0.0015	0.2400	0.0660	0.2600	3257
POL	AVFIHFKR	931	9	62	97	0.0009	0.0068	0.0006	0.0005	0.0001	3258
POL	IASHIQTK	955	9	14	22	0.0002	0.0001	0.0006	0.0069	0.0065	3259
POL	DIATDIQTK	955	9	35	55	0.0290	0.0039	0.3100	0.0008	0.0002	3260
POL	DIQTRKELQK	959	9	46	72	0.0002	0.0001	0.0006	0.0069	0.0065	3261
POL	QIKIQNFR	968	9	12	19	0.0002	0.0001	0.0006	0.0069	0.0065	3262
POL	QIKIQNFR	968	9	35	55	0.0002	0.0001	0.0006	0.0069	0.0065	3263
POL	VIQNSDIK	1003	9	37	58	0.0002	0.0001	0.0006	0.0069	0.0065	3264
POL	VIQNSDIK	1003	9	12	19	0.0002	0.0001	0.0006	0.0069	0.0065	3265
POL	NSDIKVVPR	1007	9	40	63	0.0002	0.0001	0.0006	0.0069	0.0065	3266
POL	NSEIKVVPR	1007	9	12	19	0.0002	0.0001	0.0006	0.0069	0.0065	3267
POL	DIKVVPRK	1009	9	48	75	0.0002	0.0001	0.0006	0.0069	0.0065	3268
POL	DIKVVPRK	1009	9	15	23	0.0002	0.0001	0.0006	0.0069	0.0065	3269
POL	KVVPKAK	1011	9	52	81	0.0002	0.0001	0.0006	0.0069	0.0065	3270
POL	KVVPKAK	1011	9	11	17	0.0002	0.0001	0.0006	0.0069	0.0065	3271
POL	NLAFFQGEAR	5	10	10	16	0.0002	0.0001	0.0006	0.0069	0.0065	3272
POL	NLAFFQGEAR	5	10	16	25	0.0002	0.0001	0.0006	0.0069	0.0065	3273
POL	NLAFFQGEAR	5	10	11	18	0.0002	0.0001	0.0006	0.0069	0.0065	3274
POL	QTRANSPTSR	21	10	12	19	0.0002	0.0001	0.0006	0.0069	0.0065	3275
POL	QTRANSPTSR	21	10	01	50	0.0002	0.0001	0.0006	0.0069	0.0065	3276
POL	QTRANSPTSR	24	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3277
POL	QTRANSPTSR	33	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3278
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3279
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3280
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3281
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3282
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3283
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3284
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3285
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3286
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3287
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3288
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3289
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3290
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3291
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3292
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3293
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3294
POL	QTRANSPTSR	35	10	01	33	0.0002	0.0001	0.0006	0.0069	0.0065	3295

Table IX
HIV Δ03 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SI:Q ID NO
POL	FSVPLDKDFR	305	10	18	28						3296
POL	SVPLDKDFRK	306	10	18	28						3297
POL	SINNETGIR	323	10	32	50						3298
POL	STNETTGIR	323	10	11	17						3299
POL	PAIFQSSMTK	346	10	36	56		0.0830	0.0017	0.0025	0.0046	3300
POL	SMTKILEPFR	352	10	42	66	0.0760	0.0004				3301
POL	MTKILEPFRK	353	10	22	34	0.0004	0.0004	0.0150	0.0060	0.1100	3302
POL	GSDLEIGQIR	379	10	52	81	0.0150	0.0380				3303
POL	DLEIGQIRAK	381	10	27	42						3304
POL	DLEIGQIRTK	381	10	21	33						3305
POL	FTTPDKKIQK	403	10	51	80	0.0002	0.0150	0.0010	0.0013	0.0273	3306
POL	WMGYELIPDK	418	10	60	94	0.0005	0.0004	0.0009	0.0016	0.0003	3307
POL	TVQPIQLPEK	429	10	17	27						3308
POL	TVQPIVLPEK	429	10	13	20	0.1600	5.6000				3309
POL	DSWTVNDIQK	439	10	43	67	0.0007	0.0002				3310
POL	ESWTVNDIQK	439	10	11	17						3311
POL	WASQIVAGIK	455	10	27	42						3312
POL	WASQIVYGIK	455	10	28	44						3313
POL	KVKQLCKLLR	464	10	27	42						3314
POL	KVRQLCKLLR	464	10	19	30						3315
POL	QLCKLLRGAK	467	10	25	39						3316
POL	QLCKLLRGTK	467	10	21	33						3317
POL	EAELELAENR	487	10	53	83						3318
POL	ELAENREILK	491	10	54	84	0.0002	0.0003				3319
POL	ATESIVIWGK	568	10	19	30						3320
POL	SIVWGKTPK	571	10	42	66						3321
POL	VIWGKTPKFK	573	10	17	27						3322
POL	VIWGKTPKFR	573	10	29	45						3323
POL	LVKLWYQLEK	614	10	46	72			0.0075	0.0081	0.0097	3324
POL	AANRETKLGK	637	10	30	47	0.0560	0.0820				3325
POL	KAGYVYDRGR	646	10	39	61	0.0007	0.0016				3326
POL	VSLTDTNQK	659	10	10	16						3327
POL	VSLTETNQK	659	10	20	31						3328
POL	VSQIEQLIK	710	10	19	30						3329
POL	IEQLIKKEK	713	10	30	47	0.0007	0.0370	0.0017	0.0025	0.0007	3330
POL	GIGGNEQVDK	733	10	58	91	0.0004	0.0003	0.0009	0.0008	0.0003	3331
POL	KVFLDGDIK	750	10	48	75	0.0005	0.0001	0.0009	0.0009	0.0003	3332
POL	VASCDKCKLK	789	10	43	67	0.3600	0.7800				3333
POL	QLDCTILEGK	814	10	60	95	0.0004	0.0004				3334
POL	GSNFTSAVK	870	10	26	41	0.0010	0.0003				3335
POL	GSNFTETVK	870	10	11	17						3336
POL	KAACWWAGIK	879	10	20	32	0.0300	0.0740	0.0017	0.0025	0.0002	3337
POL	VVESMNKELK	902	10	48	75						3338
POL	ELKKIGQVR	909	10	56	88						3339
POL	QVRDQAEILK	916	10	44	69	0.0089	0.0093				3340
POL	QVREQAEILK	916	10	13	20						3341
POL	QMAVFIHFK	929	10	60	94	0.6100	0.6400	0.0240	0.0083	0.0610	3342
POL	MAVFIHFKR	930	10	60	94	0.0068	0.0083				3343
POL	AVFIHFKRK	931	10	58	91	0.6600	0.8500				3344
POL	GIGGYSAGER	942	10	58	91	0.0003	0.0001	0.0010	0.0029	0.0003	3345

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	DIASDIQTK	954	10	14	22						3346
POL	DIATDIQTK	954	10	34	53						3347
POL	KIQNFRVYYR	971	10	52	81	0.0056	0.0130	0.0017	0.0025	0.0170	3348
POL	VVIQNSDIK	1002	10	37	58	0.0320	0.2100	6.6000	0.0850	0.0380	3349
POL	VVIQNSEIK	1002	10	12	19	0.0005	0.0210	0.0010	0.0013	0.0018	3350
POL	NSDIKVVPRR	1007	10	40	63						3351
POL	NSDIKVVPRR	1007	10	12	19	0.0007	0.0001				3352
POL	KAKIKDYCK	1017	10	41	64	0.0048	0.0018				3353
POL	MAGIDCVAGR	1028	10	24	38						3354
POL	MAGIDCVAGR	1028	10	19	30						3355
POL	NSPTSRELQVR	34	11	01	33						3356
POL	NSPTSRELQVR	37	11	01	50						3357
POL	NSPTRELQVR	39	11	01	50						3358
POL	FSFQITLWQR	85	11	14	22						3359
POL	TLWQRPLVTIK	91	11	17	27						3360
POL	TLWQRPLVTIK	91	11	13	20						3361
POL	LVTKIGGQGLK	97	11	13	20						3362
POL	TVLEDINLPCK	118	11	13	20						3363
POL	TVLEENLPCK	118	11	12	19						3364
POL	DINLPCKWPK	122	11	13	20						3365
POL	ENLPCKWPK	122	11	12	19						3366
POL	KMIGGIGGHIK	132	11	62	97	2.3000	0.7000				3367
POL	PSPIETVPVK	187	11	53	83						3368
POL	KVKQWPLETEK	207	11	46	72	0.0750	0.0330				3369
POL	ALVEICTEMEK	220	11	15	23						3370
POL	EICTEMEKEGK	223	11	27	42						3371
POL	AIKKKDKTKWR	251	11	57	89						3372
POL	STKWRKLVDFR	257	11	58	91						3373
POL	KLVDRELNRK	262	11	60	94						3374
POL	QLGIPHPAGLK	280	11	56	89						3375
POL	GIPHPAGLK	282	11	53	84						3376
POL	FSVPLDKDFRK	305	11	18	28						3377
POL	PSINNE:TPGIR	322	11	31	48						3378
POL	PSINNE:TPGIR	322	11	11	17						3379
POL	SSMTKILEPFR	351	11	32	50						3380
POL	SSMTKILEPFR	352	11	22	34						3381
POL	KIELREILLK	390	11	13	20						3382
POL	KIELRQHLLR	390	11	15	23						3383
POL	LLKWGHTTDDK	398	11	23	36						3384
POL	LLRWGHTTDDK	398	11	23	36						3385
POL	WTVQPIQLPEK	428	11	17	27						3386
POL	WTVQPIVLNEK	428	11	13	20	0.0011	0.0510				3387
POL	TVNDIQKLVGK	442	11	61	95	0.0400	0.1700				3388
POL	ASQIYAGIKVK	456	11	20	32						3389
POL	ASQIYAGIKVK	456	11	12	19						3390
POL	ASQIYAGIKVR	460	11	14	22						3391
POL	YAGIKVKQLCK	505	11	18	28						3392
POL	PVIIGVYDFSK	513	11	39	61						3393
POL	PSKDLIAEIQK	513	11	25	39						3394
POL	WTYQIYQEPFK	529	11	40	63	0.9200	0.0540				3395

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HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3301	A*6801	SIQ ID NO
POL	QYQEFKMLK	532	11	40	63	0.2800	0.2900			3396
POL	NLTKGYAKMR	540	11	18	29					3397
POL	NLTKGYARMR	540	11	13	21					3398
POL	RMRGATNDVK	548	11	12	19					3399
POL	DYKQLTEAVOK	556	11	33	52		0.0240			3400
POL	IATESIVWGR	567	11	14	22	0.0048				3401
POL	ESIVWGRTPK	570	11	41	65					3402
POL	IVIWGKTPFK	572	11	17	27					3403
POL	IVIWGKTPFR	572	11	29	45					3404
POL	KTPKFKLPQK	577	11	14	22					3405
POL	KTPKFKLPQK	577	11	22	34					3406
POL	PLVKLWYQLEK	613	11	45	67					3407
POL	ETFYVDGAANR	630	11	43	70					3408
POL	YVDGAANRET	633	11	44	69					3409
POL	GAANRETQK	636	11	30	47					3410
POL	KLGRAGYVTDK	643	11	24	38					3411
POL	VVSLTUTNQK	658	11	10	16					3412
POL	VVSLTUTNQK	658	11	11	17					3413
POL	ALGIQAQPDK	694	11	39	61					3414
POL	ALGIQAQPDK	694	11	15	23					3415
POL	LVNQHIEQLK	709	11	15	23					3416
POL	LVNQHIEQLK	709	11	18	28					3417
POL	VSQIEQLKK	710	11	19	30					3418
POL	QIEQLKKKK	712	11	30	47					3419
POL	KVYLAWVPAHK	722	11	20	32	8.6000	2.3000			3420
POL	KVYLSWVPAHK	722	11	23	37					3421
POL	QVDKLVSAIR	739	11	15	23					3422
POL	QVDKLVSSGR	739	11	29	45					3423
POL	GIDKAQEEIEK	756	11	25	39					3424
POL	GIDKAQEEIEK	756	11	14	22					3425
POL	VAKIVASCDK	784	11	45	71					3426
POL	IVASCDKQK	788	11	43	67	0.0970	0.1000			3427
POL	TAYFILKLAGR	849	11	31	48					3428
POL	TAYFILKLAGR	849	11	24	38					3429
POL	ILKLAGRWPK	853	11	30	47					3430
POL	LLKLACRWPK	853	11	20	31					3431
POL	QSQGVVSMNK	898	11	49	77					3432
POL	GIVVSMNKELK	901	11	48	75					3433
POL	VVESMNKELK	902	11	48	75					3434
POL	QMAVFIINFKR	929	11	60	94					3435
POL	MAVFIINFKR	930	11	57	89					3436
POL	ASDIQTKELQK	957	11	11	17					3437
POL	ATDIQTKELQK	957	11	35	55	0.0051	0.1800			3438
POL	QTKELQKQHK	961	11	10	16					3439
POL	QTKELQKQITK	961	11	32	50	0.0050	0.0100			3440
POL	AVVIQDNDIK	1000	11	37	58	0.0004	0.0150			3441
POL	AVVIQDNDSEIK	1000	11	12	19					3442
POL	NSDIKVVPRRK	1007	11	40	63					3443
POL	NSEIKVVPRRK	1007	11	11	17					3444
POL	DIKVVFRKAK	1009	11	39	61					3445

Table IX
 HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	EIKVVRKKAK	1009	11	13	20						3446
POL	VVPRRKAKIR	1012	11	42	66						3447
POL	QMGDDCVAGR	1027	11	24	38						3448
POL	QMGDDCVASR	1027	11	19	30						3449
REV	DSDELLK	7	8	12	19						3450
REV	QARKNRRR	40	8	17	27						3451
REV	QARKNRR	40	8	38	59						3452
REV	RARORQIR	50	8	12	19						3453
REV	ILSTCLGR	63	8	12	19						3454
REV	GTETGVGR	103	8	06	19						3455
REV	LLKTVRLIK	12	9	10	16						3456
REV	GTRQARKNR	36	9	15	23						3457
REV	GTRQARKNR	36	9	34	53						3458
REV	GTRQTRKNR	37	9	01	50						3459
REV	TTRQARKNR	37	9	01	50						3460
REV	QARKNRRR	40	9	16	25						3461
REV	QARKNRRR	40	9	38	59						3462
REV	RILSTCLGR	62	9	12	19						3463
REV	PLQLPIER	76	9	11	17						3464
REV	PLQLPIER	76	9	35	55						3465
REV	PSPECTRQAR	31	10	13	20						3466
REV	GTRQARKNR	36	10	15	23						3467
REV	GTRQARKNR	36	10	34	53						3468
REV	GTRQTRKNR	37	10	01	50						3469
REV	TTRQARKNR	37	10	01	50						3470
REV	RSQDSDELLK	4	11	11	17						3471
REV	PSPECTRQAR	31	11	13	20						3472
REV	GTRQARKNR	36	11	14	22						3473
REV	GTRQARKNR	36	11	34	53						3474
REV	GTRQTRKNR	37	11	01	50						3475
REV	TTRQARKNR	37	11	01	50						3476
REV	QARKNRRRWR	40	11	16	25						3477
REV	QARKNRRRWR	40	11	37	58						3478
REV	IVPLQLPIER	74	11	11	17						3479
REV	PVPLQLPIER	74	11	34	53						3480
TAT	GLGISYGR	45	8	55	87						3481
TAT	GISYGRKK	47	8	58	91						3482
TAT	ISYGRKKR	48	8	58	91						3483
TAT	PTGPKESK	88	8	20	31						3484
TAT	TACNNCYCK	23	9	17	27						3485
TAT	TACTNICYCK	23	9	10	16						3486
TAT	GLGISYGRK	45	9	55	87			0.0017	0.0020	0.0001	3487
TAT	GISYGRKKR	47	9	57	89			0.0018	0.0014	0.0001	3488
TAT	ISYGRKKRR	48	9	46	72			0.3900	0.1300	0.0032	3489
TAT	PTGPKESKK	88	9	18	28						3490
TAT	ESKKVIESK	93	9	12	19						3491
TAT	PVDPRLERWK	3	10	11	17						3492
TAT	TACNNCYCKK	23	10	11	17						3493
TAT	GLGISYGRKK	45	10	55	87						3494
TAT	GISYGRKKRR	47	10	45	70						3495

Table IX
HIV Δ03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	Δ*1101	Δ*3101	Δ*3301	Δ*6801	SEQ ID NO
TAT	PTQPKESKKK	88	10	12	19						3496
TAT	KAGGGYPRR	101	10	01	50						3497
TAT	GLGISYGRKKK	45	11	54	86						3498
TAT	ISYGRKKRRQR	48	11	39	61						3499
TAT	KAGGGYPRRK	101	11	01	50						3500
VIF	LIVWQVDR	8	8	10	16						3501
VIF	MIVWQVDR	8	8	46	72						3502
VIF	QVDRMKIR	12	8	13	20						3503
VIF	QVDRMRIR	12	8	34	53						3504
VIF	RMIRNTWK	15	8	10	16						3505
VIF	RMIRNTWK	15	8	15	23						3506
VIF	RTWKSLSVK	19	8	15	23						3507
VIF	RTWNSLSVK	19	8	27	42						3508
VIF	IIPLGDAR	56	8	13	20						3509
VIF	IIPLGEAR	56	8	20	31						3510
VIF	GVSEWRK	87	8	16	25						3511
VIF	VSIEWRLR	88	8	15	23						3512
VIF	SIEWRLRR	89	8	11	17						3513
VIF	FSDSAIRK	120	8	13	20						3514
VIF	FSESAIRK	120	8	14	22						3515
VIF	SLQYLALK	149	8	13	20						3516
VIF	LALTALIK	153	8	16	25						3517
VIF	LTALIKPK	155	8	13	20						3518
VIF	TALIKPKK	156	8	11	17						3519
VIF	LIRPKKKIK	158	8	10	16	0.0003	0.0045				3520
VIF	LTEDRWNK	178	8	31	48						3521
VIF	LVEDRWNK	178	8	11	17						3522
VIF	VMIVWQVDR	7	9	44	69	0.0034	0.0220	4.8000	5.5000	0.0010	3523
VIF	IVWQVDRMK	9	9	12	19	0.0034	0.0220	4.8000	5.5000	0.0010	3524
VIF	IVWQVDRMR	9	9	47	73	0.0008	0.0007	0.4500	0.5600	0.0048	3525
VIF	GVSEWRRLR	87	9	14	22						3526
VIF	VSIEWRLR	88	9	11	17						3527
VIF	YSLQYLALK	148	9	13	20						3528
VIF	YSLQYLALK	152	9	16	25						3529
VIF	YSLQYLALK	152	9	13	20						3530
VIF	YSLQYLALK	152	9	13	20						3531
VIF	YSLQYLALK	152	9	13	20						3532
VIF	YSLQYLALK	152	9	13	20						3533
VIF	YSLQYLALK	152	9	13	20						3534
VIF	YSLQYLALK	152	9	13	20						3535
VIF	YSLQYLALK	152	9	13	20						3536
VIF	YSLQYLALK	152	9	13	20						3537
VIF	YSLQYLALK	152	9	13	20						3538
VIF	YSLQYLALK	152	9	13	20						3539
VIF	YSLQYLALK	152	9	13	20						3540
VIF	YSLQYLALK	152	9	13	20						3541
VIF	YSLQYLALK	152	9	13	20						3542
VIF	YSLQYLALK	152	9	13	20						3543
VIF	YSLQYLALK	152	9	13	20						3544
VIF	YSLQYLALK	152	9	13	20						3545

Table IX
 HIV Δ03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	Δ*1101	Δ*3101	Δ*3301	Δ*6801	SH:Q 113 NO
VIF	ALTALIKPKK	154	10	11	17						3546
VIF	PSVKLTEDR	173	10	13	20						3547
VIF	VMIVQVDRMR	7	11	41	64						3548
VIF	IVWQVDRMKIR	9	11	12	19						3549
VIF	IVWQVDRMRIR	9	11	33	52						3550
VIF	QVDRMRINTWK	12	11	10	16						3551
VIF	QVDRMRINTWK	12	11	14	22						3552
VIF	SLVKHIIMYSK	23	11	12	19						3553
VIF	LYKHIIMYSKK	24	11	12	19						3554
VIF	TYWGLITGER	69	11	22	34						3555
VIF	IILGHGYSIEWR	83	11	22	34						3556
VIF	IILGQGVSEWR	83	11	25	39						3557
VIF	YLALTALIKPK	152	11	13	20						3558
VIF	LALTALIKPKK	153	11	11	17						3559
VIF	LTEDRWNKPKQ	178	11	21	33	0.0390	0.0130				3560
VIF	LVEDRWNKPKQ	178	11	10	16						3561
VPR	ELKNEAVR	25	8	17	27						3562
VPR	ELKNEAVR	25	8	16	25						3563
VPR	EAVRIIFR	29	8	59	92						3564
VPR	QLLFVIFR	66	8	44	69						3565
VPR	QLLFVIFR	66	8	10	16						3566
VPR	RIGCQIISR	74	8	47	73						3567
VPR	RIGCQIISR	74	8	12	19						3568
VPR	ISRIGIIR	79	8	10	16						3569
VPR	ISRIGIIR	79	8	11	17						3570
VPR	RIGITRQR	81	8	10	16						3571
VPR	RLPGRQR	85	8	01	50						3572
VPR	NIRGRVR	85	8	01	50						3573
VPR	RAKNGASR	93	8	19	30						3574
VPR	ALELLEELK	19	9	10	16						3575
VPR	TLLELLEELK	19	9	44	69						3576
VPR	WAGVEAIR	54	9	16	25						3577
VPR	FIIFRIGCR	69	9	11	17						3578
VPR	FIIFRIGCR	69	9	10	16						3579
VPR	RIGITRQR	81	9	10	16						3580
VPR	QAPEDQGRQR	3	10	39	62						3581
VPR	WALELLEELK	18	10	09	15						3582
VPR	WTLELLEELK	18	10	42	69						3583
VPR	KSEAVRIIFR	27	10	14	22						3584
VPR	ISRIGITRQR	79	10	10	16						3585
VPR	LLEELKNEAVR	22	11	17	27						3586
VPR	LLEELKSEAVR	22	11	16	25						3587
VPR	DTWAGVEAIR	52	11	16	25						3588
VPR	DTWAGVEAIR	52	11	18	28						3589
VPR	ILQQLLFIFR	63	11	35	55						3590
VPR	LLHFIFRIGCR	67	11	11	17						3591
VPR	HSRIGITRQR	79	11	10	16						3592
VPU	TIVFIEYR	35	8	10	16						3593
VPU	IVFIEYRK	36	8	12	19						3594
VPU	LVQRKQDR	43	8	01	50						3595
VPU	KIDRLIDR	52	8	15	23						3596

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 HIV Δ03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	Δ*1101	Δ*1101	Δ*1301	Δ*6801	SEQ ID NO
VPV	LIDRIR	58	8	14	22						3596
VPV	VTLLSSK	94	8	01	50						3597
VPV	WTIVFIEYR	34	9	10	16						3598
VPV	LVQRKQDRR	43	9	01	50						3599
VPV	ILRQRKIDR	46	9	15	23						3600
VPV	RLIDRIR	56	9	10	16						3601
VPV	LVTLSSK	91	9	01	50						3602
VPV	KILRQRKIDR	45	10	15	23	0.0039	0.0001				3603
VPV	KIDRLIDRIR	52	10	10	16						3604
VPV	VVWTVFIEYR	31	11	10	16						3605

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SFQ ID NO
ENV	LILGLVII	21	8	09	15		3606
ENV	KLWVTYYY	44	8	11	17		3607
ENV	NLWVTYYY	44	8	35	56		3608
ENV	VYGVVPVW	49	8	55	86		3609
ENV	DTEVIINW	75	8	19	30		3610
ENV	NVTENFM	101	8	34	53		3611
ENV	VTEFNMW	102	8	34	53		3612
ENV	SLKPCVKL	128	8	55	86		3613
ENV	LTPLCVTL	135	8	54	84		3614
ENV	IYCAPAGF	262	8	27	42		3615
ENV	IYCTPAGF	262	8	11	17		3616
ENV	CTPAGFAI	264	8	10	16		3617
ENV	TVQCTIIGI	290	8	51	80		3618
ENV	PVSTQLL	300	8	60	94		3619
ENV	VYSTQLLL	301	8	60	94		3620
ENV	QLLLNGSL	305	8	57	89		3621
ENV	NTKRSIRI	351	8	10	16		3622
ENV	RIGHQTH	357	8	11	17		3623
ENV	GIGHQTH	360	8	01	33		3624
ENV	SIGSGQAF	360	8	01	33		3625
ENV	FYATGDII	367	8	12	19		3626
ENV	KLREIROF	405	8	01	25		3627
ENV	SFNCGGEF	437	8	36	56		3628
ENV	SFNCRGEF	437	8	16	25		3629
ENV	FYCNTSGL	445	8	21	33		3630
ENV	IIEGNTIL	478	8	01	50		3631
ENV	NITLPCR	482	8	11	17		3632
ENV	TITLPCR	482	8	14	22		3633
ENV	RIKQINM	488	8	30	47		3634
ENV	RIKQIVNM	488	8	12	19		3635
ENV	QIRCSSNI	512	8	11	17		3636
ENV	STNGTETF	537	8	01	17		3637
ENV	KVKIEPL	565	8	25	39		3638
ENV	AVGIGAVF	595	8	11	17		3639
ENV	STMGAASI	614	8	39	61		3640
ENV	LTVQARQL	623	8	38	59		3641
ENV	TVQARQLL	624	8	36	56		3642
ENV	IVQQNNIL	634	8	26	41		3643
ENV	IVQQSNIL	634	8	32	50		3644
ENV	AIQAQQIL	644	8	49	77		3645
ENV	HLLKLTW	650	8	13	20		3646
ENV	HLLQLTVW	650	8	34	53		3647
ENV	IMLQLTVW	650	8	10	16		3648
ENV	TVWGIKQL	655	8	59	92		3649
ENV	RVLAVERY	665	8	33	52		3650
ENV	VLAVERYL	666	8	34	53		3651
ENV	RYLKDQQL	671	8	30	47		3652
ENV	RYLRDQQL	671	8	18	28		3653
ENV	YLRDQQL	672	8	31	48	0.0001	3654
ENV	YLRDQQL	672	8	18	28		3655

Table X
HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*2401	SEQ ID NO
ENV	IWCGSKL	681	8	48	75		3656
ENV	NVPWNSSW	693	8	13	20		3657
ENV	IWDNMTW	716	8	13	20		3658
ENV	IWDNMTWM	717	8	11	17		3659
ENV	IWNMTWM	717	8	17	27		3660
ENV	WMEWEREI	723	8	12	19		3661
ENV	DLLALDKW	734	8	21	33		3662
ENV	ELLELDKW	734	8	20	31		3663
ENV	ALDKWASL	737	8	11	17		3664
ENV	ELDKWASL	737	8	11	17		3665
ENV	KWASLWNW	760	8	26	41		3666
ENV	SLWNWFDI	763	8	17	27		3667
ENV	WFDITNWL	767	8	10	16		3668
ENV	DITNWLWY	769	8	10	16		3669
ENV	ITNWLWYI	770	8	16	25		3670
ENV	ITNWLWYI	770	8	19	30		3671
ENV	ITNWLWYI	772	8	19	30		3672
ENV	KWLWYIKI	772	8	25	39		3673
ENV	WLYWYIKI	773	8	50	78		3674
ENV	WYIKIFI	774	8	49	77		3675
ENV	WYIKIFIM	775	8	43	67		3676
ENV	YIKIFIMI	776	8	43	67		3677
ENV	FIMIVGGL	780	8	44	69		3678
ENV	IMIVGGLI	781	8	35	56		3679
ENV	IVGGLIGL	783	8	42	66		3680
ENV	IVGGLVGL	783	8	10	16		3681
ENV	GLIGLRII	786	8	15	23		3682
ENV	LIGLRIIF	787	8	16	25		3683
ENV	LIGLRIVF	787	8	29	45		3684
ENV	IIFAVLSI	792	8	15	23		3685
ENV	IVFAVLSI	792	8	20	31		3686
ENV	PLSFOTLL	809	8	10	16		3687
ENV	SIRLVNGF	842	8	13	20		3688
ENV	SIRLVSGF	842	8	13	20		3689
ENV	LVNGFLAL	845	8	14	22		3690
ENV	LVSGFLAL	845	8	19	30		3691
ENV	AWDDLRLS	853	8	20	31		3692
ENV	DLNKLCLF	856	8	17	27		3693
ENV	DLRSICLF	856	8	38	59		3694
ENV	CLESYHRL	861	8	42	66		3695
ENV	SYIHLRDL	864	8	18	28		3696
ENV	SYIHLRDL	864	8	23	36		3697
ENV	RLRDLLI	867	8	13	20		3698
ENV	ELIGHSSL	881	8	13	20		3699
ENV	ELGRRGW	881	8	23	37		3700
ENV	GWEALKYL	896	8	12	19		3701
ENV	GWEGLKYL	896	8	12	19		3702
ENV	YWNLLQY	902	8	15	23		3703
ENV	WNNLLQYW	903	8	15	23		3704
ENV	SLLNATAI	920	8	14	22		3705

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	ILIIIPRI	947	8	13	20		3706
ENV	PTIRIQGL	951	8	12	19		3707
ENV	TVYGVVW	48	9	55	86		3708
ENV	VWKEATTL	55	9	22	34	0.0300	3709
ENV	PTDPRQEI	89	9	25	39		3710
ENV	NVTENFMW	101	9	34	53		3711
ENV	NFNMWKNDM	105	9	12	19		3712
ENV	NFNMWKNNM	105	9	18	28		3713
ENV	MVEQMIEDI	113	9	23	36		3714
ENV	QMIEDISL	116	9	29	45		3715
ENV	IISLWDQSL	121	9	38	59		3716
ENV	VISLWDQSL	121	9	10	16		3717
ENV	KLTLCLVTL	134	9	52	81		3718
ENV	EIKNCSFI	181	9	13	20		3719
ENV	LINCNTSAI	237	9	15	23		3720
ENV	KVSFEIPI	252	9	30	47		3721
ENV	SFEPIIIV	254	9	31	48		3722
ENV	ILKCNDRKF	271	9	12	19		3723
ENV	STVQCTIIGI	289	9	51	80		3724
ENV	PVSTQLLL	300	9	60	94		3725
ENV	SLAEIEVVI	311	9	13	20		3726
ENV	RIGIPQTFY	357	9	11	17		3727
ENV	GIGIPQTFY	360	9	01	33		3728
ENV	SIGSQAFY	360	9	01	33		3729
ENV	ATGDIIGDI	369	9	12	19		3730
ENV	DIRQAIHNI	380	9	15	23		3731
ENV	DLEITTIISF	428	9	21	33		3732
ENV	SFNCGGEFF	437	9	35	55		3733
ENV	SFNCRGEFF	437	9	16	25		3734
ENV	FYCNCTSLG	444	9	21	33		3735
ENV	FYCNCTSLF	445	9	21	33		3736
ENV	TLPCNKIQI	484	9	26	41		3737
ENV	RIKQINMW	488	9	30	47		3738
ENV	RIKQIVNMW	488	9	12	19		3739
ENV	MWQEVGKAM	495	9	15	23		3740
ENV	MWQHVQAM	495	9	10	16		3741
ENV	IFRPGGGDM	545	9	17	27		3742
ENV	TFRPGGGDM	545	9	25	39		3743
ENV	NWRSELYKY	556	9	54	84		3744
ENV	LYKYKVVEI	561	9	13	20	0.0200	3745
ENV	LYKYKVVKI	561	9	29	45		3746
ENV	AVGIAVFL	595	9	11	17		3747
ENV	GIGAVFLGF	598	9	11	18		3748
ENV	MLGAMFLGF	599	9	04	36		3749
ENV	TIGAMFLGF	599	9	03	27		3750
ENV	FLGAAGSTM	608	9	55	86		3751
ENV	TMGAASTIL	615	9	39	61		3752
ENV	TLTVQARQL	622	9	37	58		3753
ENV	LTVQARQLL	623	9	36	56		3754
ENV	GIVQQNNL	633	9	26	41		3755

Table X
HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	GIVQQSNL	633	9	32	50		3756
ENV	IVQQNNLL	634	9	26	41		3757
ENV	IVQQSNLL	634	9	32	50		3758
ENV	ALQAQQHLL	644	9	48	75		3759
ENV	LLKLTWGI	651	9	13	20		3760
ENV	LLQLTWGI	651	9	34	53		3761
ENV	MLQLTWGI	651	9	10	16		3762
ENV	LTVWGIQL	654	9	59	92		3763
ENV	RYLAVERYL	665	9	33	52		3764
ENV	RYLKDQQL	671	9	29	45	0.7600	3765
ENV	RYLRDQQL	671	9	17	27	0.2300	3766
ENV	IGWCSGKL	680	9	48	75	0.0270	3767
ENV	IGWCSGKL	681	9	48	75		3768
ENV	LICTTAVPW	688	9	19	30		3769
ENV	LICTTNVPW	688	9	17	27		3770
ENV	LICTTTVPW	688	9	12	19		3771
ENV	EWMEWERH	722	9	12	19		3772
ENV	EWREIDNY	725	9	11	17		3773
ENV	ALDKWASLW	757	9	11	17		3774
ENV	ELDKWASLW	757	9	18	28		3775
ENV	KWASLWNWF	760	9	26	41		3776
ENV	WFDINLW	767	9	10	16		3777
ENV	DTNWLWYT	769	9	10	16		3778
ENV	KWLWYIKIF	772	9	16	25		3779
ENV	NWLWYIKIF	772	9	25	39		3780
ENV	WLWYIKIF	773	9	49	77		3781
ENV	LWYIKIFM	774	9	43	67		3782
ENV	WYIKIFMI	775	9	43	67		3783
ENV	IFMIVGGL	779	9	41	64		3784
ENV	FIMIVGGL	780	9	35	55		3785
ENV	MIVGGLIGL	782	9	36	56		3786
ENV	GLIGLRIIF	786	9	15	23		3787
ENV	GLIGLRIVF	786	9	29	45		3788
ENV	GLRIFAVL	789	9	17	27		3789
ENV	GLRIFAVL	789	9	28	44		3790
ENV	RIIFAVLSI	791	9	14	22		3791
ENV	IVNRVROGY	799	9	19	30		3792
ENV	RVROGYSPL	799	9	38	59		3793
ENV	SIRLVNGFL	802	9	55	86		3794
ENV	SIRLVNGFL	842	9	11	17		3795
ENV	RLVNGFLAL	842	9	13	20		3796
ENV	RLVSGFLAL	844	9	12	19		3797
ENV	FLALAWDDL	849	9	25	39		3798
ENV	SYHLRDFI	864	9	13	20		3799
ENV	SYHLRDLI	864	9	14	22		3800
ENV	LIAARTVEL	873	9	12	19		3801
ENV	SLKGLRLGW	889	9	11	19		3802
ENV	SLRGLQRGW	889	9	05	39		3803
ENV	GLRLGWGL	892	9	10	18		3804
ENV					32		3805

Table X
 HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	RLQWEGLY	894	9	09	29		3806
ENV	KYWNLLQY	901	9	14	22		3807
ENV	YWNLLQYW	902	9	15	23		3808
ENV	LLQYWSQEL	906	9	16	25		3809
ENV	ELKNSAINL	913	9	10	16		3810
ENV	ELKNSAISL	913	9	10	16		3811
ENV	ELKNSAVSL	913	9	12	19		3812
ENV	ELKNSAIDRI	928	9	16	25		3813
ENV	AVAEGLDRI	928	9	12	19		3814
ENV	ALIHPRRI	946	9	12	19		3815
ENV	VTYYGYVIVW	47	10	55	86		3816
ENV	PWKETATTL	54	10	54	34		3817
ENV	VWKEATTLF	55	10	22	34	0.27100	3818
ENV	LFCASDAKAY	65	10	42	66		3819
ENV	AYDTEVINVW	73	10	18	28		3820
ENV	MWKNMVEQ	108	10	35	55		3821
ENV	NMVEQMIEDI	112	10	20	31	0.00004	3822
ENV	MVEQMIEDII	113	10	23	36		3823
ENV	QMIEDIISLW	116	10	29	45		3824
ENV	DIISLWIDQSL	120	10	38	59		3825
ENV	DVLSLWIDQSL	120	10	10	16		3826
ENV	RLINCNTSAI	236	10	15	24		3827
ENV	ITQACTRVSF	245	10	29	45		3828
ENV	PIIYCAPAGF	260	10	27	42		3829
ENV	PIIYCTTAGF	260	10	10	16		3830
ENV	IYCAPAGFAI	262	10	27	42		3831
ENV	IYCTTAGFAI	262	10	10	16		3832
ENV	AILKCNDDKKF	270	10	12	19		3833
ENV	GIRPVVSTQL	297	10	33	52		3834
ENV	STQLLLNGSL	297	10	26	41		3835
ENV	NTSPRSRVAY	303	10	57	89		3836
ENV	SPNCGGEFFY	376	10	01	33		3837
ENV	SPNCGGEFFY	437	10	35	55		3838
ENV	EFFYCNISGL	443	10	16	25		3839
ENV	FFYCNISGLF	444	10	21	33		3840
ENV	ITLPCRIKQI	483	10	21	33		3841
ENV	TLPCRIKQII	484	10	25	39		3842
ENV	NMWQEVGKA	494	10	15	23		3843
ENV	MWQEVGKAM	495	10	15	23	0.00001	3844
ENV	MWQEVGQAM	495	10	15	23		3845
ENV	NTETNKITET	537	10	10	16		3846
ENV	NTETNKITET	537	10	01	17		3847
ENV	EIERPFGGDM	544	10	17	27		3848
ENV	EIERPFGGDM	544	10	21	33		3849
ENV	DMRDNRSEL	552	10	37	58		3850
ENV	ELYKYKVVEI	560	10	13	21		3851
ENV	ELYKYKVVKI	560	10	29	46		3852
ENV	KYKVVKIEPL	563	10	25	39		3853
ENV	GIGAVFLGFL	598	10	11	18		3854
ENV	MLGAMFLGFL	599	10	04	36		3855

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	TIGAMFLGFL	599	10	03	27		3856
ENV	GFLGAAGSTM	606	10	55	86		3857
ENV	STMGAASITL	614	10	39	61		3858
ENV	ITLTVQARQL	621	10	27	42		3859
ENV	TLTVQARQLL	622	10	35	55		3860
ENV	GIVQQQNLL	633	10	26	41		3861
ENV	GIVQQSNLL	633	10	32	50		3862
ENV	IILKLTWGI	650	10	13	20		3863
ENV	IILLQLTVWGI	650	10	34	53		3864
ENV	KLTWVGKQL	653	10	13	20		3865
ENV	QLTVWGIKQL	653	10	44	69		3866
ENV	GKQLQARVL	658	10	40	63		3867
ENV	YLRDQQLLGI	672	10	27	42		3868
ENV	YLRDQQLLGI	672	10	18	28		3869
ENV	GIWGCSSKLI	680	10	48	75		3870
ENV	KLICITAVPW	687	10	19	30		3871
ENV	KLICITINVPW	687	10	17	27		3872
ENV	KLICITTVPW	687	10	12	19		3873
ENV	TINVPWSS	691	10	11	17		3874
ENV	IWNMTWME	717	10	10	16		3875
ENV	MTWMEWIERE	721	10	12	19		3876
ENV	LLALDKWASL	755	10	11	17		3877
ENV	LLELDKWASL	755	10	18	28		3878
ENV	WFDITNWLW	767	10	10	16		3879
ENV	ITKWLWYIKI	770	10	15	23		3880
ENV	ITNWLWYIKI	770	10	14	22		3881
ENV	KWLWYIKIFI	772	10	16	25		3882
ENV	NWLWYIKIFI	772	10	25	39		3883
ENV	WLWYIKIFIM	773	10	43	67		3884
ENV	LWYIKIFIMI	774	10	43	67		3885
ENV	KIFIMIVGGL	778	10	38	59		3886
ENV	IIMIVGGILI	779	10	33	52		3887
ENV	IMIVGGILIGL	781	10	34	54		3888
ENV	IVGGILIGLRI	783	10	42	66		3889
ENV	SIVNLRQGY	798	10	36	56		3890
ENV	GYSILSPQTL	806	10	29	45		3891
ENV	LVSGLALAW	845	10	16	25		3892
ENV	GFLALAWDDL	848	10	25	39		3893
ENV	AWDDLRLSL	851	10	19	30		3894
ENV	DLNRLCFSY	856	10	20	31		3895
ENV	DLRSLCFSY	856	10	16	25		3896
ENV	NLCFLSYIIRL	859	10	35	55		3897
ENV	SLCLFSYIIRL	859	10	11	17		3898
ENV	LFSYIIRLRDF	862	10	31	48		3899
ENV	LFSYIIRLRDL	862	10	18	28		3900
ENV	SYIIRLRDFIL	864	10	22	34		3901
ENV	SYIIRLRDLLL	864	10	13	20		3902
ENV	LIARTVELL	873	10	12	19		3903
ENV	IVELLGRGW	879	10	11	17		3904
ENV			10	22	34		3905

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	LLGRGWEAL	882	10	09	15		3906
ENV	RLGWGLKYL	894	10	09	29		3907
ENV	KYWNLLQY	901	10	14	22		3908
ENV	NLLQYWSQEL	905	10	16	25		3909
ENV	ELKNSAVSL	913	10	10	16		3910
ENV	AVSLNATAI	918	10	11	17		3911
ENV	AVAEGTDRII	928	10	15	23		3912
ENV	AVAEGTDRVI	928	10	14	22		3913
ENV	IIPRIRIQGL	949	10	13	21		3914
ENV	NIPRIRIQGL	949	10	11	17		3915
ENV	RIRQGLERAL	953	10	34	53		3916
ENV	WVTYYGYGPV	46	11	55	86		3917
ENV	PVWKEATITL	54	11	22	34		3918
ENV	TLFCASDAKA	64	11	40	63		3919
ENV	CVPTDIPRQEI	87	11	25	39		3920
ENV	ITDIPRQEVVL	89	11	12	19		3921
ENV	NMWKNMVE	107	11	30	47		3922
ENV	NMVEQMIEDII	112	11	20	31		3923
ENV	SLKPCVKLTPL	128	11	54	84		3924
ENV	CVKLTITLCVT	132	11	52	81		3925
ENV	VITQACTKVSF	244	11	24	14		3926
ENV	KVSFEPIMHY	252	11	28	44		3927
ENV	IYCAPAGFAIL	262	11	27	42		3928
ENV	NVSTVQCTIIGI	287	11	51	80		3929
ENV	GIRPVVSTQLL	297	11	33	52		3930
ENV	GIRPVVSTQLL	297	11	26	41		3931
ENV	FYATGDIIGDI	367	11	11	17		3932
ENV	GTAGNSSRAA	375	11	01	33		3933
ENV	TTISFNCGE	432	11	16	25		3934
ENV	TTISFNCGE	432	11	12	19		3935
ENV	VMIISFNCGE	432	11	13	20		3936
ENV	EFFYCNTSGLF	443	11	21	33		3937
ENV	NITLPCRIKQI	482	11	11	17		3938
ENV	ITLPCRIKQI	483	11	13	20		3939
ENV	NMWQEVGKA	494	11	15	23		3940
ENV	EVGKAMYAPPI	498	11	15	23		3941
ENV	RVGOAMYAPPI	498	11	18	28		3942
ENV	QIRCSSNITGL	512	11	10	16		3943
ENV	DMRDINWRSEL	532	11	11	17		3944
ENV	VVEREKRAVGI	588	11	37	58		3945
ENV	AVGIGAVFLGF	595	11	11	17		3946
ENV	SITLTVQARQL	620	11	27	42		3947
ENV	ITLTVQARQLL	621	11	27	42		3948
ENV	TVQARQLLSGI	624	11	36	56		3949
ENV	LLRAIEAQHIL	641	11	45	70		3950
ENV	AIEAQHILLKL	644	11	12	19		3951
ENV	AIEAQHILLQL	644	11	35	55		3952
ENV	AVERYLKDDQ	668	11	23	36		3953
ENV	AVERYLRDQ	668	11	11	17		3954
ENV							3955

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	RYLKDQQLGI	671	11	25	39		3956
ENV	RYLRDQQLGI	671	11	17	27		3957
ENV	YLRDQQLGI	672	11	27	42		3958
ENV	YLRDQQLGI	672	11	18	28		3959
ENV	LLGIWCSGKL	678	11	46	72		3960
ENV	CTTNVWNS	690	11	11	17		3961
ENV	NMTWMEWER	720	11	12	19		3962
ENV	WMEWEREIDN	723	11	10	16		3963
ENV	ELLELDKWAS	754	11	15	23		3964
ENV	LLALDKWASL	755	11	11	17		3965
ENV	LELDKWASL	755	11	18	28		3966
ENV	ALDKWASLW	757	11	10	16		3967
ENV	ELDKWASLW	757	11	16	25		3968
ENV	KWASLWVWF	760	11	15	23		3969
ENV	WFDITNWLW	767	11	10	16		3970
ENV	ITKWLWYKIF	770	11	12	19		3971
ENV	ITNVLWYKIF	770	11	14	22		3972
ENV	KVLWYKIFIM	772	11	15	23		3973
ENV	NVLWYKIFIM	772	11	22	34		3974
ENV	WLWYKIFIM	773	11	43	67		3975
ENV	KIFIMVGGGL	778	11	31	48		3976
ENV	FIMVGGGLGL	780	11	34	53		3977
ENV	MVGGGLGLRI	782	11	36	56		3978
ENV	IVGGGLGLRI	783	11	12	19		3979
ENV	LIGLRIFAVL	787	11	15	23		3980
ENV	LIGLRIFAVL	787	11	20	31		3981
ENV	GLRIIFAVLSI	789	11	14	22		3982
ENV	GLRIIFAVLSI	789	11	19	30		3983
ENV	RVRQGYSPLSF	802	11	47	73		3984
ENV	SIRLVSGFLAL	842	11	11	17		3985
ENV	RLVSGFLALA	844	11	16	25		3986
ENV	AWDDLRLSLCL	853	11	20	31		3987
ENV	CLFSYIIRLRIDF	861	11	18	28		3988
ENV	CLFSYIIRLRIDL	861	11	20	31		3989
ENV	LFSYIIRLRIDF	862	11	13	20		3990
ENV	LFSYIIRLRIDLL	862	11	13	20		3991
ENV	SYIIRLRIDLLI	864	11	10	16		3992
ENV	RIVELLGRKG	878	11	22	34		3993
ENV	ELLGRRGWEA	881	11	09	15		3994
ENV	GLRLGWEGLK	892	11	09	29		3995
ENV	RLGWEGLKYL	894	11	07	23		3996
ENV	YWQELKNSA	909	11	12	19		3997
ENV	AIAVAECTDRI	926	11	16	25		3998
ENV	RIRQGLERALL	953	11	33	52		3999
GAG	SVLSGGEL	6	8	11	17		4000
GAG	SVLSGGKL	6	8	28	44		4001
GAG	KLDWWEKI	12	8	18	28		4002
GAG	KLDKWEKI	12	8	10	16		4003
GAG	IVWASKEL	35	8	21	33		4004
GAG	LWWSREL	35	8	36	56		4005

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	RFALNRGL	45	8	20	31		4006
GAG	REAVNRGL	45	8	16	25		4007
GAG	GTELRSL	73	8	12	19		4008
GAG	LFNTVATL	80	8	16	25		4009
GAG	LYNTVATL	80	8	22	34		4010
GAG	LYCVIQLI	87	8	13	20		4011
GAG	LYCVIQLI	87	8	18	28		4012
GAG	KVSNQYPI	148	8	15	27		4013
GAG	QVSNQYPI	148	8	27	48		4014
GAG	NYRVQNL	152	8	31	48		4015
GAG	KVIEKAF	178	8	24	38		4016
GAG	KVVEKAF	178	8	28	44		4017
GAG	VIPMESAL	189	8	46	72		4018
GAG	VIPMFTAL	189	8	14	22		4019
GAG	ATPQDLNM	200	8	12	19		4020
GAG	DLNMLNI	204	8	12	19		4021
GAG	TLQEQIAV	263	8	12	19		4022
GAG	TLQEQIGW	263	8	27	42		4023
GAG	WMTNNPII	270	8	20	31		4024
GAG	WMTSNPII	270	8	16	25		4025
GAG	PIPVGDIY	279	8	11	17		4026
GAG	PIPVGEIY	279	8	35	55		4027
GAG	DIYKRWII	284	8	17	27		4028
GAG	EYKRWII	284	8	39	61		4029
GAG	IYKRWII	285	8	54	84		4030
GAG	ILGLNKI	290	8	57	89		4031
GAG	GLNKIVRM	293	8	60	94		4032
GAG	RMYSPTS	299	8	14	22		4033
GAG	RMYSPTSI	299	8	40	63		4034
GAG	MYSPSIL	300	8	14	22		4035
GAG	MYSPVSIL	300	8	42	66		4036
GAG	ATQDVKNW	333	8	15	23		4037
GAG	ATQEVKNW	333	8	18	28		4038
GAG	NWMTDTLL	339	8	16	25		4039
GAG	NWMTETLL	339	8	36	56		4040
GAG	ALGPAATL	360	8	16	25		4041
GAG	ALGPGATL	360	8	18	28		4042
GAG	IMMQKSNF	408	8	11	17		4043
GAG	IMMQGNF	408	8	27	42		4044
GAG	CTERQANF	459	8	55	87		4045
GAG	ETIDKDLV	537	8	01	25		4046
GAG	ELYPLASL	543	8	14	22		4047
GAG	ELYPLTSL	543	8	11	17		4048
GAG	PLSLKSL	548	8	15	23		4049
GAG	PLTSIKSL	548	8	12	19		4050
GAG	PLTSLSL	548	8	12	19		4051
GAG	LTSLSL	549	8	13	20		4052
GAG	LTSLSLF	549	8	12	19		4053
GAG	SLFGNDPL	554	8	12	19		4054
GAG	SLFGSDPL	554	8	11	17		4055

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*2401	SEQ ID NO
GAG	KYKLKILVW	29	9	10	16		4056
GAG	KYRLKILVW	29	9	16	25		4057
GAG	IIVWASREL	34	9	21	33		4058
GAG	ILVWASREL	34	9	36	56		4059
GAG	RFALNPGLL	45	9	20	31		4060
GAG	RFVNPGLL	45	9	16	25	0.0100	4061
GAG	EYSEGRQI	54	9	16	25		4062
GAG	ILQLQPSL	62	9	11	17		4063
GAG	SLOTGSEL	69	9	14	22		4064
GAG	SLNTVATL	79	9	16	25		4065
GAG	SLNTVATL	79	9	22	34		4066
GAG	LFNTVATLY	80	9	15	23		4067
GAG	LYNTVATLY	80	9	22	34		4068
GAG	TYCYVHQI	86	9	12	19		4069
GAG	TYCYVHQI	86	9	15	23		4070
GAG	DVKDTKEAL	95	9	11	17		4071
GAG	EYKDTKEAL	95	9	20	31		4072
GAG	DTKEALDKI	98	9	32	50		4073
GAG	DTKEALEKI	98	9	10	16		4074
GAG	IVQNAQGM	155	9	21	33		4075
GAG	IVQNLQGM	155	9	29	45		4076
GAG	TLNAWVKVI	172	9	30	47		4077
GAG	AFSEVIFM	184	9	50	78		4078
GAG	EVIPMSAL	188	9	46	72		4079
GAG	EVIPMTAL	188	9	14	22		4080
GAG	ATPQDLNMM	200	9	12	19		4081
GAG	ATPQDLNMT	200	9	42	66		4082
GAG	IVGGHQAAAM	211	9	12	19		4083
GAG	TVGGHQAAAM	211	9	47	73		4084
GAG	AMQMLKDTI	218	9	33	52		4085
GAG	AMQMLKETI	218	9	41	61		4086
GAG	TINEEALEW	225	9	53	83		4087
GAG	DIAGTTSTL	236	9	48	75		4088
GAG	TTSTLQEQI	260	9	45	71		4089
GAG	STLQEQIAW	262	9	12	19		4090
GAG	STLQEQIGW	262	9	27	42		4091
GAG	TLQEQIAWM	263	9	12	19		4092
GAG	TLQEQIGWM	263	9	27	42		4093
GAG	GWMTNNPPI	269	9	18	28	0.0140	4094
GAG	GWMTSNPPI	269	9	10	16		4095
GAG	PVGDIYKRW	281	9	18	28		4096
GAG	PVGEIYKRW	281	9	40	63		4097
GAG	DIYKRWIL	284	9	17	27		4098
GAG	EYKRWIL	284	9	37	58		4099
GAG	WILGLNKI	289	9	57	89		4100
GAG	GLNKIVRMY	293	9	60	94		4101
GAG	RMYSPTSIL	299	9	14	22		4102
GAG	RMYSPTSIL	299	9	40	63		4103
GAG	PFROYVDRF	316	9	63	98		4104
GAG	YVDRFEKTL	320	9	27	42		4105

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*2401	SEQ ID NO
GAG	YVDREYKTL	320	9	28	44		4106
GAG	ATQDVKNWM	333	9	15	23		4107
GAG	ATQEVKNWM	333	9	18	28		4108
GAG	NIMMORGNF	407	9	10	17		4109
GAG	TIMMORGNF	407	9	13	22		4110
GAG	CTERQANFL	439	9	55	87		4111
GAG	PTAPPAESF	495	9	20	31		4112
GAG	PTAPPAESF	495	9	15	23		4113
GAG	PTAPPAESF	507	9	02	67		4114
GAG	PTAPPAESF	507	9	01	33		4115
GAG	PIDKELYPL	534	9	12	19		4116
GAG	PIDKELYPL	538	9	01	25		4117
GAG	TIDKOLYPL	538	9	01	25		4118
GAG	PLASLSKSLF	548	9	15	23		4119
GAG	PLTSLSKSLF	548	9	12	19		4120
GAG	PLTSLSKSLF	548	9	12	19		4121
GAG	VLGGKLDIAW	7	10	15	23		4122
GAG	KLDIAWEKIRL	12	10	16	25		4123
GAG	KLDIAWEKIRL	12	10	16	16		4124
GAG	RLRPGKKKY	20	10	34	53		4125
GAG	VWASHELERF	36	10	45	70		4126
GAG	ETSEGCQIL	54	10	14	22		4127
GAG	QILGLOQPSL	61	10	11	17		4128
GAG	QTGSELRSL	71	10	12	19		4129
GAG	SLNTVATLY	79	10	15	23		4130
GAG	SLNTVATLY	79	10	22	34		4131
GAG	ATLYCVIIQRI	85	10	12	19		4132
GAG	ATLYCVIIQRI	85	10	15	23		4133
GAG	PIVQNAQGQM	154	10	21	33		4134
GAG	PIVQNLQGQM	154	10	29	45		4135
GAG	ALSPRTLNAW	167	10	29	45		4136
GAG	ALSPRTLNAW	167	10	10	16		4137
GAG	RLNNAWVKVI	171	10	30	47		4138
GAG	WVKVVEEKAF	176	10	24	38		4139
GAG	WVKVVEEKAF	176	10	28	44		4140
GAG	AESPEVIMF	184	10	50	78	0.007R	4141
GAG	ATIQDLNMTML	200	10	12	19		4142
GAG	ATIQDLNMTML	200	10	42	66		4143
GAG	NIVGGHQAAM	210	10	12	19		4144
GAG	NTVGGHQAAM	210	10	47	73		4145
GAG	DTINEEAWE	224	10	31	48		4146
GAG	DTINEEAWE	224	10	22	34		4147
GAG	RLIIPVIA GPI	235	10	22	34		4148
GAG	RLIIPVIA GPI	235	10	14	22		4149
GAG	QMRPRGSDI	248	10	44	69		4150
GAG	GTTSTLQEQI	259	10	45	70		4151
GAG	STLQEQIAWM	262	10	12	19		4152
GAG	STLQEQIGWM	262	10	27	42		4153
GAG	PVGDIYKRWI	281	10	17	27		4154
GAG	PVGDIYKRWI	281	10	40	63		4155

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	IYKRWILGL	285	10	54	84	0.0140	4156
GAG	RWILGLNKI	288	10	56	88		4157
GAG	ILGLNKIVRM	291	10	57	89		4158
GAG	IVRMYSPTSI	297	10	14	22		4159
GAG	IVRMYSPTSI	297	10	40	63		4160
GAG	MYSPTSILDI	300	10	13	20		4161
GAG	MYSPTSILDI	300	10	40	63		4162
GAG	DIKQGPKEF	308	10	19	30		4163
GAG	DIRQGPKEF	308	10	41	64		4164
GAG	PFRDYVDREY	316	10	35	55		4165
GAG	PFRDYVDREY	316	10	28	44		4166
GAG	DYVDRFFKTL	319	10	27	42		4167
GAG	DYVDRFFKTL	319	10	28	44		4168
GAG	DVKNWMTDT	336	10	12	19	0.0010	4169
GAG	DVKNWMTDT	336	10	11	17		4170
GAG	EVKNWMTETL	336	10	25	39		4171
GAG	ATIMMQRGNF	406	10	11	28		4172
GAG	CFNCGKEGIII	425	10	27	42		4173
GAG	CFNCGKEGIII	425	10	27	42		4174
GAG	TTTTSOKQEPH	522	10	09	45		4175
GAG	ETIDKDLPL	537	10	01	25		4176
GAG	RTENSLYIPL	538	10	01	25		4177
GAG	LYPLASLKL	544	10	09	17		4178
GAG	SVLSGGKLDA	6	11	15	23		4179
GAG	IYVWASRELERF	35	11	19	30		4180
GAG	IYVWASRELERF	35	11	25	39		4181
GAG	ELERFALNPGI	42	11	14	22		4182
GAG	ELERFALNPGI	42	11	15	23		4183
GAG	LLETSEGRQI	52	11	16	25		4184
GAG	RIEVKIDTKEAL	93	11	12	19		4185
GAG	NLQGMVVIQA	158	11	15	23		4186
GAG	MVIQAIISPTL	163	11	27	42		4187
GAG	AWVKVVEEKA	175	11	24	38		4188
GAG	AWVKVVEEKA	175	11	28	44		4189
GAG	ALSEGATIQDL	195	11	58	91		4190
GAG	IYGGIIQAAMQ	211	11	11	17		4191
GAG	TVGGIIQAAMQ	211	11	47	73		4192
GAG	TTSTLQEQIA	260	11	11	17		4193
GAG	TTSTLQEQIG	260	11	27	43		4194
GAG	QIGWMTNNPPI	267	11	18	29		4195
GAG	QIGWMTNNPPI	267	11	10	16		4196
GAG	PIPVGEIYKRW	279	11	34	53		4197
GAG	IPVGDYKRWII	281	11	17	27		4198
GAG	IPVGEIYKRWII	281	11	39	61		4199
GAG	DIYKRWILGL	284	11	17	27		4200
GAG	EIVKRWILGL	284	11	37	58		4201
GAG	IILGLNKIVRM	290	11	56	88		4202
GAG	IILGLNKIVRM	291	11	57	89		4203
GAG	KIVRMYSPTSI	296	11	14	22		4204
GAG	KIVRMYSPTSI	296	11	39	61		4205

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HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ2401	SEQ ID NO
GAG	IVRMYSPTSIL	297	11	14	22		4206
GAG	IVRMYSVSIL	297	11	40	63		4207
GAG	RMYSPTSILDI	299	11	13	20		4208
GAG	RMYSVSILDI	299	11	38	59		4209
GAG	IVKNWMTDT	336	11	12	19		4210
GAG	IVKNWMTET	336	11	11	17		4211
GAG	IVKNWMTETL	336	11	25	39		4212
GAG	ILKALGPAATL	357	11	16	25		4213
GAG	ALGIPAATLEE	360	11	16	25		4214
GAG	ALGHGATLEE	360	11	17	27		4215
GAG	ATAQODLKGG	392	11	01	50		4216
GAG	CWKCKEGEIIQ	446	11	46	72		4217
GAG	PTAPPAESFGF	495	11	10	16		4218
GAG	PTAPPLESFRF	495	11	14	22		4219
GAG	PTAPPAESFRF	507	11	02	67		4220
GAG	PTAPPIESFRF	507	11	01	33		4221
GAG	LYPLASLSLFL	544	11	09	17		4222
GAG	SLKSLFGNDPL	551	11	12	19		4223
NEF	DLEKIIGAI	57	8	12	22		4224
NEF	ATNADCAW	71	8	12	22		4225
NEF	PVRNQVPL	95	8	48	75		4226
NEF	PMYKGAFL	105	8	12	19		4227
NEF	TYKGAFL	107	8	12	19		4228
NEF	AFDLSFLL	111	8	18	28		4229
NEF	ALDLSHFL	111	8	11	17		4230
NEF	AVDLSHFL	111	8	15	23		4231
NEF	FLKEKGGL	117	8	56	88		4232
NEF	DILDWVY	185	8	20	31		4233
NEF	EILDWVY	185	8	33	52		4234
NEF	WVYITQGF	191	8	13	20		4235
NEF	WVYITQGY	191	8	21	33		4236
NEF	VYITQGF	192	8	13	20		4237
NEF	VYITQGYF	192	8	21	33		4238
NEF	FFPDWQNY	199	8	17	27		4239
NEF	YFIDWQNY	199	8	36	56		4240
NEF	NYITGPGI	206	8	20	31		4241
NEF	GIRYPLTF	213	8	13	20		4242
NEF	GTRPLTF	213	8	13	20		4243
NEF	RYPLTFGW	216	8	22	32		4244
NEF	RYPLTFGW	216	8	22	43		4245
NEF	RLTFGWCF	219	8	43	67		4246
NEF	TFGWCFKL	222	8	40	63		4247
NEF	GVGAASQDL	45	9	11	17		4248
NEF	GVGAVSQDL	45	9	21	33		4249
NEF	GVGAVSRDL	45	9	17	27		4250
NEF	ATNADCAWL	71	9	12	22		4251
NEF	QVPLRPMTF	100	9	10	16		4252
NEF	QVPLRPMTY	100	9	46	72		4253
NEF	MTYKGAFL	106	9	12	19		4254
NEF	FELKEKGGL	116	9	26	41		4255

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HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
NEF	IIFLKEKGL	116	9	29	45		4256
NEF	IYSKKRQEI	175	9	18	29		4257
NEF	LWVYIITQGF	190	9	13	20		4258
NEF	LWVYIITQGY	190	9	21	33		4259
NEF	WVYIITQGEF	191	9	13	20		4260
NEF	WVYIITQGYF	191	9	21	33		4261
NEF	IITQGFDFD	194	9	25	22		4262
NEF	IITQGYFDFW	194	9	12	19		4263
NEF	NTQGYFDFW	194	9	17	27		4264
NEF	GFDFDQWNY	198	9	36	56		4265
NEF	GYDFDQWNY	198	9	17	27		4266
NEF	YTFGPGIRY	207	9	13	20		4267
NEF	YTFGPGTRF	207	9	39	61		4268
NEF	LTFGWCFKL	221	9	48	75	0.0002	4269
NEF	KWSKSSIVGW	4	10	20	31		4270
NEF	GFVIRQVPL	93	10	12	19		4271
NEF	PMTYKGAFDL	105	10	22	34		4272
NEF	SFLKEKQGL	115	10	18	28		4273
NEF	LIYSKKRQEI	174	10	18	29		4274
NEF	IYSKKRQEI	175	10	13	20		4275
NEF	DLWVYIITQGF	188	10	21	33		4276
NEF	DLWVYIITQGY	188	10	17	27		4277
NEF	LWVYIITQGF	190	10	13	20		4278
NEF	LWVYIITQGYF	190	10	21	33		4279
NEF	NYTFGPGIRY	206	10	17	27		4280
NEF	NYTFGPGTRF	206	10	13	20		4281
NEF	GIRYPLTFGW	213	10	13	20		4282
NEF	GTRFPLTFGW	213	10	12	19		4283
NEF	RPLTFGWCF	216	10	17	27		4284
NEF	RYPLTFGWCF	216	10	21	33		4285
NEF	PLTFGWCFKL	219	10	39	61		4286
NEF	LLIPICQIIGM	257	10	10	16		4287
NEF	LLIPMSQIIGM	257	10	12	19		4288
NEF	IIMARELIPEY	320	10	10	16		4289
NEF	NTAATNAIDCA	68	11	12	19		4290
NEF	PVRQVPLRP	95	11	47	73		4291
NEF	PLRMTYKGA	102	11	12	19		4292
NEF	FLKEKGLDGL	117	11	26	41		4293
NEF	FLKEKGLLEGL	117	11	29	45		4294
NEF	GLIYSKKRQEI	173	11	18	28		4295
NEF	LIYSKKRQEI	174	11	18	28		4296
NEF	DLWVYIITQGF	188	11	13	20		4297
NEF	VYIITQGFDFD	192	11	21	33		4298
NEF	VYIITQGYFDFD	192	11	13	20		4299
NEF	DWQNYTTPQG	203	11	21	33		4300
NEF	YTFGPGIRYPL	207	11	16	25		4301
NEF	YTFGPGTRFPL	207	11	13	20		4302
NEF	CLLIPMSQIIG	256	11	10	16		4303
NEF	IIMARELIPEY	320	11	10	16		4304
NEF							4305

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	FFREDLAF	1	8	15	23		4306
POL	FFRENLAF	1	8	41	64		4307
POL	GTLNCFQI	80	8	01	33		4308
POL	PTFNFFQI	80	8	01	33		4309
POL	NFRQITLW	86	8	22	34		4310
POL	SFQITLW	86	8	23	36		4311
POL	ITLWQRPL	90	8	47	73		4312
POL	TIKIGGQL	99	8	17	27		4313
POL	TVKIGGQL	99	8	11	17		4314
POL	TVLEENIL	118	8	13	20		4315
POL	DINLPCKW	118	8	15	23		4316
POL	EINLPCKW	122	8	13	20		4317
POL	MIGGIGGF	133	8	12	19		4318
POL	GFIKVRQY	139	8	62	97		4319
POL	KVRQYDQI	142	8	41	64		4320
POL	ECGIIKAI	152	8	19	30		4321
POL	ECGKKAI	152	8	24	38		4322
POL	NIIGKNLL	170	8	26	41		4323
POL	NIIGRNML	170	8	31	48		4324
POL	LTOIGCTL	177	8	42	66		4325
POL	LTOIGCTL	177	8	15	23		4326
POL	QIGCTLNF	179	8	41	64		4327
POL	QIGCTLNF	179	8	16	25		4328
POL	PVKLKPGM	195	8	56	88		4329
POL	KIKALTEI	217	8	28	44		4330
POL	KIKALVEI	217	8	15	23		4331
POL	LVEICTEM	221	8	15	24		4332
POL	EMEKEGKI	229	8	42	66		4333
POL	KIGPENPY	238	8	51	80		4334
POL	RIGPENPY	238	8	11	17		4335
POL	KWAKLVDF	259	8	59	92		4336
POL	KLVDREL	262	8	63	98		4337
POL	FWEVQLGI	276	8	57	89		4338
POL	GIPHPAGL	282	8	56	89		4339
POL	VLDVGDAY	297	8	60	94		4340
POL	SVPLDKDF	306	8	18	28		4341
POL	DFPKYTAF	312	8	42	66		4342
POL	GWKGPAL	341	8	59	92		4343
POL	MTKILEPF	353	8	44	69		4344
POL	DVIYQYM	366	8	18	28		4345
POL	EIVYQYM	366	8	24	38		4346
POL	IYQYMDL	369	8	61	95		4347
POL	DLYVGSOL	375	8	63	98		4348
POL	YVGSOLFI	377	8	58	91		4349
POL	FLWMGYEL	416	8	64	100		4350
POL	WTVPQIQL	428	8	28	44		4351
POL	WTVPQIVL	428	8	13	20		4352
POL	QLPEKDSW	434	8	13	20		4353
POL	VLPEKDSW	434	8	13	20		4354
POL							4355

Table X
 HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	TVNDIQKL	442	8	62	97		4356
POL	KLVGKLNW	448	8	62	97		4357
POL	KLNWASQI	452	8	61	95		4358
POL	KVKQLCKL	464	8	29	45		4359
POL	KVRQLCKL	464	8	19	30		4360
POL	LLRGAKAL	471	8	47	30		4361
POL	LLRGTKAL	471	8	24	38		4362
POL	ALTDIVPL	477	8	21	33		4363
POL	ALTEVIPL	477	8	16	25		4364
POL	PLTEAEEL	483	8	30	47		4365
POL	ELAENREI	491	8	57	89		4366
POL	YYDFSKDL	510	8	43	67		4367
POL	KTGKYAKM	542	8	19	30		4368
POL	KTGKYARM	542	8	13	21		4369
POL	IITNDVKQL	553	8	49	77		4370
POL	LTEAVQKI	560	8	34	53		4371
POL	ATIESIIV	568	8	19	30		4372
POL	IWGIKIKF	574	8	11	17		4373
POL	IWCKTIKF	574	8	48	75		4374
POL	ETWWTIDYW	591	8	10	16		4375
POL	DYWQATWI	596	8	20	31		4376
POL	EYWQATWI	596	8	37	58		4377
POL	TWIPEWIEF	601	8	52	81		4378
POL	EFVNTIPL	607	8	54	84		4379
POL	NTIPLVKL	610	8	57	89		4380
POL	LVKLWYQL	614	8	58	91		4381
POL	PIVGAETI	625	8	28	44		4382
POL	IVGAETFY	626	8	28	44		4383
POL	TTNQRTIL	664	8	55	86		4384
POL	KTELQAIY	668	8	12	19		4385
POL	NIVTDSQY	686	8	62	97		4386
POL	VTDSDYAL	688	8	59	92		4387
POL	LIRKEKVV	717	8	35	55		4388
POL	WVPAIKGI	727	8	63	98		4389
POL	GIRKVLFL	747	8	51	80		4390
POL	KVLFLDGI	750	8	50	78		4391
POL	AMASDFNL	773	8	45	70		4392
POL	QVDCSPGI	805	8	57	89		4393
POL	CTHLECKI	817	8	35	55		4394
POL	HLEGGKIL	819	8	23	36		4395
POL	IILEGKVL	819	8	31	48		4396
POL	AVIIVASGY	828	8	59	92		4397
POL	GYIEAEVI	834	8	54	84		4398
POL	ETGQETAY	844	8	39	59		4399
POL	ILKLAGRW	853	8	34	53		4400
POL	LLKLAGRW	853	8	25	39		4401
POL	HTDNGSNF	866	8	51	80		4402
POL	TTVKAACW	876	8	32	50		4403
POL	AVKAACWW	877	8	24	38		4404
POL	TVKAACWW	877	8	24	38		4405

Table X
HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	GIKQEEGI	886	8	22	34		4406
POL	GIKQEEGI	886	8	11	17		4407
POL	ILKTAVQM	923	8	57	89		4408
POL	AVQMAVFI	927	8	60	94		4409
POL	NFKRKGCI	936	8	60	94		4410
POL	GYSGAGRI	945	8	57	89		4411
POL	QIKIQNF	968	8	12	19		4412
POL	QIKIQNF	968	8	35	55		4413
POL	KIQNFRVY	971	8	52	81		4414
POL	IKWGFAPL	986	8	36	56		4415
POL	LWKGFAPL	986	8	19	30		4416
POL	VIQDNSDI	1003	8	37	58		4417
POL	VIQDNSEI	1003	8	12	19		4418
POL	PTRELQVW	30	9	13	20		4419
POL	GTILNFQI	79	9	01	17		4420
POL	AISLSLIQI	80	9	01	33		4421
POL	SFSFIQTL	84	9	14	22		4422
POL	QITLWQRP	89	9	47	73		4423
POL	LWQRPVFI	92	9	21	33	0.0190	4424
POL	VTIKGGQL	98	9	17	27		4425
POL	VTIKGGQL	98	9	11	17		4426
POL	DTGADDTVL	112	9	61	95		4427
POL	DTVLEDINL	117	9	13	20		4428
POL	DMIGGIGGF	132	9	62	22		4429
POL	DMIGGIGFI	133	9	62	97	0.0011	4430
POL	KVRQYDQIL	142	9	21	33		4431
POL	QYDQILIEI	145	9	27	42		4432
POL	QYDQIMEI	145	9	12	19		4433
POL	LYGPTPVNI	163	9	54	84		4434
POL	PVNIIGRNL	168	9	26	41		4435
POL	PVNIIGRNM	168	9	24	38		4436
POL	LLTQIGCTL	176	9	21	33		4437
POL	MLTQIGCTL	176	9	18	28		4438
POL	MLTQIGCTL	176	9	10	16		4439
POL	TLNFPISH	183	9	61	97		4440
POL	PIETVPVKL	190	9	53	83		4441
POL	QWPLTEEKI	210	9	56	88		4442
POL	LTEEKIKAL	213	9	56	88		4443
POL	ALVEICTEM	220	9	15	23		4444
POL	PYNTIPFAI	244	9	24	38	0.0310	4445
POL	PYNTIPFAI	244	9	37	58		4446
POL	ELNKRQDF	268	9	57	89		4447
POL	DFVEVQLGI	275	9	56	88		4448
POL	TVLDVGDAY	296	9	57	89		4449
POL	VLDVGDAYF	297	9	60	94		4450
POL	PLDKDFRKY	308	9	19	30		4451
POL	YTAFTIFS	316	9	37	58		4452
POL	SINNETPGI	323	9	32	50		4453
POL	STNNETPGI	323	9	11	17		4454
POL							4455

Table X
 IIIV $\Delta 24$ Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Antigen Acids	Sequence Frequency	Conservancy (%)	Δ^*2401	SI:Q ID NO
POL	ETPGRYQY	327	9	52	81		4456
POL	GIRYQYVL	330	9	52	81		4457
POL	QYNVLPQGW	334	9	63	98	0.0036	4458
POL	GWKSPAF	341	9	59	92		4459
POL	IFOSSMTKI	348	9	38	59	0.0029	4460
POL	SMTKLIEPF	352	9	43	67	0.0110	4461
POL	PFKKQNPDI	359	9	16	25		4462
POL	VYQYMDDL	368	9	51	80		4463
POL	IYQYMDILY	369	9	61	95	0.0130	4464
POL	LYVGSDEI	376	9	58	91		4465
POL	EIGQIRAKI	383	9	26	41		4466
POL	EIGQIRTKI	383	9	21	33		4467
POL	KIELREIL	390	9	19	30		4468
POL	KIELRQHIL	390	9	17	27		4469
POL	ELREHLLKW	393	9	17	27		4470
POL	ELRQHLLRW	393	9	15	23		4471
POL	PELWNGYEL	415	9	64	100		4472
POL	GYLEIIPDKW	420	9	60	94		4473
POL	KWIVQPIQL	427	9	28	44	0.0001	4474
POL	KWIVQPIVL	427	9	12	19		4475
POL	IVLEKDSW	433	9	13	20		4476
POL	WTVNDIQKL	441	9	62	97		4477
POL	DIQKLVGKL	445	9	62	97		4478
POL	KLNWASQIY	452	9	60	94		4479
POL	KVKQLCKLL	464	9	28	44		4480
POL	KVRQLCKLL	464	9	19	30		4481
POL	KLLRGAKAL	470	9	25	40		4482
POL	KLLRGTKAL	470	9	24	38		4483
POL	GKALTEVI	474	9	11	17		4484
POL	LTEEALELEL	484	9	37	58		4485
POL	ELAENREIL	491	9	57	89		4486
POL	VYVDPKDL	509	9	39	61	0.0004	4487
POL	YVDISKDLI	510	9	35	55		4488
POL	TYQIQEIPF	530	9	42	66	0.3000	4489
POL	IYQEPKNI	533	9	40	63	0.0520	4490
POL	OLTEAVQKI	559	9	34	53		4491
POL	KIATESIVI	566	9	14	22		4492
POL	VIWGTPTKF	573	9	47	73		4493
POL	KTPKFLPI	577	9	17	27		4494
POL	KTPKFLPI	577	9	29	45		4495
POL	KLPQKETW	582	9	20	31		4496
POL	RLPQKETW	582	9	26	41		4497
POL	TWETWWTDY	589	9	10	16		4498
POL	TWETWWTET	589	9	10	16		4499
POL	WTIDYQQATW	594	9	14	22		4500
POL	WTIDYQQATW	594	9	24	38		4501
POL	ATWIPEWEF	600	9	52	81		4502
POL	NTPIVLKLV	610	9	57	89		4503
POL	PLVKLVWQL	613	9	54	84		4504
POL	WYQLEKQPI	618	9	14	22		4505

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*2401	SEQ ID NO
POL	WYQLEKEPI	618	9	31	48	0.0001	4506
POL	WYQLETEPI	618	9	11	17		4507
POL	PIVGAEFFY	625	9	28	44		4508
POL	ETKLGKAGY	641	9	35	55		4509
POL	DTTNQKTEL	663	9	26	41		4510
POL	ETTNQKTEL	663	9	29	45		4511
POL	KTELQAIHL	668	9	15	23		4512
POL	KTELQAIYL	668	9	12	19		4513
POL	ELQAIHLAL	670	9	16	25		4514
POL	ELQAIYLAL	670	9	12	19		4515
POL	ILALQDSGL	675	9	15	23		4516
POL	IVTDSQYAL	687	9	59	92		4517
POL	LVNQIEQL	709	9	30	30		4518
POL	LVSQIEQL	709	9	19	30		4519
POL	OLIKKEKVV	716	9	28	44		4520
POL	LIKKEKYYL	717	9	35	55		4521
POL	AWVPALIKGI	726	9	22	34		4522
POL	SWVPALIKGI	726	9	37	58		4523
POL	KYIISNWRAM	766	9	28	44		4524
POL	KYIISNWRAM	766	9	11	17		4525
POL	NWRAMASDF	770	9	43	67	0.0016	4526
POL	QVDCSPGIW	805	9	57	89		4527
POL	IWQLDCTIHL	812	9	59	92	0.0095	4528
POL	CTHLECKII	817	9	35	55		4529
POL	CTHLECKVI	817	9	26	41		4530
POL	AVIIVASGYI	828	9	53	83		4531
POL	ETGQETAYF	844	9	57	89		4532
POL	ETAYFILKL	848	9	31	48		4533
POL	ETAYFLKL	848	9	27	42		4534
POL	FILKLAGRW	852	9	32	50		4535
POL	FLKLAGRW	852	9	25	39		4536
POL	STTVKAACW	875	9	15	23		4537
POL	TTVKAACWW	876	9	15	23		4538
POL	WWAGIKQEF	883	9	21	33	0.0120	4539
POL	WWAGIQQEF	883	9	11	17		4540
POL	VVESMNKEL	902	9	48	75		4541
POL	SMNKELKKI	905	9	53	83		4542
POL	QVRDQAEHL	916	9	48	75		4543
POL	QVREQAEIIL	916	9	13	20		4544
POL	KTAVQMAVF	925	9	57	89		4545
POL	QMAVFIINF	929	9	60	94	0.0190	4546
POL	GYSAGERII	945	9	41	64		4547
POL	IIDIASDI	952	9	12	19		4548
POL	IIDIATDI	952	9	29	45		4549
POL	IVDIATDI	952	9	12	19		4550
POL	ATDIQTKEL	957	9	35	55		4551
POL	QTKELQKQI	961	9	46	72		4552
POL	ELQKQIKI	964	9	13	21		4553
POL	ELQKQITKI	964	9	34	54		4554
POL	KIQFRVYY	971	9	52	81		4555

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*2401	SEQ ID NO
POL	YYRSDRPI	978	9	34	53		4556
POL	YYRSDRPL	978	9	14	22		4557
POL	PLWKGPAKL	985	9	36	56		4558
POL	PLWKGPAKL	985	9	19	30		4559
POL	IKWGPALKL	986	9	35	55		4560
POL	LWKGPAKLL	986	9	18	28		4561
POL	VVIQDNDI	1002	9	37	58		4562
POL	VVIQDNDI	1002	9	12	19		4563
POL	VVPRKAKI	1012	9	51	80		4564
POL	VVPRKAKI	1012	9	11	17		4565
POL	IKDYGRQM	1020	9	11	11		4566
POL	IKDYGRQM	1020	9	50	78		4567
POL	AFQGEAREF	7	10	10	16		4568
POL	STNSPTSREL	32	10	01	33		4569
POL	GTLNCPQITL	80	10	01	33		4570
POL	PTENFIQITL	80	10	01	33		4571
POL	SFSFQITLW	84	10	13	20		4572
POL	TLWQRPLVTH	91	10	21	33		4573
POL	LVTIKIGQAL	97	10	13	20		4574
POL	KIGGQLEAL	101	10	23	36		4575
POL	NLKKWKPKM	124	10	35	55		4576
POL	KWKPKMIGGI	128	10	42	66		4577
POL	RWKPKMIGGI	128	10	17	27	0.0001	4578
POL	KMIGGIGFI	132	10	62	97		4579
POL	FIKVRQYDQI	140	10	41	64		4580
POL	KVRQYDQILI	142	10	20	31		4581
POL	KVRQYDQIPI	142	10	13	20		4582
POL	LIECGIJKAI	150	10	10	16		4583
POL	LIECGKKAI	150	10	13	20		4584
POL	VLGGPIPVNI	162	10	53	83		4585
POL	LVGPIPVNII	163	10	52	81		4586
POL	PVNIIGRNLL	168	10	26	41		4587
POL	PVNIIGRNML	168	10	24	38		4588
POL	IIGRNLLTQI	171	10	21	33		4589
POL	IIGRNMLTQI	171	10	18	28		4590
POL	IIGRNMLTQL	171	10	11	17		4591
POL	NLLTQIGCTL	175	10	21	33		4592
POL	NMLTQIGCTL	175	10	18	28		4593
POL	NMLTQIGCTL	175	10	10	16		4594
POL	LTIQIGCTLNF	177	10	41	64		4595
POL	LTIQIGCTLNF	177	10	15	23		4596
POL	QIGCTLNFPI	179	10	41	64		4597
POL	QIGCTLNFPI	179	10	16	25		4598
POL	CTLNFPISPI	182	10	60	94		4599
POL	TVPVKLPKPM	193	10	54	84		4600
POL	GMDGPKVKQ	201	10	51	80		4601
POL	PLTEEKIKAL	212	10	54	84		4602
POL	CTEMEKEGKI	225	10	27	42		4603
POL	AIKKKDKTKW	231	10	57	89		4604
POL	STKWRKLVDF	257	10	58	91		4605

Table X
HIV-1 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	ELNKRTOQDFW	268	10	57	89		4606
POL	RTQDFWEVQL	272	10	53	83		4607
POL	QLGIRIPAGL	280	10	56	89		4608
POL	VIVLDVGDAY	295	10	56	88		4609
POL	TVLDVGDAYF	296	10	57	89		4610
POL	YFSVPLDKDF	304	10	18	29		4611
POL	IFPKYTAFTI	312	10	42	66		4612
POL	KYTAFTISI	315	10	37	58		4613
POL	AFQSSMTKI	347	10	36	56		4614
POL	IFQSSMTKIL	348	10	38	59	0.0002	4615
POL	IVIQYMDIDL	367	10	42	66		4616
POL	VIVQYMDIUL	368	10	51	80		4617
POL	DLYVGSDEL	375	10	58	91		4618
POL	KIELREHLL	390	10	19	30		4619
POL	KIELRQJILL	390	10	17	27		4620
POL	PIQLPEKDSW	432	10	13	20		4621
POL	PVLPEKDSW	432	10	13	20		4622
POL	SWTVNDIQKL	440	10	54	84		4623
POL	NWASQIYAGI	454	10	27	42		4624
POL	NWASQIYPGI	454	10	29	45		4625
POL	IYAGIKVKQL	459	10	18	28		4626
POL	IYPGKVKQL	459	10	11	17		4627
POL	IYPGKVRQL	459	10	15	23		4628
POL	GKVKQLCKL	462	10	28	44		4629
POL	GKVRQLCKL	462	10	18	28		4630
POL	IVPLTEFAEL	481	10	13	20		4631
POL	VIPLTEFAEL	481	10	11	17		4632
POL	PLTEFAEL	483	10	30	47		4633
POL	ELLEAENREI	489	10	53	83		4634
POL	ILKEPIIGVY	498	10	40	63		4635
POL	GVYDPSKDL	508	10	38	59		4636
POL	VYDPSKDLI	509	10	31	48	0.0150	4637
POL	EIQKQGQDQW	520	10	13	20		4638
POL	EIQKQGQGW	520	10	15	23		4639
POL	WTYQIQEPF	529	10	42	66		4640
POL	QYQIEPKNL	532	10	40	63		4641
POL	PFKNLTKGY	537	10	45	70		4642
POL	NLTKGYAKM	540	10	18	29		4643
POL	NLTKGYARM	540	10	13	21		4644
POL	AVQKIATESI	563	10	16	16		4645
POL	KIATESIVIV	566	10	14	22		4646
POL	IVWGTKPKF	572	10	47	73		4647
POL	IWGKTPKFL	574	10	17	27		4648
POL	IWKTPKFKL	574	10	30	47		4649
POL	PIKETWEAW	584	10	15	23		4650
POL	PIKETWETW	584	10	27	42		4651
POL	ETWETWETD	588	10	10	16		4652
POL	ETWETWTE	588	10	10	16		4653
POL	TWETWETDY	589	10	10	16		4654
POL	WWTDYWQAT	593	10	14	22		4655

Table X
 HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*2401	SEQ ID NO
POL	WWTEYWQAT	593	10	23	16		4656
POL	WTDYWQATW	594	10	14	22		4657
POL	WTEYWQATW	594	10	24	38		4658
POL	YWQATWIPE	597	10	52	81	0.0660	4659
POL	EWIEFVNTIPL	605	10	50	78		4660
POL	FVNTIPLVKL	608	10	54	86		4661
POL	NTHPLVKLWY	610	10	57	89		4662
POL	LWYQLEKDP	617	10	14	22		4663
POL	LWYQLEKEPI	617	10	31	48		4664
POL	LWYQLETEPI	617	10	11	17		4665
POL	EVNIVTDSQY	684	10	59	92		4666
POL	NIVTDSQYAL	686	10	59	92		4667
POL	VTDQYALGI	688	10	58	91		4668
POL	ELVSNQIEQL	708	10	18	28		4669
POL	ELVSNQIEQL	708	10	19	30		4670
POL	LVNQHIEQL	709	10	19	30		4671
POL	LVNQHIEQL	709	10	19	30		4672
POL	QLIKKEKVVYL	716	10	28	44		4673
POL	QVDKLVLSAGI	719	10	15	23		4674
POL	QVDKLVSSGI	719	10	29	45		4675
POL	LVNAGIRKVL	743	10	15	23		4676
POL	LVSSGIRKVL	743	10	26	41		4677
POL	NLPVIVAKEI	779	10	26	41		4678
POL	IVASCDKQCL	779	10	42	67		4679
POL	GIWQLDCTIIL	811	10	43	67		4680
POL	CTHILEGKIL	817	10	31	48		4681
POL	CTHILEGKVL	817	10	23	36		4682
POL	LVAVIIVASGY	826	10	31	48		4683
POL	ETGQETAYFI	844	10	53	83		4684
POL	ETGQETAYFL	844	10	26	41		4685
POL	YFLKLAGRW	851	10	31	48		4686
POL	YFLKLAGRW	851	10	25	39		4687
POL	THITDNGSNF	864	10	14	22		4688
POL	VHITDNGSNF	864	10	24	38		4689
POL	STTVKACW	875	10	15	23		4690
POL	CWWAGIKQEF	882	10	21	33		4691
POL	CWWAGIKQEF	882	10	11	17		4692
POL	GIKQEFIPY	886	10	22	34		4693
POL	GIKQEFIPY	886	10	11	17		4694
POL	GVVSMINKEL	901	10	48	75		4695
POL	SMNKELKII	905	10	53	83		4696
POL	KTAVQMAVFI	925	10	56	88		4697
POL	RIIDIASDI	951	10	12	19		4698
POL	RIIDIIATDI	951	10	29	45		4700
POL	RIVDIATDI	951	10	12	19		4701
POL	QTKELQKQII	961	10	10	16		4702
POL	IIKIQNFRVY	969	10	12	19		4703
POL	ITKIQNFRVY	969	10	36	57		4704
POL	VYYRDSRDPI	977	10	34	53		4705

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	VYRDSRDPL	977	10	14	22		4706
POL	VYRDSRDPLW	978	10	34	53		4707
POL	VYRDSRDPLW	978	10	14	22		4708
POL	PLWKGPAKLL	985	10	35	55		4709
POL	PLWKGPAKLL	985	10	18	28		4710
POL	PLWKGPAKLLW	986	10	35	55		4711
POL	PLWKGPAKLLW	986	10	18	28		4712
POL	LWKGEGAVVI	994	10	59	92		4713
POL	AVVIQINSDI	1000	10	37	58		4714
POL	AVVIQINSEI	1000	10	12	19		4715
POL	KVPRRKAKI	1011	10	51	80		4716
POL	KVPRRKAKI	1011	10	17	17		4717
POL	VVPRRKAKII	1012	10	50	78		4718
POL	VVPRRKAKII	1012	10	11	17		4719
POL	KIKDYGRQM	1019	10	11	17		4720
POL	KIKDYGRQM	1019	10	50	78		4721
POL	GTTLNIPQITF	79	11	01	17		4722
POL	ATLSLIQITL	80	11	01	33		4723
POL	GTLSLIQITL	80	11	01	33		4724
POL	PTFNFQITLW	80	11	01	33		4725
POL	ITLWQPLVTH	90	11	19	30		4726
POL	LWQPLVTH	92	11	14	22		4727
POL	LWQPLVTH	92	11	12	19		4728
POL	PLVTIKIGGQL	96	11	13	20		4729
POL	KIGGQLKEALL	101	11	23	36		4730
POL	LLDYGADDTV	110	11	61	95		4731
POL	VLEDINLIGRW	119	11	13	13		4732
POL	VLEENLIGRW	119	11	12	19		4733
POL	NLPGRWKPKM	124	11	35	55		4734
POL	GIGGFIKVRQY	136	11	53	83		4735
POL	GIGGFIKVRQY	139	11	41	64		4736
POL	FIKVRQYDQIL	140	11	21	33		4737
POL	ILIEICGKKAI	149	11	13	20		4738
POL	TVLVGHTPVNI	161	11	53	83		4739
POL	VLVGHTPVNI	162	11	51	80		4740
POL	PTPVNIIGRNL	166	11	26	41		4741
POL	PTPVNIIGRNM	166	11	24	38		4742
POL	NIIGRNLITQI	170	11	21	33		4743
POL	NIIGRNLITQI	170	11	18	28		4744
POL	NIIGRNLITQI	170	11	11	17		4745
POL	LLTQIGCTLNF	176	11	21	33		4746
POL	MLTQIGCTLNF	176	11	17	27		4747
POL	MLTQIGCTLNF	176	11	10	16		4748
POL	ETVPVKLKP	192	11	51	80		4749
POL	EMEKEGKISKI	229	11	32	50		4750
POL	KISKIGPENPY	235	11	41	64		4751
POL	KISKIGPENPY	235	11	11	17		4752
POL	KWRKLVDFRE	259	11	59	92		4753
POL	GLKKKKSIVT	288	11	49	77		4754
POL	SVTVLDVGDG	294	11	56	88		4755

Table X
 IIIY Δ2-4 Super MuIf Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*2401	SI:Q ID NO
POL	VTVLVDVGDAY	295	11	56	88		4756
POL	DVGDAYFSVP	299	11	54	84		4757
POL	AYFSVPLDKDF	303	11	18	28		4758
POL	SVPLDKDFRK	306	11	18	28		4759
POL	SINNETGIRY	323	11	32	50		4760
POL	STNETGIRY	323	11	11	17		4761
POL	RYQYNVLQK	332	11	63	98		4762
POL	AIQSSMTKIL	347	11	36	56		4763
POL	PERKQNPDI	359	11	14	22		4764
POL	DIVYQYMDL	366	11	18	28		4765
POL	EIVYQYMDL	366	11	24	38		4766
POL	IVYQYMDLY	367	11	42	66		4767
POL	YMDLYVGSID	372	11	61	95		4768
POL	DLHGQIRAKI	381	11	26	41		4769
POL	DLHGQIRTKI	381	11	20	31		4770
POL	RTKIELRQIIL	388	11	14	22		4771
POL	ELREILLKWI	393	11	14	22		4772
POL	ELRQIILLRWG	393	11	12	19		4773
POL	WMGYELIIPDK	418	11	60	94		4774
POL	DIQKLVGKLN	445	11	62	97		4775
POL	LYCKLNWASQ	449	11	60	94		4776
POL	QIYAGIKVKQL	458	11	18	29		4777
POL	QIYPIGKVKQL	458	11	11	17		4778
POL	QIYPIGKVRQL	458	11	14	22		4779
POL	GKVKQLCKLL	462	11	27	42		4780
POL	GKVRQLCKLL	462	11	18	28		4781
POL	LLRGAKALTDI	471	11	22	34		4782
POL	GKALTEVIVL	474	11	11	17		4783
POL	DIVPLTEAEI	480	11	13	20		4784
POL	EVIPLTEAEI	480	11	11	17		4785
POL	ELELAENREIL	489	11	53	83		4786
POL	EILKEPIVIGVY	497	11	40	63		4787
POL	ILKEPIVIGVY	498	11	38	59		4788
POL	GVYYDPSKDLI	508	11	31	48		4789
POL	QWYQIYQEP	528	11	42	66		4790
POL	SIVWGTTPKF	571	11	41	64		4791
POL	VIWGTTPKF	573	11	17	27		4792
POL	VIWGTTPKFR	573	11	29	45		4793
POL	KFKLPIQKETW	580	11	20	31		4794
POL	KFKLPIQKETW	580	11	26	41		4795
POL	PIQKETWEAW	584	11	15	23		4796
POL	PIQKETWEAW	584	11	27	42		4797
POL	ETWETWWTID	588	11	10	16		4798
POL	TWWTDYWQA	592	11	10	16		4799
POL	TWWTDYWQA	592	11	12	19		4800
POL	WWTDYWQAT	593	11	14	22		4801
POL	WWTEYWQAT	593	11	23	36		4802
POL	DYWQATWIPE	596	11	19	30		4803
POL	EYWQATWIPE	596	11	33	52		4804
POL	EFVNTPLVKL	607	11	54	84		4805

Table X
HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ2401	SI:Q ID NO
POL	FVNTPLVLKL	608	11	54	86		4806
POL	KLWYQLEKPH	616	11	14	22		4807
POL	KLWYQLEKEH	616	11	31	48		4808
POL	KLWYQLETEH	616	11	11	17		4809
POL	LTDTTNQKTE	661	11	19	30		4810
POL	LTEITNOKTE	661	11	25	39		4811
POL	TTNQKTELHAI	664	11	12	19		4812
POL	TTNQKTELQAI	664	11	42	66		4813
POL	KTELQAIHIAL	668	11	15	23		4814
POL	KTELQAIYLAL	668	11	12	19		4815
POL	AIHIALQDSGL	673	11	15	23		4816
POL	ALQDSGLEVNI	677	11	27	42		4817
POL	ALQDSGSEVNI	677	11	25	39		4818
POL	IVTDSQYALGI	687	11	58	91		4819
POL	VITDSQYALGII	688	11	58	91		4820
POL	ELVNOIHQOLI	708	11	18	28		4821
POL	ELVSOIHQOLI	708	11	19	30		4822
POL	LIKKEKYVLA	717	11	20	31		4823
POL	LIKKEKYVLSW	717	11	13	20		4824
POL	YLAWVPAIKG	724	11	22	34		4825
POL	YLSWVPAIKG	724	11	37	58		4826
POL	GIGGNEQVDKL	733	11	58	91		4827
POL	KLVSAGIRKVL	742	11	26	23		4828
POL	KLVSAGIRKVL	742	11	15	23		4829
POL	LVSAGIRKVL	743	11	15	23		4830
POL	LVSSGIRKVL	743	11	26	41		4831
POL	GIRKVLFLDGI	747	11	49	77		4832
POL	NWRMASIDF	770	11	41	64		4833
POL	AMASIDENLPH	773	11	18	28		4834
POL	EIVASCDKQCL	787	11	43	67		4835
POL	QVDCSPGIWQ	805	11	56	88		4836
POL	QLDCTHLEGI	814	11	33	52		4837
POL	ILVAVIIVASGY	825	11	53	83		4838
POL	LVAVIIVASGYI	826	11	47	73		4839
POL	ETGQETAYFIL	844	11	31	48		4840
POL	ETGQETAYFLL	844	11	26	41		4841
POL	AYFLKLGR	850	11	31	48		4842
POL	AYFLKLGR	850	11	25	39		4843
POL	KLGRWPVKV	855	11	13	20		4844
POL	KLGRWPVKV	855	11	22	34		4845
POL	KVIITDQSNF	863	11	21	33		4846
POL	FTSAAYKAAC	873	11	27	42		4847
POL	FTSTTVKAAC	873	11	14	22		4848
POL	AVKAACWWA	877	11	10	16		4849
POL	TVKAACWWA	877	11	20	31		4850
POL	WWAGIKQEF	883	11	21	33		4851
POL	WWAGIKQEF	883	11	17	17		4852
POL	IILKTAVQMAY	923	11	57	89		4853
POL	AVQMAVFIIN	927	11	60	94		4854
POL	FIINFRKKG	933	11	58	91		4855

Table X
 HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	NFKRKGIGGY	936	11	59	92		4856
POL	GIGGYAGIERI	942	11	57	89		4857
POL	GYSAGIERIDI	945	11	40	63		4858
POL	GYSAGIERIVDI	945	11	14	22		4859
POL	IASDIQIKEL	955	11	14	22		4860
POL	IATDIQIKEL	955	11	34	53		4861
POL	DIQIKELQKQI	959	11	44	69		4862
POL	QIKIQNFVY	968	11	12	19		4863
POL	QIKIQNFVY	968	11	35	55		4864
POL	IKIQNFVY	969	11	12	19		4865
POL	ITKIQNFVY	969	11	36	57		4866
POL	RVYIDSRDPI	976	11	34	53		4867
POL	RVYIDSRDPI	976	11	14	22		4868
POL	VYRDSRDI	977	11	34	53		4869
POL	VYRDSRDI	977	11	14	22		4870
POL	FWKGPALKL	985	11	35	55		4871
POL	PLWKGPALKL	985	11	18	28		4872
POL	LLWKGEAVV	993	11	59	92		4873
POL	KVPRIRKAKII	1011	11	50	78		4874
POL	KVPRIRKAKII	1011	11	11	17		4875
REV	LLKTVRLI	12	8	11	17		4876
REV	AVRIKIL	17	8	13	20		4877
REV	ILYQSNPY	23	8	27	42		4878
REV	QLPIERL	78	8	14	22		4879
REV	QLPIERL	78	8	37	58		4880
REV	LVESPAVL	114	8	11	17		4881
REV	AVRIKILY	17	9	13	20		4882
REV	KILYQSNPY	22	9	26	41		4883
REV	RWRARQRI	48	9	35	55		4884
REV	RWRERQRI	48	9	11	17		4885
REV	PVPLQLPI	74	9	11	17		4886
REV	PVPLQLPI	74	9	35	55		4887
REV	PLQPLPIERL	76	10	11	17		4888
REV	PLQPLPIERL	76	10	34	53		4889
REV	QLPIERLTL	78	10	18	28		4890
REV	QIQGVGSPI	97	10	11	18		4891
REV	IKILYQSNPY	20	11	18	28		4892
TAT	CYCKKCCF	28	8	11	17		4893
TAT	CYCKKCCY	28	8	11	17		4894
TAT	CFICQVCF	34	8	11	17		4895
TAT	FLNKGGLI	41	8	14	22		4896
TAT	PVDNLEPW	3	9	20	31		4897
TAT	PVDNLEPW	3	9	14	22		4898
TAT	CFLNKGGLI	40	9	14	22		4899
TAT	FLNKGGLISY	41	10	14	22		4900
TAT	CFLNKGGLISY	40	11	14	22		4901
VIF	RWQVLIVW	4	8	10	16		4902
VIF	RWQVMIVW	4	8	43	67		4903
VIF	IVWQVDRM	9	8	59	92		4904
VIF	KIRTWNSL	17	8	12	19		4905

Table X
HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	RRTWKS	17	8	15	23		4906
VIF	RRTWNSL	17	8	15	23		4907
VIF	SLVKIIMY	23	8	44	69		4908
VIF	LVKIIIMY	24	8	19	30		4909
VIF	GWFYRIIY	37	8	20	31		4910
VIF	KISSEVIII	50	8	15	23		4911
VIF	KVSEVIII	50	8	20	31		4912
VIF	RISSEVIII	50	8	15	23		4913
VIF	RLVITYW	65	8	12	19		4914
VIF	VIKTYWGL	67	8	10	16		4915
VIF	VITYWGL	67	8	22	34		4916
VIF	VVRTYWGL	67	8	10	16		4917
VIF	VVTYWGL	67	8	11	17		4918
VIF	HLGIGVSI	83	8	25	39		4919
VIF	HLGIGVSI	83	8	26	41		4920
VIF	GVSEIVRL	87	8	18	28		4921
VIF	STQIDPDL	100	8	12	19		4922
VIF	STQVDIPL	100	8	11	17		4923
VIF	QLIILYYF	110	8	14	22		4924
VIF	QLIIMITYF	110	8	14	22		4925
VIF	ILYYFDYF	113	8	16	25		4926
VIF	IMIIYFDCF	113	8	15	23		4927
VIF	IVSRCEY	133	8	14	22		4928
VIF	KVSLQYL	146	8	52	81		4929
VIF	QYLALAL	151	8	12	19		4930
VIF	QYLALKAL	151	8	11	17		4931
VIF	QYLALTAL	151	8	33	52		4932
VIF	YLALTALI	152	8	28	44		4933
VIF	ALIKPKKI	157	8	10	16		4934
VIF	PLPSVKKL	168	8	21	33		4935
VIF	PLPSVKKL	168	8	14	22		4936
VIF	MIVWQVDRM	8	9	46	72		4937
VIF	VWQVDRMKI	10	9	13	20		4938
VIF	VWQVDRMKI	10	9	48	75		4939
VIF	SLVKIIMYI	23	9	19	30		4940
VIF	IIPLGDAKL	36	9	13	20		4941
VIF	IIPLGEARL	36	9	20	31		4942
VIF	PLGEARLVI	38	9	10	16		4943
VIF	LVIKTYWGL	66	9	10	16		4944
VIF	LVITYWGL	66	9	22	34		4945
VIF	GLITGERDW	73	9	22	34		4946
VIF	GLTGERDW	73	9	12	19		4947
VIF	ITGERDWIL	75	9	21	33		4948
VIF	QTGERDWIIL	75	9	12	19		4949
VIF	SIEVRLRRY	89	9	11	17		4950
VIF	DLADQLIIL	106	9	18	28		4951
VIF	GLADQLIIM	106	9	15	23		4952
VIF	QYLALTALI	151	9	28	44		4953
VIF	VMIWQVDIR	7	10	44	69		4954
VIF	IVWQVDRMKI	9	10	12	19		4955

Table X
 HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	IVWQVDRMRI	9	10	47	73		4956
VIF	QVDRMKIRTW	12	10	12	19		4957
VIF	QVDRMRINTW	12	10	10	16		4958
VIF	QVDRMRIRTW	12	10	31	48		4959
VIF	RMKIRTWNSL	15	10	12	19		4960
VIF	RMKIRTWKSL	15	10	15	23		4961
VIF	RMKIRTWNSL	15	10	15	23		4962
VIF	TWKSLSVKIII	20	10	25	25		4963
VIF	TWNSLVKIII	20	10	25	39		4964
VIF	KISSEVHIPL	50	10	14	22		4965
VIF	KVSSEVHIPL	50	10	19	30		4966
VIF	RISSEVHIPL	50	10	13	20		4967
VIF	RLVITYWGL	65	10	12	19		4968
VIF	DWILGIGVSI	81	10	21	33		4969
VIF	DWILGQGVSI	81	10	18	28		4970
VIF	IILHIGVSI	83	10	25	39		4971
VIF	IILGQGVSI	83	10	26	41		4972
VIF	IYSLQVDRGL	98	10	10	16		4973
VIF	QIIMDLADQL	102	10	10	16		4974
VIF	QVDRGLADQL	102	10	14	22		4975
VIF	LHILYYDFCF	111	10	16	25		4976
VIF	LHIMHYDFCF	111	10	15	23		4977
VIF	YFDCFSASAI	116	10	28	44		4978
VIF	KVGSQYLAL	146	10	51	80		4979
VIF	SLQYLALAL	149	10	12	19		4980
VIF	SLQYLALKAL	149	10	11	17		4981
VIF	SLQYLALTAL	149	10	31	48		4982
VIF	SVKLLTDRW	174	10	13	20		4983
VIF	QVMIVWQVDR	6	11	43	67		4984
VIF	MIVWQVDRM	8	11	43	67		4985
VIF	RTWKSLSVKIII	19	11	14	22		4986
VIF	RTWNSLVKIII	19	11	24	38		4987
VIF	TWKSLSVKIII	20	11	16	25		4988
VIF	TWNSLVKIII	20	11	22	34		4989
VIF	EVHIIPLGDAKL	54	11	13	20		4990
VIF	EVHIIPLGEARL	54	11	20	31		4991
VIF	IHIIPLGEARLVI	56	11	10	16		4992
VIF	YWGLITGERD	71	11	22	34		4993
VIF	YWGLITGERD	71	11	12	19		4994
VIF	GLIITGERDWII	73	11	21	33		4995
VIF	GLITGERDWII	73	11	12	19		4996
VIF	GVSEWRRLR	87	11	10	16		4997
VIF	QIDPDLADQLI	102	11	10	16		4998
VIF	QVDFGLADQLI	102	11	14	22		4999
VIF	GLADQLIIMII	106	11	11	17		5000
VIF	QLIILYYDFCF	110	11	13	20		5001
VIF	QLIIMHYDFCF	110	11	22	33		5002
VIF	YYFDCFSASAI	115	11	20	31		5003
VIF	CFSDSAIRKAI	119	11	10	16		5004
VIF	CFSESAIRKAI	119	11	12	19		5005

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	Nn. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	CFSESJAUNAI	119	11	12	19		5006
VIF	SLQYLALYALI	149	11	27	42		5007
VIF	LIKPKIKKIPPL	158	11	10	16		5008
VIF	KTKGIRGSIIIT	188	11	15	23		5009
VPR	ALELELEL	19	8	10	16		5010
VPR	TLELELEL	19	8	44	69		5011
VPR	AVRIIFPRI	30	8	14	22		5012
VPR	WLHGLQGY	38	8	11	17		5013
VPR	TWAGVEAI	53	8	16	25		5014
VPR	TWEGVEAI	53	8	20	31		5015
VPR	GVEAIIRI	56	8	34	53		5016
VPR	IRILQQL	60	8	42	66		5017
VPR	RILOQLLF	62	8	45	70		5018
VPR	ILQQLFI	63	8	37	58		5019
VPR	LLFIIFRI	67	8	44	69		5020
VPR	LLFVIFRI	67	8	12	19	0.1400	5021
VPR	PYNEWTELEL	14	9	30	47		5022
VPR	WTLELELEL	18	9	42	69		5023
VPR	AVRIIFPRIW	30	9	14	22		5024
VPR	AVRIIFRPFW	30	9	34	53		5025
VPR	PWLHGLQGY	37	9	11	17		5026
VPR	WLHGLQGH	38	9	20	31		5027
VPR	IYETYGDTW	46	9	31	48		5028
VPR	IYNTYGDW	46	9	18	28	0.0580	5029
VPR	DTWAGVEAI	52	9	16	25		5030
VPR	DTWEGVEAI	53	9	20	31		5031
VPR	TWAGVEAI	53	9	16	25		5032
VPR	TWEGVEAI	53	9	19	30		5033
VPR	GVEAIIRL	56	9	34	53		5034
VPR	AIIRILQQL	59	9	39	61		5035
VPR	RILOQLLF	60	9	42	66		5036
VPR	QLLFIFRI	62	9	36	56		5037
VPR	QLLFVIFRI	66	9	44	69		5038
VPR	RIGCQISR	74	9	10	16		5039
VPR	RIGCIRISR	74	9	47	73		5040
VPR	PYNEWTELEL	74	9	12	19		5041
VPR	EWLELELEL	17	10	30	47		5042
VPR	ELKNEAVRIIF	25	10	40	63		5043
VPR	ELKSEAVRIIF	25	10	17	27		5044
VPR	AVRIIFPRIWL	30	10	15	23		5045
VPR	AVRIIFPRIWL	30	10	14	22		5046
VPR	HFPRIRWLISL	33	10	34	53		5047
VPR	HFPRIRWLIGL	33	10	10	16		5048
VPR	PWLHGLQGH	37	10	24	38		5049
VPR	WLHGLQGH	38	10	12	19		5050
VPR	IYETYGDTW	45	10	20	31		5051
VPR	IYETYGDTW	45	10	17	27		5052
VPR	IYETYGDTW	45	10	14	22		5053
VPR	IYETYGDTW	45	10	14	22		5054
VPR	DTWAGVEAI	52	10	16	25		5055

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SI:Q ID NO
VPR	DTWEGVEAH	52	10	19	30		5056
VPR	AIRILOQLL	59	10	39	61		5057
VPR	IRILOQLLF	60	10	41	64		5058
VPR	ILQQLLFHIF	63	10	35	55		5059
VPR	PWLHGLGQH	37	11	12	19		5060
VPR	QYIYETGDT	44	11	14	22		5061
VPR	TWAGVEAIRI	53	11	15	23		5062
VPR	TWEGVEAIRI	53	11	14	22		5063
VPR	AIRILOQLLF	59	11	38	59		5064
VPR	IRILOQLLF	60	11	33	52		5065
VPR	RILQQLFHIF	62	11	34	53		5066
VPR	IIFRIGCRHSKI	71	11	44	69		5067
VPR	IIFRIGCRHSKI	71	11	11	17		5068
VPR	RIGCQHSRIGI	74	11	45	70		5069
VPR	RIGCQHSRIGI	74	11	11	11		5070
VPU	KVIDYRVI	7	8	01	33		5071
VPU	LIAIVVW	26	8	10	16		5072
VPU	IVVWTVF	30	8	15	23		5073
VPU	VVWTVF	31	8	15	23		5074
VPU	WTIVFIEY	34	8	12	19		5075
VPU	VIEYRKI	37	8	12	19		5076
VPU	KILQRKI	45	8	15	23		5077
VPU	EMGHIAFW	89	8	11	17		5078
VPU	NYELAVGAL	5	9	25	01		5079
VPU	DYKLGVGAL	10	9	02	29		5080
VPU	DYKLGVGAL	10	9	03	43		5081
VPU	IIAIVVWTI	27	9	23	36		5082
VPU	AIVVWTVF	29	9	22	14		5083
VPU	IVVWTVF	30	9	15	23		5084
VPU	VWTVFIEY	33	9	12	19		5085
VPU	IVFIEYRKI	36	9	12	19		5086
VPU	KIDRLIRI	52	9	14	22		5087
VPU	VTLSSSKL	94	9	01	50		5088
VPU	NYELAVGALI	5	10	01	25		5089
VPU	DYKLGVGALI	10	10	02	29		5090
VPU	DYKLGVGALI	10	10	03	43		5091
VPU	AIVVWTVF	29	10	14	22		5092
VPU	VVWTVFIEY	31	10	12	19		5093
VPU	ILRQRKIDRL	46	10	15	23		5094
VPU	GVEMGHIAF	91	10	01	50		5095
VPU	LVTLLSSKL	91	10	01	50		5096
VPU	KVDYRIVIVAF	7	11	01	33		5097
VPU	KVDYRIVIVAF	7	11	01	33		5098
VPU	RIDYRLGVGAL	7	11	01	33		5099
VPU	IVVWTVFIEY	30	11	12	19		5100
VPU	EYRKILRQRKI	41	11	13	21		5101
VPU	KILRQRKIDRL	45	11	15	23		5102
VPU	ILRQRKIDRL	46	11	13	20		5103
VPU	RIKEIRDDSDY	64	11	01	50		5104
VPU	RIKEIRDDSDY	64	11	01	50		5105

Table XI
 HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
ENV	DINPQEVV	91	8	13	20		5106
ENV	APAGFAIL	265	8	29	45		5107
ENV	KPVVSTQL	299	8	34	53		5108
ENV	RPVVSTQL	299	8	26	41		5109
ENV	GKQTFYA	362	8	11	17		5110
ENV	LPCRIKQI	485	8	31	48		5111
ENV	SPLSFQTL	808	8	30	47		5112
ENV	GIDRPEEI	822	8	15	23		5113
ENV	EPDRPEEI	823	8	01	33		5114
ENV	IPDRPEEI	823	8	12	19		5115
ENV	DINPQEVVL	91	9	01	33	0.00012	5116
ENV	KPCVKLTPL	130	9	55	86	0.41000	5117
ENV	CPKVSFEPI	250	9	30	47	0.05500	5118
ENV	DIPHIYCA	256	9	12	19	0.00001	5119
ENV	EPRIIYCA	256	9	26	41	0.01300	5120
ENV	IPHIYCAPA	259	9	36	56		5121
ENV	IPHIYCTPA	259	9	18	28		5122
ENV	GPCKNVSTV	283	9	15	23	0.00019	5123
ENV	GPCTNVSTV	283	9	11	17	0.00012	5124
ENV	KPVVSTQLL	299	9	34	53	0.00044	5125
ENV	RPVVSTQLL	299	9	26	41		5126
ENV	DPEIVMISF	428	9	14	22	0.00001	5127
ENV	LPCRIKQII	485	9	20	31	0.00011	5128
ENV	LPCRIKQIV	485	9	10	16		5129
ENV	APTKAKRRV	575	9	22	34	0.00082	5130
ENV	SPLSFQTL	808	9	10	16		5131
ENV	IPRRIRQGF	950	9	10	16		5132
ENV	IPRRIRQGL	950	9	24	38		5133
ENV	IPTRIRQGL	950	9	11	17		5134
ENV	VPIDPNPQEI	88	10	25	39	0.00008	5135
ENV	VPIDPNPQEV	88	10	21	33		5136
ENV	KPVVSTQLL	299	10	34	53		5137
ENV	RPVVSTQLL	299	10	26	41	0.00038	5138
ENV	RPNNTRKSI	347	10	17	27		5139
ENV	EPLGVAPTKA	570	10	21	33	0.00005	5140
ENV	APTKAKRRVV	575	10	22	34	0.12000	5141
ENV	VPVWKEATT	53	11	22	34	0.00022	5142
ENV	VPIDPNPQEV	88	11	13	20		5143
ENV	KPCVKLTPLC	130	11	54	84	0.00004	5144
ENV	CPKVSFEPII	250	11	30	47		5145
ENV	DIPHIYCAPA	256	11	10	16		5146
ENV	EPDHIYCAPA	256	11	24	38		5147
ENV	EPDHIYCTPA	256	11	10	16		5148
ENV	IPHIYCAPAGF	259	11	26	41		5149
ENV	IPHIYCTPAGF	259	11	10	16		5150
ENV	LPCRIKQIIM	485	11	18	28		5151
ENV	RPGGDMRDN	547	11	38	59		5152
GAG	RPGGKKKY	22	8	35	55		5153
GAG	NPGLLETA	49	8	15	23		5154
GAG	SPRTLNAW	169	8	57	89	0.00036	5155

Table XI
 IIIV D07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	P<0.001	SEQ ID NO.
GAG	SPEVPMF	186	8	55	86	0.0012	5156
GAG	TPQDLNMM	201	8	12	19		5157
GAG	TPQDLNTM	201	8	42	66	0.0001	5158
GAG	IIPVIAQPI	237	8	38	59	0.0012	5159
GAG	GPIAPQOM	242	8	19	30	0.0005	5160
GAG	GPIPPQOM	242	8	17	27		5161
GAG	GPIVAPQOM	242	8	10	16		5162
GAG	EPKGSQIA	251	8	56	88	0.0001	5163
GAG	PIPVGDI	278	8	10	16		5164
GAG	PIPVGEI	278	8	35	55	0.0001	5165
GAG	SPVSILDI	302	8	13	20		5166
GAG	NPDC'KSIL	351	8	40	63		5167
GAG	NPDC'KTIL	351	8	11	17		5168
GAG	GPGLIKARV	379	8	46	72	0.0003	5169
GAG	GPSIKARV	379	8	36	56	0.0002	5170
GAG	APRKKGCW	400	8	19	30		5171
GAG	PPAESFGF	498	8	55	86	0.0004	5172
GAG	PPAESFRF	498	8	10	16		5173
GAG	PPAESFRF	510	8	15	23		5174
GAG	PPAESFRF	510	8	02	67		5175
GAG	PPAESFRF	510	8	04	33		5176
GAG	EPDKELY	533	8	12	19		5177
GAG	EPDKELY	537	8	01	25		5178
GAG	SPKTLNAAWV	169	9	57	89	0.5500	5179
GAG	TPQDLNMMML	201	9	12	19		5180
GAG	TPQDLNTML	201	9	42	66	0.0008	5181
GAG	IIPVIAQPIA	237	9	19	30	0.0590	5182
GAG	NPPIPVGDI	277	9	10	16		5183
GAG	NPPIPVGEI	277	9	34	54	0.0002	5184
GAG	PIPVGDIY	278	9	10	16		5185
GAG	PIPVGEIY	278	9	35	55	0.0002	5186
GAG	GPKEPRDY	312	9	63	98	0.0002	5187
GAG	GPAATLEEM	362	9	16	25	0.0014	5188
GAG	GPGATLEEM	362	9	18	28		5189
GAG	GPSIKARVL	379	9	35	55	0.0290	5190
GAG	GPSIKARVL	379	9	19	30		5191
GAG	RPEPTAPPA	490	9	30	47	0.0014	5192
GAG	APPAESFGF	497	9	10	16		5193
GAG	APPAESFRF	497	9	15	23	0.0046	5194
GAG	RPEPTAPPA	504	9	01	50	0.0014	5195
GAG	APPAESFRF	509	9	02	67		5196
GAG	APPAESFRF	509	9	01	33		5197
GAG	TPSQKQEI	537	9	10	17		5198
GAG	YPLASLKS	545	9	08	17	0.9900	5199
GAG	YPLASLKS	545	9	07	15		5200
GAG	PPLASLKS	546	9	04	24		5201
GAG	EPLTALRS	547	9	01	33		5202
GAG	PPLASLKS	547	9	01	33		5203
GAG	PPLSLSKS	547	9	01	33		5204
GAG	RPGKKKKYKL	22	10	10	16		5205

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Antibody Acids	Sequence Frequency	Conservancy (%)	11*0702	SEQ ID NO.
GAG	RPGGKKKYRL	22	10	16	25		5206
GAG	SPEVPMFSA	186	10	41	64	0.0002	5207
GAG	SPEVPMFETA	186	10	13	20		5208
GAG	NIPVIGDIY	277	10	10	16		5209
GAG	NIPVIGELY	277	10	34	54	0.0002	5210
GAG	IPVGIYKRW	280	10	11	17		5211
GAG	IPVGEYKRW	280	10	34	53	0.0002	5212
GAG	GPKPEYDYV	312	10	63	98	0.0002	5213
GAG	EPEDYVDIF	315	10	63	98	0.0002	5214
GAG	NPDCKTLKA	351	10	28	44	0.0002	5215
GAG	NPDCKTLRA	351	10	18	28		5216
GAG	GPAATLEMM	362	10	16	25	0.0020	5217
GAG	GPGATLEMM	362	10	18	28		5218
GAG	GPGIKARVLA	379	10	35	55	0.0002	5219
GAG	GPGIKARVLA	379	10	19	30		5220
GAG	IPAEPTAPPA	491	10	01	50		5221
GAG	EPTAIPAESE	494	10	20	31		5222
GAG	EPTAIPAESE	494	10	15	23	0.0002	5223
GAG	EPTAIPAESE	506	10	01	50		5224
GAG	EPTAIPAESE	506	10	01	50		5225
GAG	PPESFRFEA	511	10	01	33	0.0019	5226
GAG	EPIDKELYPL	533	10	12	19	0.0019	5227
GAG	EPIDKELYPL	537	10	01	25	0.0019	5228
GAG	YPLASLKSIF	545	10	08	17		5229
GAG	YPLASLKSIF	545	10	07	15	0.0140	5230
GAG	PPLASLKSIF	546	10	04	24		5231
GAG	EPLTALRSIF	547	10	01	33		5232
GAG	PPLASLKSIF	547	10	01	33		5233
GAG	PPLASLKSIF	547	10	01	33		5234
GAG	QPSLQTGEEL	67	11	13	20		5235
GAG	YPIVQNAQQQ	153	11	20	31		5236
GAG	YPIVQNLQQQ	153	11	29	45		5237
GAG	SPRTLNAAWK	169	11	55	86	0.0076	5238
GAG	SPEVPMFSAI	186	11	41	64	0.0003	5239
GAG	SPEVPMFSAI	186	11	13	20		5240
GAG	IPMFSAISEGA	190	11	45	70	0.0004	5241
GAG	IPMFSAISEGA	190	11	15	23		5242
GAG	TPQDLNMMMLN	201	11	11	17		5243
GAG	IPVGIYKRWI	280	11	10	16		5244
GAG	IPVGEYKRWI	280	11	10	16		5245
GAG	EPFRDYVDIFF	315	11	35	55	0.0001	5246
GAG	EPFRDYVDIFF	315	11	28	44	0.0001	5247
GAG	NPDCKTLKAL	351	11	28	44	0.0001	5248
GAG	NPDCKTLKAL	351	11	18	28		5249
GAG	WPSIKGRPGN	474	11	23	36		5250
GAG	WPSIKGRPGN	474	11	14	22		5251
GAG	WPSKGRPGN	474	11	11	17		5252
GAG	PPPSFRFEA	510	11	01	33		5253
NEF	APTAAKGV	34	8	01	33		5254
NEF	VPLRPMTF	101	8	10	16		5255

Table XI
 HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	P*0702	SEQ ID NO.
NEF	VPLRPMTY	101	8	46	73	0.0001	5256
NEF	RPMTYKAA	104	8	23	36		5257
NEF	RPMTYKGA	104	8	25	39		5258
NEF	TPGIGIRY	208	8	17	27		5259
NEF	TPGIGTRF	208	8	13	20		5260
NEF	GPGRYPL	210	8	17	27		5261
NEF	GPGRFPL	210	8	13	20		5262
NEF	VPVIRREV	210	8	11	17		5263
NEF	IIPICQIIGM	259	8	10	16		5264
NEF	IIPMSQIIGM	259	8	12	19		5265
NEF	EPAADGVGA	40	9	05	19	0.0001	5266
NEF	PAAEGVGA	40	9	04	15		5267
NEF	FPVRPQVPL	94	9	48	75	0.7600	5268
NEF	RPQVPLRPM	98	9	47	73	1.7000	5269
NEF	RPMTYKGA	104	9	12	19		5270
NEF	FPLTFGWCF	217	9	17	27		5271
NEF	YPLTFGWCF	217	9	24	38		5272
NEF	APTAAGVGGA	34	10	01	33		5273
NEF	EPAADGVGAV	40	10	04	15		5274
NEF	VPLRPMTYKA	101	10	20	32	0.0001	5275
NEF	TPGIGIRYPL	208	10	16	25		5276
NEF	TPGIGTRFPL	208	10	13	20		5277
NEF	GPGRYPLTF	210	10	13	20		5278
NEF	GPGRYPLTF	210	10	13	20		5279
NEF	APTAAGVGGA	34	11	01	33		5280
NEF	RPQVPLRPMIT	98	11	10	16		5281
NEF	RPQVPLRPMIT	98	11	36	56		5282
NEF	VPLRPMTYKA	101	11	19	30		5283
NEF	VPLRPMTYKG	101	11	23	37		5284
NEF	RPMTYKGAFD	104	11	12	19		5285
NEF	FPLTFGWCFK	217	11	17	27		5286
NEF	YPLTFGWCFK	217	11	20	31		5287
POL	EPGIEDREL	69	8	01	17		5288
POL	GPGRALSV	70	8	01	20		5289
POL	RPLVTIKI	95	8	14	22		5290
POL	RPLVTIKI	95	8	12	19		5291
POL	KPKMIGGI	130	8	60	94	0.0023	5292
POL	GTPVNI	165	8	54	84	0.0001	5293
POL	SPIETVPV	189	8	56	88	0.0021	5294
POL	WPLTEEKI	211	8	56	88	0.0001	5295
POL	NPYNTPIF	243	8	24	38		5296
POL	NPYNTPIF	243	8	38	59	0.0008	5297
POL	TPGIRYQY	328	8	52	81	0.0001	5298
POL	PPFLWMGY	414	8	64	100	0.0001	5299
POL	EPVHGVY	504	8	41	64	0.0001	5300
POL	DPSKDLIA	512	8	34	53		5301
POL	TPKFKLPI	578	8	17	27		5302
POL	TPKFKLPI	578	8	30	47		5303
POL	LPIQKETW	583	8	47	73	0.0001	5304
POL	TPPLVKLW	611	8	57	89	0.0001	5305

Table XI
IIIY B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	U*0702	SIQ ID NO.
POL	PPLVKLWY	612	8	57	89	0.0001	5306
POL	PIVVAKEI	781	8	27	42		5307
POL	PIVVAKEI	781	8	29	45	0.0001	5308
POL	PIVVAKEI	781	8	29	45	0.0001	5309
POL	PIVVAKEI	781	8	29	45	0.0001	5310
POL	PIVVAKEI	781	8	29	45	0.0001	5311
POL	PIVVAKEI	781	8	29	45	0.0001	5312
POL	PIVVAKEI	781	8	29	45	0.0001	5313
POL	PIVVAKEI	781	8	29	45	0.0001	5314
POL	PIVVAKEI	781	8	29	45	0.0001	5315
POL	PIVVAKEI	781	8	29	45	0.0001	5316
POL	PIVVAKEI	781	8	29	45	0.0001	5317
POL	PIVVAKEI	781	8	29	45	0.0001	5318
POL	PIVVAKEI	781	8	29	45	0.0001	5319
POL	PIVVAKEI	781	8	29	45	0.0001	5320
POL	PIVVAKEI	781	8	29	45	0.0001	5321
POL	PIVVAKEI	781	8	29	45	0.0001	5322
POL	PIVVAKEI	781	8	29	45	0.0001	5323
POL	PIVVAKEI	781	8	29	45	0.0001	5324
POL	PIVVAKEI	781	8	29	45	0.0001	5325
POL	PIVVAKEI	781	8	29	45	0.0001	5326
POL	PIVVAKEI	781	8	29	45	0.0001	5327
POL	PIVVAKEI	781	8	29	45	0.0001	5328
POL	PIVVAKEI	781	8	29	45	0.0001	5329
POL	PIVVAKEI	781	8	29	45	0.0001	5330
POL	PIVVAKEI	781	8	29	45	0.0001	5331
POL	PIVVAKEI	781	8	29	45	0.0001	5332
POL	PIVVAKEI	781	8	29	45	0.0001	5333
POL	PIVVAKEI	781	8	29	45	0.0001	5334
POL	PIVVAKEI	781	8	29	45	0.0001	5335
POL	PIVVAKEI	781	8	29	45	0.0001	5336
POL	PIVVAKEI	781	8	29	45	0.0001	5337
POL	PIVVAKEI	781	8	29	45	0.0001	5338
POL	PIVVAKEI	781	8	29	45	0.0001	5339
POL	PIVVAKEI	781	8	29	45	0.0001	5340
POL	PIVVAKEI	781	8	29	45	0.0001	5341
POL	PIVVAKEI	781	8	29	45	0.0001	5342
POL	PIVVAKEI	781	8	29	45	0.0001	5343
POL	PIVVAKEI	781	8	29	45	0.0001	5344
POL	PIVVAKEI	781	8	29	45	0.0001	5345
POL	PIVVAKEI	781	8	29	45	0.0001	5346
POL	PIVVAKEI	781	8	29	45	0.0001	5347
POL	PIVVAKEI	781	8	29	45	0.0001	5348
POL	PIVVAKEI	781	8	29	45	0.0001	5349
POL	PIVVAKEI	781	8	29	45	0.0001	5350
POL	PIVVAKEI	781	8	29	45	0.0001	5351
POL	PIVVAKEI	781	8	29	45	0.0001	5352
POL	PIVVAKEI	781	8	29	45	0.0001	5353
POL	PIVVAKEI	781	8	29	45	0.0001	5354
POL	PIVVAKEI	781	8	29	45	0.0001	5355

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	U*0702	SEQ ID NO.
POL	NPYNTPIFAI	243	10	24	38		5356
POL	NPYNTPIFAI	243	10	37	58	0.0034	5357
POL	VPLDKDFRKY	307	10	18	28	0.0002	5358
POL	TPGIRYQYNV	328	10	51	80	0.0044	5359
POL	LPQGWKGSFA	338	10	58	92	0.0120	5360
POL	EPFKQNPDI	358	10	16	25	0.0002	5361
POL	NPIDIVIYQM	364	10	17	27	0.0005	5362
POL	NPIDIVIYQM	364	10	23	36		5363
POL	NPFLWMGYEL	414	10	64	100	0.0002	5364
POL	IPDKWTVOPI	424	10	53	83	0.0012	5365
POL	DPSKDLIAEI	512	10	26	41	0.0002	5366
POL	LPIQKETWEA	583	10	15	23		5367
POL	PFLVKLWYQL	612	10	53	83	0.0002	5368
POL	EPVGAETFY	624	10	21	33	0.0002	5369
POL	QPIKSESELY	701	10	37	58	0.0002	5370
POL	LPIVAKIEIV	780	10	26	41		5371
POL	LPIVAKIEIV	780	10	27	42	0.0002	5372
POL	LPIVVAKEIV	781	10	25	39		5373
POL	LPIVVAKEIVA	781	10	28	44	0.0066	5374
POL	IPVETQGETA	841	10	58	91		5375
POL	IPVETQGETA	841	10	63	98	0.0023	5376
POL	DPIWKGPAKL	984	10	35	55		5377
POL	DPLWKGPAKL	984	10	15	23		5378
POL	VPTFNFPQITL	79	11	01	17	0.0001	5379
POL	FRQTLWQRPL	87	11	40	63		5380
POL	KPKMGIGIGF	130	11	60	94	0.0004	5381
POL	TPVNIIGNRNL	167	11	26	41	0.0012	5382
POL	TPVNIIGNRNL	167	11	24	38		5383
POL	FRISPIETVIV	186	11	55	86	0.0067	5384
POL	WPLTEKKIKAL	211	11	54	84	0.0001	5385
POL	GPENFYNTPIF	240	11	24	38		5386
POL	GPENFYNTPIF	240	11	38	59	0.0001	5387
POL	IPAGLKKKKKS	285	11	50	78	0.0001	5388
POL	IPSNINETIGI	321	11	31	48		5389
POL	IPSTNNETIGI	321	11	11	17		5390
POL	TPGIRYQYNVL	328	11	51	80	0.0015	5391
POL	LPQGWKGSFAI	338	11	58	92	0.0002	5392
POL	EPFKQNPDIIV	358	11	14	22		5393
POL	EPFLWMGYE	413	11	63	98	0.0001	5394
POL	IPDKWTVOPI	424	11	12	19		5395
POL	QPIQLPEKDSW	431	11	13	20		5396
POL	QPIVLPEKDSW	431	11	13	20		5397
POL	IPLTEEALEL	482	11	11	17		5398
POL	VPLTEEALEL	482	11	19	30		5399
POL	EPFKNLTKGK	536	11	45	70	0.0001	5400
POL	LPIQKETWEA	583	11	15	23		5401
POL	LPIQKETWEA	583	11	27	42		5402
POL	TPPLVKLWYQ	611	11	53	83	0.0001	5403
POL	EPVGAETFYV	624	11	21	33		5404
POL	LPIVAKIEIVA	780	11	25	39		5405

Table XI
HIV D07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	D*0702	SEQ ID NO.
POL	LPPVVAKEIVA	780	11	27	42	0.0001	5406
POL	IPAEIQGETAY	841	11	58	91	0.0001	5407
POL	IPYNPOSQGVV	893	11	59	92	0.0120	5408
POL	NPQSQGVVES	896	11	53	83	0.0001	5409
POL	DPIWKGPAAKL	984	11	34	53		5410
POL	DPLWKGPAKL	984	11	14	22		5411
REV	SPIETRQA	33	8	13	20		5412
REV	RPAEPVPL	70	8	20	31		5413
REV	VPLQLPPI	75	8	11	17		5414
REV	VPLQLPPL	75	8	36	56	0.0490	5415
REV	PPLERLTL	80	8	19	30	0.0001	5416
REV	LPLERLTL	79	9	19	30	0.3100	5417
REV	QIQGTETGV	100	9	05	18		5418
REV	PPSEGTQA	30	10	12	19		5419
REV	RPAEPVPLQL	70	10	20	31		5420
REV	EPVRLQPMI	73	10	11	17		5421
REV	EPVHLQPL	73	10	34	53	0.0023	5422
REV	PPISPEGTQA	29	11	12	19		5423
REV	VPLQLPHERL	75	11	11	17		5424
REV	VPLQLPPLERL	75	11	34	53	0.0001	5425
TAT	IPGSPQPKTA	16	9	26	41	0.0007	5426
TAT	IPGSPQRTA	16	9	10	16		5427
TAT	GPESKKV	90	9	13	20		5428
TAT	EPVDNLEPW	2	10	14	22		5429
TAT	EPVDPRLEPW	2	10	13	20	0.0001	5430
VIF	IPKISSEV	48	8	13	20		5431
VIF	IPKVSSEV	48	8	19	30		5432
VIF	IPKISSEV	48	8	13	20		5433
VIF	IPLGIDARL	57	8	14	22		5434
VIF	IPLGEARL	57	8	20	31		5435
VIF	DPLADQL	104	8	19	30		5436
VIF	DPLADQL	104	8	19	30		5437
VIF	SPRCYQA	135	8	21	33	0.0008	5438
VIF	IPLGIDARLV	57	9	11	17		5439
VIF	IPLGIDARLV	57	9	19	30		5440
VIF	DPLADQLI	104	9	19	30	0.0002	5441
VIF	DPLADQLI	104	9	19	30		5442
VIF	KPKKIKPPL	160	9	10	16		5443
VIF	PPLPSVKKL	167	9	21	33		5444
VIF	PPLPSVKKL	167	9	14	22		5445
VIF	IPKISSEVIII	48	10	13	20		5446
VIF	IPKVSSEVIII	48	10	19	30		5447
VIF	IPKISSEVIII	48	10	13	20	0.0330	5448
VIF	IPLGIDARLV	57	10	16	10		5449
VIF	KPLPSVKKL	166	10	20	31		5450
VIF	DPLADQLIIL	104	11	18	28		5451
VPR	EPYNEWTL	13	8	30	47		5452
VPR	FPRIWLHSL	34	9	16	10		5453
VPR	FPRIWLHGL	34	9	24	38		5454
VPR	GPRQEPYNEW	9	10	37	58	0.0001	5455

Table XI
 HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	U*0702	SEQ ID NO.
VPR	EPYNEWTLLEL	13	10	29	45	0.0054	5456
VPR	RPWLIIGLGQY	36	10	10	16		5457
VPR	EPYNEWTLLEL	13	11	29	45		5458
VPR	RPWLIIGLGQH	36	11	12	19		5459
VPU	APWDYDDL	99	8	12	19		5460

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HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	KKLWTLYL	9	8	01	50	5461
ENV	RKSWSLYL	9	8	01	50	5462
ENV	WRWGTFL	15	8	01	50	5463
ENV	WRWGTMLL	15	8	01	50	5464
ENV	EKLWVTY	43	8	09	15	5465
ENV	WKEATTL	56	8	23	36	5466
ENV	MIEDIISL	117	8	29	45	5467
ENV	IKNCSFNI	182	8	13	20	5468
ENV	PKVSFEIH	251	8	30	47	5469
ENV	LKCNIDKKF	272	8	13	20	5470
ENV	AKTIIVQL	330	8	14	22	5471
ENV	QRGGRAF	360	8	01	33	5472
ENV	KKKKTGYI	374	8	01	50	5473
ENV	IRQAHCNI	381	8	17	27	5474
ENV	IKQINMIW	489	8	33	52	5475
ENV	IKQIVNMW	489	8	13	21	5476
ENV	QRVGOANY	497	8	11	17	5477
ENV	FRPGKIDNI	546	8	43	67	5478
ENV	WRSELYKY	557	8	54	84	5479
ENV	YKYKVVHI	562	8	13	20	5480
ENV	YKYKVVKI	562	8	29	45	5481
ENV	ARQLISGI	627	8	38	59	5482
ENV	VRQLLSGI	627	8	10	16	5483
ENV	LKLTIVWGI	652	8	13	20	5484
ENV	EKNEQDLL	749	8	17	27	5485
ENV	EKNEQELL	749	8	18	28	5486
ENV	LRIFAVL	790	8	17	27	5487
ENV	LRIFAVL	790	8	28	44	5488
ENV	VIQGYSHL	803	8	56	88	5489
ENV	IRLVNGFL	843	8	11	17	5490
ENV	IRLVSGFL	843	8	13	20	5491
ENV	YIIRLDIF	865	8	13	20	5492
ENV	YIIRLDLL	865	8	15	23	5493
ENV	IRLRDIFL	866	8	13	20	5494
ENV	IRLRDILL	866	8	13	20	5495
ENV	GRIGWEAL	884	8	09	15	5496
ENV	LKGLRLGW	890	8	12	40	5497
ENV	LKGLQKQW	890	8	05	17	5498
ENV	LRIGWIEGL	893	8	10	32	5499
ENV	LKYLWNLL	900	8	14	22	5500
ENV	LKYWWNLL	900	8	14	22	5501
ENV	LKNSAINL	914	8	10	16	5502
ENV	LKNSAISL	914	8	10	16	5503
ENV	LKNSAVSL	914	8	13	20	5504
ENV	PRIRIQGF	951	8	11	17	5505
ENV	PRIRIQGL	951	8	26	41	5506
ENV	GKDLWVTY	42	9	01	33	5507
ENV	EKLWVTYV	43	9	09	15	5508
ENV	WKEATTLF	56	9	23	36	5509
ENV	WKNNMVEQM	109	9	35	55	5510

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HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	MIEDIISLW	117	9	29	45	5511
ENV	GKNEINDTY	218	9	01	20	5512
ENV	IIYCAPAGF	261	9	27	42	5513
ENV	IIYCTPAGF	261	9	10	16	5514
ENV	IKPVVSTQL	298	9	33	52	5515
ENV	IRPVVSTQL	298	9	26	41	5516
ENV	CRKQIINM	487	9	30	47	5517
ENV	CRKQIVNM	487	9	12	19	5518
ENV	GRAMYAPPI	501	9	23	36	5519
ENV	GRAMYAPPI	501	9	12	19	5520
ENV	MKDNWSEL	553	9	40	63	5521
ENV	YKVKIEPL	564	9	25	39	5522
ENV	EREKRAVGI	590	9	1	17	5523
ENV	QIILLKLTW	649	9	13	20	5524
ENV	QIILLQLTW	649	9	34	53	5525
ENV	QIIMLQLTW	649	9	10	16	5526
ENV	IKQLQARVL	659	9	40	63	5527
ENV	ARVLAVEIK	664	9	33	52	5528
ENV	ERYLKDQQL	670	9	30	47	5529
ENV	ERYLNIDQQL	670	9	18	28	5530
ENV	LKDQQLGI	673	9	27	42	5531
ENV	LRDQQLGI	673	9	19	30	5532
ENV	DKWASLWNW	759	9	26	41	5533
ENV	TKWLWYIKI	771	9	15	23	5534
ENV	LRNLCLFSY	857	9	16	25	5535
ENV	LRSLCLFSY	857	9	35	55	5536
ENV	YIIRLRDFIL	865	9	13	20	5537
ENV	YIIRLRDLLL	865	9	13	20	5538
ENV	IIRLRDLLL	866	9	11	17	5539
ENV	LKNSAVSLL	914	9	11	17	5540
ENV	IRQGLERAL	954	9	34	53	5541
ENV	KKLWTLYLAM	9	10	01	50	5542
ENV	RKSWSLYLAM	9	10	01	50	5543
ENV	WRWGTFLGIM	15	10	01	50	5544
ENV	WRWGTMLLGM	15	10	01	50	5545
ENV	GKDLWVTIVY	42	10	01	33	5546
ENV	LKPCVKLTPL	129	10	55	86	5547
ENV	VKLTPLCVTL	133	10	52	81	5548
ENV	PKVSFEPII	251	10	30	47	5549
ENV	IKPVVSTQLL	298	10	33	52	5550
ENV	IRPVVSTQLL	298	10	26	41	5551
ENV	MLSFNCGGIEF	433	10	13	20	5552
ENV	THSFNCGGIEF	433	10	22	34	5553
ENV	THSFNCRGIEF	433	10	13	20	5554
ENV	CRKQIINMW	487	10	30	47	5555
ENV	CRKQIVNMW	487	10	12	19	5556
ENV	IRCSNITGL	513	10	12	19	5557
ENV	MKDNWSEL	553	10	40	63	5558
ENV	KRAVGIGAVF	593	10	11	17	5559
ENV	LRAIEAQQL	642	10	45	70	5560

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HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	ARVLAVERYL	664	10	33	52	5561
ENV	ERYLKDQQL	670	10	29	45	5562
ENV	ERYLRDQQL	670	10	17	27	5563
ENV	LKDQQLGIW	673	10	27	42	5564
ENV	LRDQQLGIW	673	10	19	30	5565
ENV	EKNEQDLAL	749	10	17	27	5566
ENV	EKNEQELLE	749	10	13	20	5567
ENV	DKWASLWNWF	759	10	26	41	5568
ENV	TKWLWYKIF	771	10	12	19	5569
ENV	LRIFAFLSI	790	10	14	22	5570
ENV	LRIFAFLSI	790	10	19	30	5571
ENV	NIRVQGSPL	801	10	52	81	5572
ENV	VRQGSPLSF	803	10	48	75	5573
ENV	PRGPRPEGI	820	10	12	19	5574
ENV	IRLVSGFLAL	843	10	11	17	5575
ENV	YHRLDILLI	865	10	11	17	5576
ENV	LKLGWEGIKY	893	10	09	29	5577
ENV	LKYWWNLQY	900	10	14	22	5578
ENV	IRQLERALL	954	10	33	52	5579
ENV	WRWGTILFLGML	15	11	01	50	5580
ENV	WRWGTMLLGML	15	11	01	50	5581
ENV	YRLNCTSAT	235	11	15	24	5582
ENV	IIHYCAPAGFAI	261	11	27	42	5583
ENV	IKPVVSTQLLI	298	11	33	52	5584
ENV	IRPVVSTQLLI	298	11	26	41	5585
ENV	TRPNNTRKSI	346	11	12	19	5586
ENV	QRGPRAFVTI	360	11	01	33	5587
ENV	MIISFNCGGIEFF	433	11	13	20	5588
ENV	THSFNCGGIEFF	433	11	21	33	5589
ENV	THSFNCGGIEFF	433	11	13	20	5590
ENV	IRCSNITGLL	513	11	10	16	5591
ENV	YKYKVVKIEPL	562	11	25	39	5592
ENV	EKRAVGIGAVF	592	11	10	16	5593
ENV	KRAYGIGAVFL	593	11	11	17	5594
ENV	LRAIEAQQHIL	642	11	44	69	5595
ENV	QILLKLTWGI	649	11	13	20	5596
ENV	QILLQLTVWGI	649	11	34	53	5597
ENV	LKLTVWGIKQL	652	11	13	20	5598
ENV	GKLICTTAVPW	686	11	19	30	5599
ENV	GKLICTTNVW	686	11	17	27	5600
ENV	GKLICTTVPW	686	11	12	19	5601
ENV	TKWLWYKIFI	771	11	12	19	5602
ENV	IKIFIMIVGGL	777	11	38	59	5603
ENV	LKGLRLGWEG	890	11	08	27	5604
ENV	LKLGWEGIKYL	893	11	09	29	5605
ENV	LKYWWNLQYW	900	11	14	22	5606
ENV	LIIPRRIRQGL	948	11	12	19	5607
ENV	RIRROGLERAL	952	11	16	25	5608
ENV	TRIRQGLERAL	952	11	11	17	5609
GAG	DKWEKIRL	14	8	18	28	5610

Table XII
HIV D27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
GAG	KYKLIKIL	28	8	10	16	5611
GAG	KYKLIKIL	28	8	16	25	5612
GAG	YKLIKILW	30	8	13	20	5613
GAG	YKLIKILW	30	8	17	27	5614
GAG	CRQLGQL	59	8	15	23	5615
GAG	IKDTKEAL	96	8	10	16	5616
GAG	VKDTKEAL	96	8	33	52	5617
GAG	VRDTKEAL	96	8	10	16	5618
GAG	TKALDKI	99	8	33	52	5619
GAG	TKALEKI	99	8	10	16	5620
GAG	GIQAAMQM	214	8	61	95	5621
GAG	KRWILGL	287	8	55	86	5622
GAG	PKEPNDY	313	8	63	98	5623
GAG	FRDYVDRF	317	8	64	100	5624
GAG	CKTILKAL	354	8	28	44	5625
GAG	CKTILKAL	354	8	18	28	5626
GAG	AKVLAEM	384	8	57	89	5627
GAG	IKQIRPGNF	477	8	23	37	5628
GAG	NKGRPGNF	477	8	14	23	5629
GAG	SKQIRPGNF	477	8	11	18	5630
GAG	LKDKEPFL	535	8	01	25	5631
GAG	ERTENSLY	537	8	01	25	5632
GAG	EKEEGGLY	538	8	01	25	5633
GAG	GKLDWKEI	11	9	17	27	5634
GAG	LRPGKKKY	21	9	35	55	5635
GAG	KKYKLIKIL	27	9	13	20	5636
GAG	SRELERFAL	39	9	22	34	5637
GAG	ERFALNPGL	44	9	15	23	5638
GAG	ERFALNPGL	44	9	15	23	5639
GAG	VKVEEKAF	177	9	24	38	5640
GAG	VKVEEKAF	177	9	28	44	5641
GAG	EKAFSPEVI	182	9	48	75	5642
GAG	GIQAAMQML	214	9	61	95	5643
GAG	LIIPVHAGPI	236	9	22	34	5644
GAG	VIIPVHAGPI	236	9	14	22	5645
GAG	MIKPRGSDI	249	9	44	69	5646
GAG	YKRWILGL	286	9	55	86	5647
GAG	VRMYSPTSI	298	9	14	22	5648
GAG	VRMYSPTSI	298	9	40	63	5649
GAG	IKQGPKEPF	309	9	20	31	5650
GAG	IRQGPKEPF	309	9	42	66	5651
GAG	FRDYVDRFF	317	9	35	55	5652
GAG	FRDYVDRFY	317	9	29	45	5653
GAG	VKNWMTIDL	337	9	16	25	5654
GAG	VKNWMTIDL	337	9	36	56	5655
GAG	SIKGRPGNF	476	9	23	37	5656
GAG	IKGRPGNFI	477	9	23	37	5657
GAG	NKGRPGNFI	477	9	09	15	5658
GAG	RKEPTAPPL	492	9	01	50	5659
GAG	DKDKELYPL	536	9	01	25	5660

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HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	GKKKYRLKIL	25	10	12	19	5661
GAG	KKYRLKILVW	28	10	10	16	5662
GAG	KKYRLKILVW	28	10	16	25	5663
GAG	KILVWASREL	33	10	21	33	5664
GAG	KILVWASREL	33	10	36	56	5665
GAG	ERFALNPGLL	44	10	15	23	5666
GAG	ERFALNPGLL	44	10	15	23	5667
GAG	VIIQALSPRTL	164	10	27	42	5668
GAG	VIIQALSPRTL	164	10	11	17	5669
GAG	VRMYSPTSIL	298	10	14	22	5670
GAG	VRMYSPTSIL	298	10	40	63	5671
GAG	VKNWMTDTLL	337	10	16	25	5672
GAG	VKNWMTDTLL	337	10	36	56	5673
GAG	LKALGPAATL	358	10	16	25	5674
GAG	IKARVLAIEAM	438	10	57	89	5675
GAG	CHAPIKKGCW	447	10	53	83	5676
GAG	WKCCKEIGHQM	476	10	46	72	5677
GAG	ERQANFLGKI	491	10	54	84	5678
GAG	SIKGRIGNFL	530	10	23	37	5679
GAG	TRKEPTAPPL	538	10	01	50	5680
GAG	QKQEHDKIL	541	10	12	19	5681
GAG	EKEKGLYPL	541	10	01	25	5682
GAG	DKELYPLASL	552	10	13	21	5683
GAG	DKELYPLTSL	552	10	10	16	5684
GAG	LKSLFGNDPL	3	10	12	19	5685
GAG	ARASVLSGGEL	3	11	11	17	5686
GAG	ARASVLSGGKL	11	11	28	44	5687
GAG	GKLDAREKIRL	19	11	16	25	5688
GAG	IRLRPGGKKKY	21	11	33	52	5689
GAG	LRPGGKKKYKL	21	11	10	16	5690
GAG	LRPGGKKKYRL	27	11	16	25	5691
GAG	KKKYRLKILVW	32	11	13	20	5692
GAG	LKILVWASREL	32	11	21	33	5693
GAG	LKILVWASREL	32	11	22	34	5694
GAG	LKSLYNTVATL	77	11	13	20	5695
GAG	VKDTKEALDKI	96	11	16	25	5696
GAG	PRTLNAAWVKVI	170	11	30	48	5697
GAG	EKAFSPEVIM	182	11	48	75	5698
GAG	DRLLIPVIA GPI	234	11	22	34	5699
GAG	DRVLPVIA GPI	239	11	14	22	5700
GAG	VIIAGPIAFQGM	239	11	17	27	5701
GAG	VIIAGPIPFQGM	287	11	17	27	5702
GAG	KRWILGLNKI	381	11	55	86	5703
GAG	GIHKARVLAIEAM	381	11	35	55	5704
GAG	SIHKARVLAIEAM	456	11	19	30	5705
GAG	MKDCTERQANF	464	11	50	78	5706
GAG	ERQANFELKIW	530	11	54	84	5707
GAG	QKQEPIDKELY	535	11	12	19	5708
GAG	LKDKPEPLASL	537	11	01	25	5709
GAG	ERTENSLYPPPL		11	01	25	5710

Table XII
 HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	GKWSKSSI	3	8	18	28	5711
NEF	SKSSVGV	6	8	20	31	5712
NEF	EKGGLDGL	121	8	26	41	5713
NEF	EKGGLGL	121	8	34	53	5714
NEF	SKRQEL	177	8	25	39	5715
NEF	KRQDILD	181	8	18	28	5716
NEF	KRQELDL	181	8	32	50	5717
NEF	ARELIPEF	322	8	11	17	5718
NEF	ARELIPEY	322	8	24	38	5719
NEF	EKGGLDGLI	121	9	23	36	5720
NEF	EKGGLGLI	121	9	27	42	5721
NEF	KRQELDL	179	9	25	39	5722
NEF	KRQDILD	179	9	12	19	5723
NEF	KRQDILDW	181	9	18	28	5724
NEF	KRQELDLW	181	9	32	50	5725
NEF	IRYPLTFGW	214	9	13	20	5726
NEF	TRPPLTFGW	214	9	12	19	5727
NEF	LIIPMSQIGM	258	9	10	16	5728
NEF	ARELIPEFY	322	9	12	19	5729
NEF	ARELIPEY	322	9	11	17	5730
NEF	ARELIPEY	322	9	21	33	5731
NEF	SRDLEKIGAI	50	10	14	22	5732
NEF	VRQVPLRPM	97	10	47	73	5733
NEF	LRPMYKGF	103	10	12	19	5734
NEF	SIPLKEGGL	115	10	29	45	5735
NEF	LKEKGLDGL	118	10	26	42	5736
NEF	EKGGLDGLI	121	10	29	47	5737
NEF	EKGGLGLIY	121	10	21	33	5738
NEF	SKRQELDL	177	10	19	30	5739
NEF	KRQDILDW	179	10	25	39	5740
NEF	KRQDILDW	179	10	25	39	5741
NEF	YITQGFPPDW	193	10	14	22	5742
NEF	YITQGFPPDW	193	10	25	39	5743
NEF	GKWSKSSIVGW	3	11	25	39	5744
NEF	LKEKGLDGLI	118	11	23	37	5745
NEF	LKEKGLGLI	118	11	24	39	5746
NEF	SKRQELDLW	177	11	25	39	5747
NEF	KRQDILDWVY	181	11	16	25	5748
NEF	KRQDILDWVY	181	11	29	45	5749
NEF	TRPPLTFGWCF	214	11	10	16	5750
POL	TRRELQVW	43	8	13	20	5751
POL	GKWKPKMI	127	8	41	64	5752
POL	GRWPKNI	127	8	16	25	5753
POL	VRQYDQIL	143	8	21	33	5754
POL	IKKIGTVL	156	8	20	31	5755
POL	KKKIGTVL	156	8	29	45	5756
POL	GRNLLTQI	173	8	21	33	5757
POL	GRNMLTQI	173	8	19	30	5758
POL	GRNMLTQI	173	8	11	17	5759
POL	GRNMLTQI	173	8	11	17	5760

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HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PKVKQWPL	206	8	51	80	5761
POL	KKKDSFKW	233	8	57	89	5762
POL	NKRTQDFW	270	8	57	89	5763
POL	KKKSVTVL	291	8	50	78	5764
POL	RKYTAFTI	314	8	62	97	5765
POL	IRYQYNVL	331	8	53	83	5766
POL	WKGSPAIF	342	8	59	92	5767
POL	FRQNPDII	360	8	16	25	5768
POL	IRAKIEEL	387	8	26	41	5769
POL	IRTKIEEL	387	8	22	34	5770
POL	LREHLLKW	394	8	17	27	5771
POL	LRQHLLRW	394	8	15	23	5772
POL	EHLLKWCIF	396	8	14	22	5773
POL	QHLLRWGF	396	8	12	19	5774
POL	KIQKEPIF	409	8	62	97	5775
POL	QKEPIFLW	411	8	63	98	5776
POL	DKWTVQM	426	8	54	84	5777
POL	VRQLCKLL	465	8	28	44	5778
POL	VRQLCKLL	465	8	19	30	5779
POL	TKALTEVI	475	8	11	17	5780
POL	SKDLIAEI	514	8	27	42	5781
POL	QKQQQDQW	522	8	16	25	5782
POL	QKQQGQW	522	8	24	38	5783
POL	OKIATESI	565	8	14	22	5784
POL	GKTIKFKL	576	8	17	27	5785
POL	GKTPKFRL	576	8	30	47	5786
POL	QKETWEAW	586	8	15	23	5787
POL	QKETWETW	586	8	27	42	5788
POL	TKIGKAGY	642	8	10	16	5789
POL	TKLGRAGY	642	8	36	56	5790
POL	GRQKVVSLL	654	8	24	38	5791
POL	QKTELIHAI	667	8	12	19	5792
POL	QKTELQAI	667	8	42	66	5793
POL	IKKEKVYL	718	8	35	55	5794
POL	DKLVSAH	741	8	16	25	5795
POL	DKLVSSGI	741	8	29	45	5796
POL	YIINNWRAM	767	8	10	16	5797
POL	YIISNWRAM	767	8	39	61	5798
POL	WRAMASDF	771	8	43	67	5799
POL	THLEGRKII	818	8	35	55	5800
POL	THLEGRKVI	818	8	26	41	5801
POL	VIIIVASGYI	829	8	53	83	5802
POL	GRWPKVTI	858	8	13	21	5803
POL	GRWPKVVI	858	8	22	35	5804
POL	NKELKKII	907	8	57	89	5805
POL	VRDQAEIIL	917	8	48	75	5806
POL	VREQAEIIL	917	8	13	20	5807
POL	RKGGIGGY	939	8	59	92	5808
POL	TKELQKQI	962	8	47	75	5809
POL	YRDSRDPI	979	8	35	55	5810

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HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	YRDSRDPL	979	8	14	22	5811
POL	WKGPAKLL	987	8	59	92	5812
POL	PRRKAKII	1014	8	50	78	5813
POL	PRRKVKII	1014	8	11	17	5814
POL	IKDYGKQM	1021	8	11	17	5815
POL	IRDYGRQM	1021	8	50	78	5816
POL	QRPLVTIKI	94	9	14	22	5817
POL	QRPLVTIKI	94	9	12	19	5818
POL	WKPKMIGGI	129	9	60	94	5819
POL	IKVRQYIQI	141	9	41	64	5820
POL	VROYIQILI	143	9	20	31	5821
POL	VRQYIQIH	143	9	13	20	5822
POL	GIKAIGTVL	155	9	20	31	5823
POL	GIKAIGTVL	155	9	29	45	5824
POL	GIKAIGTVL	155	9	28	44	5825
POL	EKIKALTEI	216	9	15	23	5826
POL	EKIKALVHI	216	9	36	56	5827
POL	EKEGKISKI	231	9	42	66	5828
POL	SKIGPENPY	237	9	11	17	5829
POL	SKIGPENPY	237	9	57	89	5830
POL	IKKKDSTKW	252	9	59	92	5831
POL	TKWRKLVDI	258	9	63	98	5832
POL	RKLVDREL	261	9	50	78	5833
POL	KKKKSVTYL	290	9	61	97	5834
POL	FRKYTAFTI	313	9	14	22	5835
POL	RKQNPDI	361	9	26	41	5836
POL	QIRAKIEEL	386	9	22	34	5837
POL	QIRAKIEEL	386	9	60	94	5838
POL	RKIQKEPPF	408	9	62	97	5839
POL	RKIQKEPPF	409	9	63	98	5840
POL	QKEPPFLWM	411	9	62	97	5841
POL	QKLVGKLNW	447	9	61	95	5842
POL	QKLVGKLNW	451	9	29	45	5843
POL	IKVKQLCKL	463	9	18	28	5844
POL	IKVROLCKL	463	9	41	64	5845
POL	LKEPVIGVY	502	9	45	70	5846
POL	FKNLKTGKY	538	9	10	16	5847
POL	YKNLKTGKY	538	9	19	30	5848
POL	LKTGYAKM	541	9	13	20	5849
POL	LKTGYARM	541	9	46	72	5850
POL	AHINDVKQL	552	9	15	23	5851
POL	QKETWEAWW	586	9	27	42	5852
POL	QKETWEAWW	586	9	12	19	5853
POL	QKTELQAIY	667	9	20	32	5854
POL	KKEKYLAW	719	9	13	21	5855
POL	KKEKYLAW	719	9	50	78	5856
POL	RKVLFLDGI	749	9	10	16	5857
POL	DHEKYIISNW	763	9	20	31	5858
POL	EHEKYIISNW	763	9	13	20	5859
POL	EHEKYIISNW	763	9	31	48	5860
POL	TIIEGKIIL	818	9			

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SI:Q ID NO.
POL	THLECKVIL	818	9	23	36	5861
POL	IIITDNGSNF	865	9	42	66	5862
POL	IKQEFQIPY	887	9	26	41	5863
POL	EILKLTAVQM	922	9	57	89	5864
POL	KRKGGIGGY	938	9	59	92	5865
POL	TKELQKQII	962	9	10	16	5866
POL	IKIQNFRVY	970	9	12	19	5867
POL	TKIQNFRVY	970	9	37	58	5868
POL	YRDSKDPW	979	9	35	55	5869
POL	YRDSRDPLW	979	9	14	22	5870
POL	WKGPAKLLW	987	9	59	92	5871
POL	WKGGAIVI	995	9	61	95	5872
POL	RKAKIRDY	1016	9	41	64	5873
POL	PKMIGGIGF	131	10	62	97	5874
POL	IKVIQYDQIL	141	10	21	33	5875
POL	KKDSTKWRKL	254	10	58	91	5876
POL	WRKLVDFREL	260	10	63	98	5877
POL	LKKKKSIVTL	289	10	49	78	5878
POL	DKDFRKYTAF	310	10	18	28	5879
POL	FRKQNPDI	360	10	14	22	5880
POL	IKQNPDIIVY	361	10	14	22	5881
POL	AKIEELREHL	389	10	13	20	5882
POL	TKIEELRQIL	389	10	14	22	5883
POL	LRHILLKWGF	394	10	14	22	5884
POL	LRQHLLRWGF	394	10	12	19	5885
POL	DKKHQKEPFL	407	10	60	94	5886
POL	KKHQKEPFL	408	10	60	94	5887
POL	KHQKEPFLW	409	10	62	97	5888
POL	DKWTVPQIQL	426	10	28	44	5889
POL	DKWTVPQIVL	426	10	12	19	5890
POL	EKDSWTVNDI	437	10	41	64	5891
POL	GKLNWASQIY	451	10	60	94	5892
POL	IKVKQLCKLL	463	10	28	44	5893
POL	IKVRQLCKLL	463	10	18	28	5894
POL	CKLLRGAKAL	469	10	25	39	5895
POL	CKLLRGTKAL	469	10	24	38	5896
POL	LRGAKALTDI	472	10	22	34	5897
POL	AKALTDIIVPL	475	10	17	27	5898
POL	TKALTEVIPL	475	10	11	17	5899
POL	LKEPVIIGVY	502	10	39	61	5900
POL	QKQGGQDQWTY	522	10	15	23	5901
POL	QKQGGQDQWTY	522	10	24	38	5902
POL	OKIATESIVI	565	10	14	22	5903
POL	GKTPKFKLPI	576	10	17	27	5904
POL	GKTPKFKLPI	576	10	29	45	5905
POL	FKLPQKETW	581	10	20	32	5906
POL	FKLPQKETW	581	10	26	41	5907
POL	DRQKQKVWSL	652	10	18	28	5908
POL	QKTELQAIHL	667	10	15	23	5909
POL	QKTELQAIYL	667	10	12	19	5910

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IIIY B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	IIILALQDSGL	674	10	15	23	5911
POL	IKKEKVLAW	718	10	20	31	5912
POL	IKKEKVLWS	718	10	13	20	5913
POL	IRKVLFLDGI	748	10	49	77	5914
POL	DKAQEEIEKY	738	10	25	39	5915
POL	DKAQEEIEERY	738	10	15	23	5916
POL	EKYIISNWARM	765	10	28	44	5917
POL	EKYIISNWRM	765	10	10	16	5918
POL	WRAMASDFNL	771	10	41	64	5919
POL	DKCOLKGEAM	793	10	44	69	5920
POL	VKAACWWAGI	878	10	31	48	5921
POL	LKTAVQMAVF	924	10	57	89	5922
POL	IIINFRRKGGI	934	10	58	91	5923
POL	FKKKGGIGGY	937	10	59	92	5924
POL	QKQIKIQNF	966	10	12	19	5925
POL	QKQITRIQNF	966	10	34	53	5926
POL	IKIONFRVYY	970	10	12	19	5927
POL	IKIONFRVYY	970	10	37	58	5928
POL	RRKAKIIRDY	1015	10	41	64	5929
POL	TRANSPTREL	22	11	11	17	5930
POL	ERAIISPATREL	25	11	01	50	5931
POL	SRANSPTSREL	25	11	01	50	5932
POL	TRANSPTSREL	34	11	01	33	5933
POL	TRANSPTREL	36	11	01	33	5934
POL	IKIGGOLKEAL	100	11	19	30	5935
POL	GKWKPKMIGGI	127	11	41	64	5936
POL	GKWKPKMIGGI	127	11	16	25	5937
POL	PKMIGGIGGI	131	11	62	97	5938
POL	IKVROYDQILI	141	11	20	31	5939
POL	IKVRQYDQIH	141	11	13	20	5940
POL	VRQYDQILIEI	143	11	20	31	5941
POL	VRQYDQIEI	143	11	12	19	5942
POL	VKQWPLTEEKI	208	11	52	81	5943
POL	IKALVEICTEM	218	11	15	23	5944
POL	KKDSTKWRKL	253	11	57	89	5945
POL	FRELNRKTQDF	266	11	57	89	5946
POL	KRTQDFWEVOL	271	11	52	81	5947
POL	RKYTAFITIS	314	11	37	58	5948
POL	FRKQNPDIIVY	360	11	14	22	5949
POL	AKIEELREILL	389	11	13	20	5950
POL	TKIEELRQILL	389	11	14	22	5951
POL	DKKHQKEPPL	407	11	60	94	5952
POL	KKHQKEPPLW	408	11	60	94	5953
POL	KKHQKEPPLWM	409	11	62	97	5954
POL	QKEPFLWMGY	411	11	63	98	5955
POL	LIPDKWTVMH	423	11	53	83	5956
POL	LRGTRKALTEVI	472	11	11	17	5957
POL	VKQITEAVQKI	557	11	30	47	5958
POL	QKIATESIVW	565	11	14	22	5959
POL	EKEPIVGAETF	622	11	16	25	5960

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HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	NRETKLGKAGY	639	11	28	44	5961
POL	DKSESELVNQI	703	11	18	28	5962
POL	DKSESELVSQI	703	11	19	30	5963
POL	MHGQVDCSIGH	802	11	52	81	5964
POL	LKTAVQMAVFI	924	11	56	88	5965
POL	ERIDIIASDI	950	11	12	19	5966
POL	ERIDIIATDI	950	11	29	45	5967
POL	ERIVDIIATDI	950	11	11	17	5968
POL	TKELQKQIKI	962	11	10	16	5969
POL	TKELQKQITKI	962	11	31	49	5970
POL	IKVVPKPKAKI	1010	11	51	80	5971
POL	IKVVPKPKVKI	1010	11	11	17	5972
POL	PRKAKIIRIY	1014	11	41	64	5973
POL	AKIIRIDYGRQM	1018	11	42	66	5974
REV	VRIKILY	18	8	18	28	5975
REV	IKNRRRW	42	8	21	31	5976
REV	IKNRRRW	42	8	40	63	5977
REV	WRARQRI	49	8	36	56	5978
REV	WRERQRI	49	8	11	17	5979
REV	ERILSTCL	61	8	11	17	5980
REV	ARKNRRRW	41	9	18	28	5981
REV	ARRNRRRW	41	9	39	61	5982
REV	ARQKHISI	51	9	18	16	5983
REV	GRPAEPVPL	69	9	20	31	5984
REV	GRSAEPVPL	69	9	12	19	5985
REV	GRGDSDEEL	3	10	17	27	5986
REV	IKILYQSNFY	21	10	25	39	5987
REV	RRWRARQRI	47	10	34	53	5988
REV	RRWRERQRI	47	10	11	17	5989
REV	RRWRARQRI	46	11	16	25	5990
REV	RRWRERQRI	46	11	34	53	5991
REV	RRWRERQRI	49	11	11	17	5992
REV	WRARQKHISI	69	11	10	16	5993
REV	GRPAEPVPLQL	69	11	20	31	5994
REV	GRSAEPVPLQL	69	11	12	19	5995
TAT	KKGLGISY	43	8	15	23	5996
TAT	NKGLGISY	43	8	14	22	5997
TAT	TKGLGISY	43	8	19	30	5998
VIF	DRMKIRTW	14	8	12	19	5999
VIF	DRMRINTW	14	8	10	16	6000
VIF	DRMRIRTW	14	8	32	50	6001
VIF	AKLVITTY	64	8	11	17	6002
VIF	LIITGERDW	74	8	22	34	6003
VIF	GHOVSIEW	85	8	31	48	6004
VIF	GIINKVGSL	143	8	47	73	6005
VIF	NKVGSLQY	143	8	47	75	6006
VIF	PKKIKPPL	161	8	19	30	6007
VIF	KKLTEDRW	176	8	13	21	6008
VIF	GIIRGSITM	191	8	25	39	6009
VIF	NRWQVLIVW	3	9	10	16	6010

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HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	NRQVMIVW	3	9	42	66	6011
VIF	MKRTWNSL	16	9	12	19	6012
VIF	MIRITWKS	16	9	15	23	6013
VIF	MIRITWNSL	16	9	15	23	6014
VIF	WKSIVKIHIM	21	9	18	28	6015
VIF	WKSIVKIHIM	21	9	10	16	6016
VIF	PKISSEVH	49	9	15	23	6017
VIF	PKISSEVH	49	9	20	31	6018
VIF	PKISSEVH	49	9	15	23	6019
VIF	ARLVITYW	64	9	11	17	6020
VIF	WILGIGVSI	82	9	23	36	6021
VIF	WILGIGVSI	82	9	26	41	6022
VIF	IILYFDCF	112	9	16	25	6023
VIF	IILYFDCF	112	9	15	23	6024
VIF	NKVGSLQYL	145	9	47	75	6025
VIF	VKKLTEDRW	175	9	13	20	6026
VIF	WKSIVKIHIM	21	10	18	28	6027
VIF	AKGWFYHIIY	35	10	10	16	6028
VIF	VHPLGDARL	55	10	13	20	6029
VIF	VHPLGEARL	55	10	20	31	6030
VIF	LITGERDWII	74	10	21	33	6031
VIF	GIIGVSIWRL	85	10	15	23	6032
VIF	GIIGVSIWRL	85	10	47	73	6033
VIF	GIIGVSIWRL	85	10	10	16	6034
VIF	IKPKIKRPL	159	10	18	29	6035
VIF	TKGIKRSITM	189	10	12	19	6036
VIF	DRMKRTWNSL	14	11	15	23	6037
VIF	DRMKRTWNSL	14	11	15	23	6038
VIF	DRMKRTWNSL	14	11	15	23	6039
VIF	WKSIVKIHIM	21	11	11	17	6040
VIF	RHPKVSSEVH	47	11	16	25	6041
VIF	PKISSEVH	49	11	14	22	6042
VIF	PKISSEVH	49	11	19	30	6043
VIF	PKISSEVH	49	11	13	20	6044
VIF	ARLVITYWGL	64	11	11	17	6045
VIF	WILGIGVSIW	82	11	23	36	6046
VIF	WILGIGVSIW	82	11	26	41	6047
VIF	GIIGVSIWRL	143	11	47	73	6048
VIF	NKVGSLQYL	145	11	46	73	6049
VPR	QREPYNEW	11	8	38	59	6050
VPR	VRIIFRIW	31	8	14	22	6051
VPR	VRIIFRIW	31	8	34	53	6052
VPR	RIFPRPW	32	8	14	22	6053
VPR	RIFPRPW	32	8	34	53	6054
VPR	PRWLHSL	35	8	10	16	6055
VPR	PRWLHSL	35	8	24	38	6056
VPR	LIIGLQHI	39	8	20	31	6057
VPR	IRILQQL	61	8	45	70	6058
VPR	CRISIRIGI	77	8	11	17	6059
VPR	QISIRIGI	78	8	16	25	6060
VPR	LKNEAVRIIF	26	9	18	28	6061

Table XII
HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SFQ ID NO.
VPR	LKQAVRIIF	26	9	11	17	6061
VPR	LKSEAVRIIF	26	9	15	23	6062
VPR	VRIIFPRIWL	31	9	14	22	6063
VPR	VRIIFPRWL	31	9	34	53	6064
VPR	LHGLQHIY	39	9	20	31	6065
VPR	IRILQQLIF	61	9	44	69	6066
VPR	QREFYNEWTL	11	10	30	47	6067
VPR	IRILQQLFI	61	10	36	56	6068
VPR	FRIGCQHSKI	73	10	44	69	6069
VPR	FRIGCRHSKI	73	10	12	19	6070
VPR	RIFPRWLHSL	32	11	10	16	6071
VPR	RIFPRWLIGL	32	11	24	38	6072
VPR	PRPWLIHGGY	35	11	10	16	6073
VPR	QHLYETYGDTW	44	11	17	27	6074
VPR	QHLYNTYGDTW	44	11	13	20	6075
VPU	QRKIDRLI	49	8	21	33	6076
VPU	AKVDYRIV	6	9	01	33	6077
VPU	RKILRQKI	44	9	13	21	6078
VPU	LRQKIDRL	47	9	17	27	6079
VPU	YRKILRQKI	42	10	13	21	6080
VPU	#KKLLKQKKI	43	10	01	50	6081
VPU	LRQKIDRLI	47	10	15	24	6082
VPU	RKIDRLIDRI	51	10	12	19	6083
VPU	QRKIDRLIDRI	49	11	12	19	6084

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	NTSPSRV	376	8	01	33	6085
ENV	NTSPSRVAY	376	10	01	33	6086
ENV	TAGNSSRAAY	376	10	01	33	6087
ENV	TSNSSSSTPI	160	11	01	33	6088
ENV	GTAGNSSRAAY	375	11	01	33	6089
ENV	ITEGNITL	478	8	01	50	6090
ENV	NANITIKRI	478	10	01	50	6091
ENV	STRTHIREKRAY	586	11	01	50	6092
ENV	DSSNSTGNY	218	9	01	20	6093
ENV	STNGTETP	537	8	01	17	6094
ENV	NETINKTETP	537	10	01	17	6095
ENV	NTTGNTEIF	537	10	01	17	6096
ENV	GSENGTETP	538	9	02	18	6097
ENV	NTRKSIRI	331	8	10	16	6098
ENV	SSLKGLRL	886	8	10	16	6099
ENV	SSLKGLRLGW	886	10	10	16	6100
ENV	CTPAIFAI	264	8	10	16	6101
ENV	QSSGDDPEI	423	9	10	16	6102
ENV	QSSGDDPEIV	423	10	10	16	6103
ENV	WSEELKNSAV	910	10	10	16	6104
ENV	FAIKCNDKRF	269	11	10	16	6105
ENV	RAYGIGAVF	594	9	11	17	6106
ENV	RAYGIGAVFL	594	10	11	17	6107
ENV	AARTVELL	876	8	11	17	6108
ENV	GTDRIEIV	932	8	11	17	6109
ENV	LALDKWASL	736	9	11	17	6110
ENV	IAARTVELL	874	9	11	17	6111
ENV	VSLNATAI	919	9	11	17	6112
ENV	YATGDIIGDI	368	10	11	17	6113
ENV	TTNVPWNSSW	691	10	11	17	6114
ENV	LALDKWASLW	736	10	11	17	6115
ENV	ISNWLWYIKI	770	10	11	17	6116
ENV	RSIRLVNGFL	841	10	11	17	6117
ENV	CTTNVWNSW	690	11	11	17	6118
ENV	ISNWLWYIKIF	770	11	11	17	6119
ENV	SAVSLNATAI	917	11	11	17	6120
ENV	VSLNATAIIV	919	11	11	17	6121
ENV	RAYGIGAV	594	8	12	19	6122
ENV	EAQIILLKL	646	9	12	19	6123
ENV	EAQIILLKLTV	646	11	12	19	6124
ENV	RAYAIPPI	502	8	12	19	6125
ENV	GALFLGFL	601	8	12	19	6126
ENV	IAARTVEL	874	8	12	19	6127
ENV	PTRIROGL	951	8	12	19	6128
ENV	ATGDIHDI	369	9	12	19	6129
ENV	RSIRLVNGF	841	9	12	19	6130
ENV	MTWMEWEREI	721	10	12	19	6131
ENV	RAIIIPRI	945	10	12	19	6132
ENV	PTDNPQEVVL	89	11	12	19	6133
ENV	TSVITQACPKV	242	11	12	19	6134

Table XIII
J11V B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID No.
ENV	GTGCKNVSTV	281	11	12	19	6135
ENV	TTISFNCRGEF	432	11	12	19	6136
ENV	CSGKLCITTV	684	11	12	19	6137
ENV	ITKWLWYKIF	770	11	12	19	6138
ENV	FSYIIRLDLL	863	11	12	19	6139
ENV	LAFEEVVI	312	8	13	20	6140
ENV	GAMFLGFL	601	8	13	20	6141
ENV	RSIRLVSGF	841	9	13	20	6142
ENV	PTDPIQEVV	89	10	13	20	6143
ENV	SATQACPKV	243	10	13	20	6144
ENV	GSLAEVVI	310	10	13	20	6145
ENV	SSGGDPEVM	424	10	13	20	6146
ENV	RSIRLVSGFL	841	10	13	20	6147
ENV	FSYIIRLDH	863	10	13	20	6148
ENV	TSATQACPKV	242	11	13	20	6149
ENV	FSYIIRLDPEIL	863	11	13	20	6150
ENV	NAKTIIVQL	329	9	14	22	6151
ENV	QAMYAPPI	502	8	14	22	6152
ENV	ISNWLWYI	770	8	14	22	6153
ENV	GSLAEVVI	310	9	14	22	6154
ENV	ITNWLWYIKI	770	10	14	22	6155
ENV	FSYIIRLDLL	863	10	14	22	6156
ENV	IAVAEGTDIV	927	10	14	22	6157
ENV	ITNWLWYKIF	770	11	14	22	6158
ENV	IAVAEGTDIV	927	11	14	22	6159
ENV	ITKWLWYIKI	770	10	15	23	6160
ENV	ITLPCRKQII	483	11	15	23	6161
ENV	IAVAEGTDRII	927	11	15	23	6162
ENV	GSLAEVVI	310	8	16	25	6163
ENV	SSGGDLEI	424	8	16	25	6164
ENV	ITKWLWYI	770	8	16	25	6165
ENV	VAEGTDIV	929	8	16	25	6166
ENV	ISFNCRGEF	434	9	16	25	6167
ENV	VSGFLALAW	846	9	16	25	6168
ENV	VAEGTDIV	929	9	16	25	6169
ENV	ISFNCRGEF	434	10	16	25	6170
ENV	IAVAEGTDRI	927	10	16	25	6171
ENV	TTISFNCGGEF	432	11	16	25	6172
ENV	ISFNCRGEFF	434	11	16	25	6173
ENV	GTGCKNV	281	8	17	27	6174
ENV	DAKAYDTEV	70	9	17	27	6175
ENV	ASLWNWFDI	762	9	17	27	6176
ENV	KAYDTEVINV	72	10	17	27	6177
ENV	VAPTKAKRRV	574	10	17	27	6178
ENV	WASLWNWFDI	761	10	17	27	6179
ENV	ASDAKAYDTEV	68	11	17	27	6180
ENV	KAYDTEVINVW	72	11	17	27	6181
ENV	VAPTKAKRRV	574	11	17	27	6182
ENV	CSGKLCITTV	684	11	17	27	6183
ENV	SSGGDPEIV	424	9	18	28	6184

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SiQ ID NO.
ENV	FSYIIRLDF	863	9	18	28	6185
ENV	VAEGTDRII	929	9	18	28	6186
ENV	DTEVINWV	75	8	19	30	6187
ENV	SSNITGILL	516	8	19	30	6188
ENV	ITNLWYI	770	8	19	30	6189
ENV	VAEGTDRI	929	8	19	30	6190
ENV	CSSNITGILL	515	9	19	30	6191
ENV	SSNITGILL	516	9	19	30	6192
ENV	CSSNITGILL	515	10	19	30	6193
ENV	CSGKICTTAV	684	11	19	30	6194
ENV	LALAWDLKSL	850	11	19	30	6195
ENV	LAWDLKSL	852	9	20	31	6196
ENV	LAWDLKSLCL	852	11	20	31	6197
ENV	CSSNITGL	515	8	21	31	6198
ENV	PTDIPNQEV	89	9	21	31	6199
ENV	ETFRVGGIDM	544	10	21	31	6200
ENV	PTKAKRRV	576	8	22	34	6201
ENV	GAVFLGFL	601	8	22	34	6202
ENV	PTKAKRRV	576	9	22	34	6203
ENV	KAMYAPPI	502	8	23	36	6204
ENV	FSYIIRLDF	863	9	23	36	6205
ENV	SSGGIDPEI	424	8	24	38	6206
ENV	LALAWDDL	850	8	25	39	6207
ENV	PTDIPNQEI	89	9	25	39	6208
ENV	ITLPCRIKQI	483	10	25	39	6209
ENV	LSGIVQQNNL	631	11	25	39	6210
ENV	CTHIGIRPV	294	8	26	41	6211
ENV	QSNLLRAI	638	8	26	41	6212
ENV	CTHIGIRPV	294	9	26	41	6213
ENV	ITLTVQARQL	621	10	27	42	6214
ENV	ITLTVQARQLL	621	11	27	42	6215
ENV	VSFEPIMTY	253	10	28	44	6216
ENV	YSPLSFQTL	807	9	29	46	6217
ENV	CAPAGFAI	264	8	29	45	6218
ENV	CAPAGFAI	264	9	29	45	6219
ENV	ITQACTKVSF	245	10	29	45	6220
ENV	VSFEPIMI	253	8	30	47	6221
ENV	WASLWNWF	761	8	30	47	6222
ENV	QACPKVSFEPI	248	11	30	47	6223
ENV	FAVLSVNRV	794	10	31	48	6224
ENV	RSCLFSYIIRL	858	11	31	48	6225
ENV	CTHIGIKPV	294	9	32	50	6226
ENV	LSGIVQQSNL	631	11	32	50	6227
ENV	CTHIGIKPV	294	8	33	52	6228
ENV	QARVLAVERY	663	10	33	52	6229
ENV	QARVLAVERYL	663	11	33	52	6230
ENV	EAQIILLQLTV	646	11	34	54	6231
ENV	VTFNFMW	102	8	34	53	6232
ENV	AAGSTMGAASI	611	11	34	53	6233
ENV	LSVNRVRQGY	797	11	34	53	6234

Table XIII
IIIY B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	EAQQHLLQL	646	9	35	56	6235
ENV	ISLCLFSY	858	8	35	55	6236
ENV	IISFNCGEFF	434	10	35	55	6237
ENV	IISFNCGEFF	434	11	35	55	6238
ENV	AASITLV	618	8	36	56	6239
ENV	IISFNCGEFF	434	9	36	56	6240
ENV	GAASITLV	617	9	36	56	6241
ENV	LTQARQLL	623	9	36	56	6242
ENV	ITQACTKV	245	8	37	58	6243
ENV	LTQARQL	623	8	38	59	6244
ENV	QARQLLSGI	626	9	38	59	6245
ENV	QARQLLSGIV	626	10	38	59	6246
ENV	STMGAASI	614	8	39	61	6247
ENV	GSTMGAASI	613	9	39	61	6248
ENV	STMGAASITL	614	10	39	61	6249
ENV	GSTMGAASITL	613	11	39	61	6250
ENV	QACIKVSF	248	8	40	63	6251
ENV	CASDAKAY	67	8	42	66	6252
ENV	KAIEAQQHLL	643	10	44	69	6253
ENV	RAIEAQQHLL	643	9	45	70	6254
ENV	ISLWDOSL	122	8	48	75	6255
ENV	QSLKPCVKL	127	9	48	75	6256
ENV	RSELYKYKV	558	10	49	77	6257
ENV	RSELYKYKV	558	9	50	78	6258
ENV	STVQCTIGI	289	9	51	80	6259
ENV	VSTVQCTHGI	288	10	51	80	6260
ENV	LTPLCVTL	135	8	54	84	6261
ENV	VTVYGVV	47	9	55	86	6262
ENV	VTVYGVVFW	47	10	55	86	6263
ENV	STOLLNGSL	303	10	57	89	6264
ENV	VSTQLLNGSL	302	11	57	89	6265
GAG	LTWGIKQL	654	9	59	92	6266
GAG	TAPPESEF	508	8	01	33	6267
GAG	ETIDKIDLY	537	8	01	25	6268
GAG	PTAPPESEF	507	9	01	33	6269
GAG	ETIDKIDLY	537	10	01	33	6270
GAG	RTENSLYPL	538	10	01	25	6271
GAG	AAAIMQKSNF	405	11	01	25	6272
GAG	SATIMMQKSNF	405	11	01	25	6273
GAG	PTAPPESEF	507	11	01	25	6274
GAG	GAAAATDSNI	123	10	01	33	6275
GAG	AADKGVSNY	130	10	01	50	6276
GAG	AAGTGNSQV	130	10	01	50	6277
GAG	GANSIPVGD	276	10	01	50	6278
GAG	SAQQLKGGY	393	10	01	50	6279
GAG	TAQQLKGGY	393	10	01	50	6280
GAG	GANSIPYGDY	276	11	01	50	6281
GAG	ASAQQLKGGY	392	11	01	50	6282
GAG	ATAQQLKGGY	392	11	01	50	6283
						6284

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Coverage (%)	SEQ ID NO.
GAG	PAETAPPAEI	492	11	01	50	6285
GAG	TAPPAESF	508	8	02	67	6286
GAG	PTAPPAESF	507	9	02	67	6287
GAG	TAPPAESFR	508	10	02	67	6288
GAG	PTAPPAESFR	507	11	02	67	6289
GAG	GTRPGNYV	480	8	02	100	6290
GAG	AADKGVSNY	129	11	02	18	6291
GAG	EADGVSNY	129	10	04	36	6292
GAG	AAMMOKSNF	406	10	06	15	6293
GAG	TITSQKEH	522	10	09	45	6294
GAG	GASLEEM	364	8	10	16	6295
GAG	DTKEALEKI	98	9	10	16	6296
GAG	TAPPAESFGF	496	10	10	16	6297
GAG	QALSPTLNAW	166	11	10	16	6298
GAG	PTAPPAESFGF	495	11	10	16	6299
GAG	ATMMQKGNF	406	10	11	28	6300
GAG	PSQKQEH	528	8	11	18	6301
GAG	SSKGRPGNF	476	9	11	18	6302
GAG	TTSTLQEQIAW	260	11	11	17	6303
GAG	QALSPTIL	166	8	11	17	6304
GAG	ASQEVKNW	333	9	11	17	6305
GAG	ASVLSGIEL	5	9	11	17	6306
GAG	QASQEVKNW	332	9	11	17	6307
GAG	ASQEVKNWM	333	9	11	17	6308
GAG	NANPDCKSI	349	9	11	17	6309
GAG	IASVLSGGEL	4	10	11	17	6310
GAG	QASQEVKNWM	332	10	11	17	6311
GAG	NANPDCKSIL	349	10	11	17	6312
GAG	PSKGRPGNF	475	10	11	17	6313
GAG	QTGSEELRSL	71	10	12	19	6314
GAG	GSEELKSL	73	8	12	19	6315
GAG	GTEELKSL	73	8	12	19	6316
GAG	ATPQDLNM	200	8	12	19	6317
GAG	LTSLSLF	549	8	12	19	6318
GAG	GSEELKSLY	73	9	12	19	6319
GAG	GATPQDLNM	199	9	12	19	6320
GAG	ATPQDLNMM	200	9	12	19	6321
GAG	STLQEQIAW	262	9	12	19	6322
GAG	RAHQASQEV	329	9	12	19	6323
GAG	KSLFGNDPL	553	9	12	19	6324
GAG	ATLYCVIIQKI	85	10	12	19	6325
GAG	GATPQDLNMM	199	10	12	19	6326
GAG	ATPQDLNMMML	200	10	12	19	6327
GAG	TSTLQEQIAW	261	10	12	19	6328
GAG	STLQEQIAWM	262	10	12	19	6329
GAG	VATLYCVIIQKI	84	11	12	19	6330
GAG	GATPQDLNMMML	199	11	12	19	6331
GAG	TSTLQEQIAWM	261	11	12	19	6332
GAG	TSNPFVPGEL	272	11	12	19	6333
GAG	LTSLSLSLF	549	8	13	20	6334

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	YSPTSLDI	301	9	13	20	6335
GAG	PSLOTGSEEL	68	10	13	20	6336
GAG	NSSQVSQNY	144	9	14	31	6337
GAG	NSSQVSQNYPI	144	11	14	31	6338
GAG	TSEGCROIL	55	9	14	22	6339
GAG	ETSEGCROIL	54	10	14	22	6340
GAG	AAEWDRVPIV	230	10	14	22	6341
GAG	PSNKGRPGNF	475	10	14	22	6342
GAG	TAPPESEFR	496	10	14	22	6343
GAG	FAAEWDRVPIV	229	11	14	22	6344
GAG	PTAPPESEFR	495	11	14	22	6345
GAG	SSQVSQNY	145	8	15	31	6346
GAG	SSQVSQNYII	145	10	15	31	6347
GAG	SSQVSQNYIV	145	11	15	31	6348
GAG	RSLYNTVATL	78	10	15	24	6349
GAG	RSLYNTVATLY	78	11	15	24	6350
GAG	FAAEWDRV	229	8	15	23	6351
GAG	ATQDVKNW	333	8	15	23	6352
GAG	TAPPESEF	496	8	15	23	6353
GAG	LASLKSLE	549	8	15	23	6354
GAG	RAEQATQIV	329	9	15	23	6355
GAG	QATQDVKNW	332	9	15	23	6356
GAG	ATQDVKNWM	333	9	15	23	6357
GAG	PTAPPESEF	495	9	15	23	6358
GAG	ATLYCVIIQRI	85	10	15	23	6359
GAG	QATQDVKNWM	332	10	15	23	6360
GAG	VATLYCVIIQRI	84	11	15	23	6361
GAG	FAVNPGLL	46	8	16	35	6362
GAG	TSEGCROI	55	8	16	25	6363
GAG	GSEELRSL	73	8	16	25	6364
GAG	TSNPPIV	272	8	16	25	6365
GAG	PAATLEEM	363	8	16	25	6366
GAG	PAATLEEM	364	8	16	25	6367
GAG	LSGCKLDAA	8	9	16	25	6368
GAG	ETSEGCROI	54	9	16	25	6369
GAG	MTSNPIV	271	9	16	25	6370
GAG	KALGPAATL	359	9	16	25	6371
GAG	PAATLEEM	363	9	16	25	6372
GAG	DAWEKIRL	14	8	17	27	6373
GAG	LSPTLNAAW	168	9	17	27	6374
GAG	ASRELERFAV	38	10	17	27	6375
GAG	LSPTLNAAW	168	10	17	27	6376
GAG	IIAGPIPPGOM	240	10	17	27	6377
GAG	WASRELERFAV	37	11	17	27	6378
GAG	ATQEVKNW	333	8	18	28	6379
GAG	QATQEVKNW	332	9	18	28	6380
GAG	ATQEVKNWM	333	9	18	28	6381
GAG	IIAGPIAPGQM	240	10	18	28	6382
GAG	QATQEVKNWM	332	10	18	28	6383
GAG	PSIIKARVL	380	8	19	30	6384

Table XIII
HIV B58 Super Modified Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	TAPPAESF	496	8	20	31	6385
GAG	MTNNPIPIV	271	9	20	31	6386
GAG	PTAPPAESF	495	9	20	31	6387
GAG	FALNPGLL	46	8	22	34	6388
GAG	ASRELERFAL	38	10	22	34	6389
GAG	ETINEEAAEW	224	10	22	34	6390
GAG	WASRELERFAL	37	11	22	34	6391
GAG	PSIHKGRFGNF	475	10	23	36	6392
GAG	PSIHKGRFGNEL	475	11	23	36	6393
GAG	AAMQMLKETI	217	10	26	41	6394
GAG	AAMQMLKETI	216	11	26	41	6395
GAG	TTSTLQEQIGW	260	11	27	43	6396
GAG	STLQEQIGW	262	9	27	42	6397
GAG	RAEQATQEV	329	9	27	42	6398
GAG	TSFLQEQIGW	261	10	27	42	6399
GAG	STLQEQIGWM	262	10	27	42	6400
GAG	TSFLQEQIGWM	261	11	27	42	6401
GAG	VSONYPIVQNL	149	11	28	48	6402
GAG	ASVLSGKGL	5	9	28	44	6403
GAG	RSVLSGKGL	4	10	28	44	6404
GAG	QAISPTIL	166	8	29	45	6405
GAG	GATLEEMM	364	8	29	45	6406
GAG	QAISPTILNAW	166	11	29	45	6407
GAG	RTLNAWVKV	171	10	30	47	6408
GAG	RTLNAWVKV	171	10	31	48	6409
GAG	DTINEEAAEW	224	10	31	48	6410
GAG	DTKEALDKI	98	9	32	50	6411
GAG	AAMQMLKDTI	217	10	33	52	6412
GAG	QAAMQMLKDTI	216	11	33	52	6413
GAG	AAEWDRLIIV	230	10	34	53	6414
GAG	EAEWDRLIIV	229	11	34	53	6415
GAG	LAIEAMSV	387	8	36	57	6416
GAG	ISPRTLNAW	168	9	36	56	6417
GAG	ISPRTLNAWV	168	10	36	56	6418
GAG	EAEWDRL	229	8	39	61	6419
GAG	YSIVSILDI	301	9	40	63	6420
GAG	NTVATLYCV	82	9	41	64	6421
GAG	ATPQDLNTM	200	9	42	66	6422
GAG	GATPQDLNTM	199	10	42	66	6423
GAG	ATPQDLNTML	200	10	42	66	6424
GAG	GATPQDLNTML	199	11	42	66	6425
GAG	TTSTLQEQI	260	9	45	71	6426
GAG	NANPDCKTI	349	9	45	70	6427
GAG	GTTSTLQEQI	259	10	45	70	6428
GAG	NANPDCKTIL	349	10	45	70	6429
GAG	ASRELERF	38	8	46	72	6430
GAG	WASRELERF	37	9	46	72	6431
GAG	TSFLQEQI	261	8	47	73	6432
GAG	NTVUGIQAAAM	210	10	47	73	6433
GAG	GSDIAGTTSTL	254	11	47	73	6434

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	VSNYIV	149	8	48	83	6435
GAG	IAGTTSTL	257	8	48	75	6436
GAG	KAFSPYVI	183	8	50	78	6437
GAG	KAFSPYIM	183	10	50	78	6438
GAG	KAFSPYIMF	183	11	50	78	6439
GAG	RAPRKGCW	439	9	53	83	6440
GAG	FSPEVIN	185	8	54	84	6441
GAG	FSPEVIMF	185	9	54	84	6442
GAG	CTERQANF	459	8	55	87	6443
GAG	CTERQANFL	459	9	55	87	6444
GAG	QANFLGKI	466	8	57	89	6445
GAG	KARVLAEM	383	9	57	89	6446
GAG	QANFLGKIW	466	9	57	89	6447
GAG	LSEGATPQDL	196	10	58	91	6448
GAG	RYLNAWVKV	171	9	61	95	6449
NEF	QAEPAAGV	34	9	01	33	6450
NEF	QTEPAAGV	32	9	01	17	6451
NEF	RAEPAAGV	32	9	01	17	6452
NEF	RTEPAAGV	32	9	01	17	6453
NEF	QAEPAAGV	33	9	01	17	6454
NEF	QAEPAAGV	33	9	01	17	6455
NEF	QAEPAAGV	33	9	01	17	6456
NEF	QAEPAAGV	33	11	01	17	6457
NEF	GAPDLSEF	110	8	10	16	6458
NEF	GAPDLSEFL	110	9	10	16	6459
NEF	MARELIPEY	321	9	10	16	6460
NEF	MARELIPEY	321	10	10	16	6461
NEF	AADGVGAV	42	8	11	18	6462
NEF	PAADGVGAV	41	9	11	17	6463
NEF	VSRDLKIIIGAI	49	11	11	17	6464
NEF	ATNADCAW	71	8	12	22	6465
NEF	AATNADCAW	70	9	12	22	6466
NEF	ATNADCAWL	71	9	12	22	6467
NEF	ATNADCAWL	70	10	12	22	6468
NEF	PAEGVGAV	41	9	12	19	6469
NEF	NTYKGAFL	106	9	12	19	6470
NEF	NTQGYFHW	194	9	12	19	6471
NEF	TAATNADCAW	69	10	12	19	6472
NEF	QTRFLTFGW	213	10	12	19	6473
NEF	NTAATNADCAW	68	11	12	19	6474
NEF	TAATNADCAWL	69	11	12	19	6475
NEF	QTRFLTF	213	8	13	20	6476
NEF	YTPGTRF	207	9	13	20	6477
NEF	YTPGTRFPL	207	11	13	20	6478
NEF	HTQGFHDW	194	9	14	22	6479
NEF	EAQEELEV	82	8	16	25	6480
NEF	EAQEELEVGF	82	10	16	25	6481
NEF	YTPGIRYPL	207	11	16	25	6482
NEF	AAEGVGAV	42	8	17	28	6483
NEF	YTPGIRY	207	9	17	27	6484
NEF	WSKSSIVGW	5	9	20	31	6484

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	YSKKHQEI	176	8	22	34	6485
NEF	YSKKRQEI	176	9	22	34	6486
NEF	LSFFLKEKGGIL	114	11	22	34	6487
NEF	YSKKHQEILD	176	11	22	34	6488
NEF	ITQGYFFDW	194	9	25	39	6489
NEF	LSIIFLKEKGGIL	114	11	27	42	6490
NEF	LTFGWCFKL	221	10	35	55	6491
NEF	LTFGWCFKL	221	9	35	55	6492
POL	NSPTSREL	34	8	39	61	6493
POL	ITSRELQV	36	8	01	33	6494
POL	GTLNCQI	80	8	01	33	6495
POL	PTFNPQI	80	8	01	33	6496
POL	STNSPTSREL	32	10	01	33	6497
POL	NSPTSRELQV	34	10	01	33	6498
POL	RANSPTSREL	35	10	01	33	6499
POL	GTLNCPQITL	80	10	01	33	6500
POL	PTFNPQITL	80	10	01	33	6501
POL	STNSPTSREL	31	11	01	33	6502
POL	GTLNCPQITLW	80	11	01	33	6503
POL	PTFNPQITLW	80	11	01	33	6504
POL	NSPTSREL	37	8	01	50	6505
POL	NSPTSREL	39	8	01	50	6506
POL	ITSRELQV	39	8	01	50	6507
POL	NSPTSRELQV	37	10	01	50	6508
POL	RANSPTSREL	37	10	01	50	6509
POL	NSPTSRELQV	39	10	01	50	6510
POL	GADROGIV	70	8	01	20	6511
POL	GSGRAVVI	70	8	01	20	6512
POL	GADROGIVSF	70	10	01	20	6513
POL	GSGRAVHCL	70	10	01	20	6514
POL	GTLNCPQI	79	9	01	17	6515
POL	GAISLSLQI	79	10	01	17	6516
POL	GTLNCPQITF	79	11	01	17	6517
POL	PSLSFPQI	79	8	02	33	6518
POL	PSLSFPQITL	79	10	02	33	6519
POL	PSLSFPQITLW	79	11	02	33	6520
POL	SSFSFPQI	82	8	03	30	6521
POL	SSFSFPQITL	82	10	03	30	6522
POL	SSFSFPQITLW	82	11	03	30	6523
POL	VSFSFPQITLW	78	11	07	15	6524
POL	VSFSFPQI	78	8	08	17	6525
POL	VSFSFPQITL	78	10	08	17	6526
POL	ETWWTQYW	591	8	10	16	6527
POL	RANSPTSREL	26	10	10	16	6528
POL	ETWWTQITDY	588	10	10	16	6529
POL	ETWWTQITDY	588	10	10	16	6530
POL	QTKELQKQI	961	10	10	16	6531
POL	LAFIQGEAREF	6	11	10	16	6532
POL	RSALTNDVKQL	550	11	10	16	6533
POL	EAVQKIATESI	562	11	10	16	6534

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Coincidence (%)	SEQ ID NO.
POL	ETWETWTDYW	588	11	10	16	6535
POL	RTAHITNDV	550	8	11	17	6536
POL	WAGIQQEF	884	8	11	17	6537
POL	VTVKIGQL	98	9	11	17	6538
POL	STNNETGI	323	9	11	17	6539
POL	GTRKALTEVI	474	9	11	17	6540
POL	GSNFTSTTV	870	9	11	17	6541
POL	GADDTVLEEM	114	10	11	17	6542
POL	ISRIGPENPY	236	10	11	17	6543
POL	PSTNNETIKI	322	10	11	17	6544
POL	TAHTNDYKQL	551	10	11	17	6545
POL	WAGIQQEFGI	884	10	11	17	6546
POL	STNNETGIRY	323	11	11	17	6547
POL	ESWTVNDIOKL	439	11	11	17	6548
POL	GTRKALTEVIFL	474	11	11	17	6549
POL	ESWTVNDI	439	8	12	19	6550
POL	KTELQAIY	668	8	12	19	6551
POL	KTELQAIYL	668	9	12	19	6552
POL	NSPTRRELQVW	28	11	12	19	6553
POL	ITNOKTELIAI	664	11	12	19	6554
POL	KTELQAIYLAL	668	11	12	19	6555
POL	GAVVIQDNSEI	999	11	12	19	6556
POL	KTKKYARM	542	8	13	21	6557
POL	WTVQPIVL	428	8	13	20	6558
POL	PTRELQVW	30	9	13	20	6559
POL	ITVLEDINL	117	9	13	20	6560
POL	NSPTRRELQV	28	10	13	20	6561
POL	LAGRWPKTI	856	10	13	20	6562
POL	RAKIELREIL	388	11	13	20	6563
POL	IATESIVI	567	8	14	22	6564
POL	IATESIVIW	567	9	14	22	6565
POL	NSPTSREL	28	8	14	22	6566
POL	PTRELQV	30	8	14	22	6567
POL	FSFIQITLW	85	9	14	22	6568
POL	DTVLEENL	117	9	14	22	6569
POL	WTDYWQATW	594	9	14	22	6570
POL	SAGERIVDI	947	9	14	22	6571
POL	ASDIQIKEL	957	9	14	22	6572
POL	WTDYWQATWI	594	10	14	22	6573
POL	TSTTVKAAACW	874	10	14	22	6574
POL	YSAGERIVDI	946	10	14	22	6575
POL	SAGERIVDI	947	10	14	22	6576
POL	IASDIQIKEL	956	10	14	22	6577
POL	RTKIELRQIIL	388	11	14	22	6578
POL	FTSTTVKAAACW	873	11	14	22	6579
POL	TSTTVKAAACW	874	11	14	22	6580
POL	YSAGERIVDI	946	11	14	22	6581
POL	KALVEICTEM	219	10	15	24	6582
POL	FSFIQITL	85	8	15	23	6583
POL	LTQLGCTL	177	8	15	23	6584

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	RSALTNDV	550	8	15	23	6585
POL	VSAGIRKV	744	8	15	23	6586
POL	SAGIRKVL	745	8	15	23	6587
POL	TTVKAACW	876	8	15	23	6588
POL	KTELQAIHL	668	9	15	23	6589
POL	VSAGIRKVL	744	9	15	23	6590
POL	SAGIRKVL	745	9	15	23	6591
POL	STTVKAACW	875	9	15	23	6592
POL	TTVKAACW	876	9	15	23	6593
POL	GADDTVLEDI	114	10	15	23	6594
POL	LTQLGCTLNF	177	10	15	23	6595
POL	LTEKIKALV	213	10	15	23	6596
POL	VSAGIRKVL	744	10	15	23	6597
POL	SAGIRKVL	745	10	15	23	6598
POL	STTVKAACW	875	10	15	23	6599
POL	KTELQAIHLAI	668	11	15	23	6600
POL	VSAGIRKVL	744	11	15	23	6601
POL	KAQEHRY	759	9	16	25	6602
POL	VSAGIRV	946	8	16	25	6603
POL	KALTEVPL	476	9	16	25	6604
POL	RANSPTRREL	26	10	16	25	6605
POL	SAITNDVKQL	551	10	16	25	6606
POL	NSPTRREL	28	8	17	27	6607
POL	VTIKIGGQL	98	9	17	27	6608
POL	KTKFKFLM	577	9	17	27	6609
POL	GAKALTDIVPL	474	11	17	27	6610
POL	FSVPLDKDF	305	9	18	28	6611
POL	YAGIKVKQL	460	9	18	28	6612
POL	GADDTVLEH	114	10	18	28	6613
POL	ITLWQRPLVT	90	11	18	28	6614
POL	KTGKYAKM	542	8	19	30	6615
POL	GTKALTEV	474	8	19	30	6616
POL	ATESIVW	568	8	19	30	6617
POL	GAITNDVKQL	551	10	19	30	6618
POL	KSESELVNQI	704	10	19	30	6619
POL	KSESELVSQI	704	10	19	30	6620
POL	ITLWQRPLVTI	90	11	19	30	6621
POL	LTDTTNQKTEL	661	11	19	30	6622
POL	KSESELVNQII	704	11	19	30	6623
POL	KSESELVSQII	704	11	19	30	6624
POL	VSQIIEQL	710	8	20	31	6625
POL	VSQIIEQLI	710	9	20	31	6626
POL	MASDFNLPIV	774	11	20	31	6627
POL	ESELVSQI	706	8	21	33	6628
POL	WAGIKQEF	884	8	21	33	6629
POL	KALTDIVPL	476	9	21	33	6630
POL	ESELVSQII	706	9	21	33	6631
POL	ASDFNLPIV	775	10	21	33	6632
POL	WAGIKQEFGI	884	10	21	33	6633
POL	LAWVPAIKGI	725	10	22	34	6634

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	MASDFNLPII	774	10	22	34	6635
POL	LAGRWPKVI	856	10	22	34	6636
POL	ASDFNLPII	775	9	23	36	6637
POL	CTHLEKGVIL	817	10	23	36	6638
POL	CTHLEKGVILV	817	11	23	36	6639
POL	GAKALTIIV	474	9	24	38	6640
POL	WTEYWQATW	594	9	24	38	6641
POL	WTEYWQATWI	594	10	24	38	6642
POL	PTPVNIQRNM	166	11	24	38	6643
POL	GAKALTDI	474	8	25	39	6644
POL	DSGSEVNI	680	8	25	39	6645
POL	DSGSEVNIIV	680	9	25	39	6646
POL	ASDFNLPIV	775	9	25	39	6647
POL	LALQDSGSEV	676	10	25	39	6648
POL	SSGIRKVLFL	745	10	25	39	6649
POL	MASDFNLPIV	774	10	25	39	6650
POL	ASDFNLPIV	775	10	25	39	6651
POL	LTETTNQKTEL	661	11	25	39	6652
POL	VSSGIRKVLFL	744	11	25	39	6653
POL	MASDFNLPIV	774	11	25	39	6654
POL	ASQIYAGIKV	456	10	26	41	6655
POL	VSSGIRKV	744	8	26	41	6656
POL	SSGIRKVL	745	8	26	41	6657
POL	CTHLEKGV	817	8	26	41	6658
POL	PSKDLIAEI	513	9	26	41	6659
POL	DTTNQKTEL	663	9	26	41	6660
POL	VSSGIRKVL	744	9	26	41	6661
POL	SSGIRKVLV	745	9	26	41	6662
POL	CTHLEKGV	817	9	26	41	6663
POL	GSNFTSAAV	870	9	26	41	6664
POL	VSSGIRKVLV	744	10	26	41	6665
POL	ETQETAYFL	844	10	26	41	6666
POL	PTPVNIQRNL	166	11	26	41	6667
POL	WASQIYAGIKV	455	11	26	41	6668
POL	ETQETAYFL	844	11	26	41	6669
POL	ASQIYAGI	456	8	27	43	6670
POL	KAQEHKRY	759	9	27	43	6671
POL	ASQIYAGIKV	456	10	27	43	6672
POL	LALQDSGL	676	8	27	42	6673
POL	ESELVNOI	706	8	27	42	6674
POL	TAYFLKL	849	8	27	42	6675
POL	WASQIYAGI	455	9	27	42	6676
POL	ESELVNOI	706	9	27	42	6677
POL	ETAYFLKL	848	9	27	42	6678
POL	CTEMEKEGKI	225	10	27	42	6679
POL	LALQDSGLV	676	10	27	42	6680
POL	TSAAVKACW	874	10	27	42	6681
POL	WASQIYAGIKV	455	11	27	42	6682
POL	FTSAAVKACW	873	11	27	42	6683
POL	TSAAVKACW	874	11	27	42	6684

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	WTVQPIQL	428	8	28	44	6685
POL	DSGLEVNI	680	8	28	44	6686
POL	AAVKAACW	876	8	28	44	6687
POL	DSGLEVNIV	680	9	28	44	6688
POL	SAAVKAACW	875	9	28	44	6689
POL	AAVKAACWW	876	9	28	44	6690
POL	VDRGRQKVV	650	10	28	44	6691
POL	SAAVKAACWW	875	10	28	44	6692
POL	ASQIVYGI	436	8	29	46	6693
POL	WASQIYRGI	455	9	29	45	6694
POL	KTPKFRLP	577	9	29	45	6695
POL	ETNQKTEL	663	9	29	45	6696
POL	AAANRETKL	637	8	30	47	6697
POL	GAANRETKL	636	9	30	47	6698
POL	VTDGRQKVV	650	9	30	47	6699
POL	LAGRWPVKV	856	9	30	47	6700
POL	KAACWWAGI	879	9	31	49	6701
POL	ETAYFILKL	848	9	31	48	6702
POL	PSINNETPGI	322	10	31	48	6703
POL	CTHLEGGKIL	817	10	31	48	6704
POL	ETQGETAYFI	844	10	31	48	6705
POL	CTHLEGGKILV	817	11	31	48	6706
POL	ETQGETAYFIL	844	11	31	48	6707
POL	TAYFILKL	849	8	32	50	6708
POL	AACWWAGI	880	8	32	50	6709
POL	IISNWRAMASDF	768	11	32	50	6710
POL	SSMTKILEPF	351	10	33	52	6711
POL	QSSMTKILEPF	350	11	33	52	6712
POL	LTEAVQKI	560	8	34	53	6713
POL	CTHLEGGKI	817	8	35	55	6714
POL	ETKLGKAGY	641	9	35	55	6715
POL	CTHLEGGKI	817	9	35	55	6716
POL	ATDIQTKEL	957	9	35	55	6717
POL	ETKLGKAGYV	641	10	35	55	6718
POL	IATDIQTKEL	956	10	35	55	6719
POL	ITKIQNFRV	969	9	36	57	6720
POL	ITKIQNFRVY	969	10	36	57	6721
POL	ITKIQNFRVY	969	11	36	57	6722
POL	PAIFQSSMTKI	346	11	36	56	6723
POL	QAQPKSESIL	699	11	36	56	6724
POL	TAFTIPS	317	8	37	58	6725
POL	YTAFTIPS	316	9	37	58	6726
POL	LTEEAGLEL	484	9	37	58	6727
POL	LSWVVAIRGI	725	10	37	58	6728
POL	GAVVIQNSDI	999	11	37	58	6729
POL	QSSMTKIL	350	8	38	59	6730
POL	KAKIRDY	1017	8	41	64	6731
POL	RAMASDFNL	772	9	41	64	6732
POL	SAGERIIDI	947	9	41	64	6733
POL	LTQIGCTLNF	177	10	41	64	6734

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	YSAGERIIDI	946	10	41	64	6735
POL	SAGERIIDI	947	10	41	64	6736
POL	YSAGERIIDI	946	11	41	64	6737
POL	LTIQICTL	177	8	42	66	6738
POL	PAIFQSSM	346	8	42	66	6739
POL	YSAGERII	946	8	42	66	6740
POL	ISKIGPENPY	236	10	42	66	6741
POL	GSPAIFQSSM	344	10	42	66	6742
POL	WTYQIQEIFF	529	10	42	66	6743
POL	TTNQKTELQAI	664	11	42	66	6744
POL	DSWTYNDI	439	8	43	67	6745
POL	ASCDKCOL	790	8	43	67	6746
POL	VASCIKCOL	789	9	43	67	6747
POL	DSWTYNDI	439	11	43	67	6748
POL	MITKILIFF	353	8	44	69	6749
POL	QIKELQKQI	961	9	46	72	6750
POL	ITLWQRPL	90	8	47	73	6751
POL	ITLWQRPLV	90	9	47	73	6752
POL	KAIGTVLV	157	8	48	75	6753
POL	ITNDVKQL	553	8	49	77	6754
POL	PAGLKKKRSV	286	10	50	78	6755
POL	QATWIPEWFEV	599	11	51	81	6756
POL	KSVTVLDV	293	8	51	80	6757
POL	ITDNGSNF	866	8	51	80	6758
POL	ATWIPEWFEV	600	10	51	80	6759
POL	ETVIVKLTGGM	192	11	51	80	6760
POL	ETVIRYQYNV	327	11	51	80	6761
POL	QATWIPEWFEV	599	10	52	83	6762
POL	ETVIRYQY	327	9	52	81	6763
POL	ATWIPEWFEV	600	9	52	81	6764
POL	VASGYIEAEV	831	10	52	81	6765
POL	VASGYIEAEV	831	11	52	81	6766
POL	ASGYIEAEV	832	9	53	83	6767
POL	QSQGVVIESM	898	9	53	83	6768
POL	GTVLVGHTV	160	10	53	83	6769
POL	RTQDFWEVQL	272	10	53	83	6770
POL	VAVIVASGYI	827	10	53	83	6771
POL	ASGYIEAEV	832	10	53	83	6772
POL	ESMNKELKKI	904	10	53	83	6773
POL	ISPIETVPKL	188	11	53	83	6774
POL	ESMNKELKKI	904	11	53	83	6775
POL	QATWIPEW	599	8	54	86	6776
POL	RTQDFWEV	272	8	55	86	6777
POL	DAYFSYPL	302	8	55	86	6778
POL	TTNQKTEL	664	8	55	86	6779
POL	ISPIETVPV	188	9	56	88	6780
POL	LTEEKIKAL	213	9	56	88	6781
POL	VTVLVDGDAY	295	10	56	88	6782
POL	KTAVQMAVFI	925	10	56	88	6783
POL	VTVLVDGDAYF	295	11	56	88	6784

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PAETGQETAYF	842	11	56	88	6785
POL	LAENREIL	492	8	57	89	6786
POL	NTPLVKL	610	8	57	89	6787
POL	CSPGIWQL	808	8	57	89	6788
POL	KTAVQNAV	925	8	57	89	6789
POL	NTPLVKLW	610	9	57	89	6790
POL	ETGQETAYF	844	9	57	89	6791
POL	KTAVQMAVF	925	9	57	89	6792
POL	NTPLVKLWY	610	10	57	89	6793
POL	FAIKKDKSTKW	250	11	57	89	6794
POL	QAEILKTAVQM	920	11	57	89	6795
POL	STKWRKLVDF	257	10	58	91	6796
POL	VDSQYALGI	688	10	58	91	6797
POL	PAETGQETAY	842	10	58	91	6798
POL	DSTKWRKLVDF	256	11	58	91	6799
POL	VDSQYALGII	688	11	58	91	6800
POL	DSTKWRKL	256	8	59	92	6801
POL	STKWRKLV	257	8	59	92	6802
POL	VDSQYAL	688	8	59	92	6803
POL	DSQYALGI	690	8	59	92	6804
POL	ETGQETAY	844	8	59	92	6805
POL	DSTKWRKLV	256	9	59	92	6806
POL	DSQYALGII	690	9	59	92	6807
POL	VAVIVASGY	827	9	59	92	6808
POL	QAEILKTAV	920	9	59	92	6809
POL	TAVQMAVFI	926	9	59	92	6810
POL	MAVEIINF	930	8	60	94	6811
POL	CTLNFIHSI	182	10	60	94	6812
POL	TAVQMAVF	926	8	61	95	6813
POL	DTGADDTVL	112	9	61	95	6814
POL	WTYNDIQKLV	441	10	61	95	6815
POL	WTYNDIQKL	441	9	62	97	6816
POL	DTGADDTV	112	8	63	98	6817
REV	RAIKRQIHISI	50	10	10	16	6818
REV	GTQGVGSHQI	97	10	11	18	6819
REV	RSAPVPL	70	8	12	19	6820
REV	SAEIVPLQL	71	9	12	19	6821
REV	SAEIVPLQL	70	10	12	19	6822
REV	RSQDSDELL	4	10	16	25	6823
REV	QARKNRRRW	40	10	16	25	6824
REV	RSQDSDELL	4	9	17	27	6825
REV	GTSGTQGV	94	8	21	33	6826
REV	PAEPVPLQL	71	9	21	33	6827
REV	QARRNRRRW	40	10	38	59	6828
TAT	PTGPKSKKKV	88	11	12	19	6829
VIF	KSIVKYIIM	22	8	10	16	6830
VIF	FDSAIRKAI	120	10	10	16	6831
VIF	YSTQIDPUL	99	9	11	17	6832
VIF	YSTQVDIPL	99	9	11	17	6833
VIF	STQVDIPL	100	8	11	17	6834

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	KSLVKIIMYI	22	10	11	17	6835
VIF	VSIEWLRRY	88	10	11	17	6836
VIF	FSESAIRKAIL	120	11	11	17	6837
VIF	GSLOYLALAKAI	148	11	11	17	6838
VIF	STQIDPDL	100	8	12	19	6839
VIF	ESAIRNAI	122	8	12	19	6840
VIF	SAIRNAIL	123	8	12	19	6841
VIF	QTGERDWIIL	75	9	12	19	6842
VIF	ESAIRNAIL	122	9	12	19	6843
VIF	KTKPPLPSV	164	9	12	19	6844
VIF	FSESAIRKAI	120	10	12	19	6845
VIF	FSESAIRNAI	120	10	12	19	6846
VIF	FSESAIRNAIL	120	11	12	19	6847
VIF	GSLOYLALAL	148	11	12	19	6848
VIF	LADQLHIMYI	107	10	13	20	6849
VIF	ESRIIPKVSSEV	45	11	13	20	6850
VIF	LADQLHIMYI	107	11	13	20	6851
VIF	PSVKKLTIEDRW	173	11	13	20	6852
VIF	NSLVKIHIMYV	22	10	14	22	6853
VIF	LADQLHIMYY	107	10	14	22	6854
VIF	RTWKSLSVKIIM	19	11	14	22	6855
VIF	LADQLHIMLYF	107	11	14	22	6856
VIF	LADQLHIMLY	107	9	15	23	6857
VIF	KTKGIIRGSHIM	188	11	15	23	6858
VIF	ESAIRKAIL	122	9	16	25	6859
VIF	LADQLHIM	107	8	17	27	6860
VIF	ESAIRKAI	122	8	17	27	6861
VIF	KSLVKIHIM	22	8	18	28	6862
VIF	KSLVKIHIMY	22	9	18	28	6863
VIF	DSAIRKAIL	122	9	19	30	6864
VIF	DSAIRKAI	122	8	20	31	6865
VIF	IITGERDWIIL	75	9	21	33	6866
VIF	NSLVKIHIMY	22	9	24	38	6867
VIF	RTWNSLVKIHIM	19	11	24	38	6868
VIF	LADQLHIM	107	8	25	39	6869
VIF	NSLVKIHIM	22	8	27	42	6870
VIF	ISSEVIHIMPL	51	9	27	42	6871
VIF	VSSEVIHIMPL	51	9	27	42	6872
VIF	GSLOYLALAL	148	11	31	48	6873
VIF	SAIRKAIL	123	8	35	55	6874
VIF	QAGINKVGSGL	141	10	38	59	6875
VIF	SSEVIHIMPL	52	8	55	86	6876
VIF	GSLOYLAL	148	8	58	91	6877
VPR	WALELLEEL	18	9	09	15	6878
VPR	ETYGDTWTGV	48	10	11	17	6879
VPR	EAVRIIFPRI	29	9	14	22	6880
VPR	EAVRIIFPRIW	29	10	14	22	6881
VPR	EAVRIIFRIWL	29	11	14	22	6882
VPR	KSEAVRIIF	27	8	15	23	6883
VPR	WAGVEAIIIRI	54	10	15	23	6884

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	WAGVEAIRIL	54	11	15	23	6885
VPR	WAGVEAIL	54	8	16	25	6886
VPR	DTWAGVEAIL	52	9	16	25	6887
VPR	ETYGDTWAGIV	48	10	16	25	6888
VPR	NTYGDWAGIV	48	10	16	25	6889
VPR	DTWAGVEAIL	52	10	16	25	6890
VPR	DTWAGVEAIL	52	10	19	30	6891
VPR	DTWEGVEAIL	52	9	20	31	6892
VPR	EAIRILQQL	58	10	33	52	6893
VPR	EAIRILQQLL	58	11	33	52	6894
VPR	EAVRIIFRPW	29	10	34	53	6895
VPR	EAVRIIFRPWL	29	11	34	53	6896
VPR	WTLLELLEL	18	9	42	69	6897
VPU	LAKVDYRI	5	8	01	25	6898
VPU	LAKVDYRL	5	8	01	25	6899
VPU	LAKVDYRIV	5	9	01	25	6900
VPU	LAKVDYRIVI	5	10	01	25	6901
VPU	LAKVDYRLGV	5	10	01	25	6902
VPU	LAKVDYRIVIV	5	11	01	25	6903
VPU	VTLSSSKL	94	9	01	50	6904
VPU	LAIVALVY	13	8	12	20	6905
VPU	WTIVFIEY	34	8	12	19	6906
VPU	ESEGDDQEEL	75	9	13	20	6907
VPU	ESEGDTTEEL	75	9	13	20	6908
VPU	LAIVVWTV	28	9	20	31	6909
VPU	LAIVVWTVI	28	8	23	36	6910

Table XIV
H1V B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	GIGPGQTF	360	8	01	33	6911
ENV	SIGSQAF	360	8	01	33	6912
ENV	KLEIRQF	405	8	01	25	6913
ENV	FPDRPERI	823	8	01	33	6914
ENV	PPDRPEGI	823	8	01	33	6915
ENV	GIGPGQTFY	360	9	01	33	6916
ENV	SIGSQAFY	360	9	01	33	6917
ENV	SIGSQAFYV	360	10	01	33	6918
ENV	KQLYATVY	34	8	01	50	6919
ENV	QLYATVYAGV	34	10	01	50	6920
ENV	KQLYATVYSGV	34	11	01	50	6921
ENV	TIGAMFLGF	599	9	03	27	6922
ENV	MLGAMFLGF	599	9	04	36	6923
ENV	SLRGLQRGW	889	9	05	18	6924
ENV	RLGWEGLYLW	894	11	07	23	6925
ENV	RLGWEGLY	894	9	09	29	6926
ENV	GLRLGWEGLY	892	11	09	29	6927
ENV	LILGLVII	21	8	09	15	6928
ENV	IPRRIRQGF	950	9	10	16	6929
ENV	ALFYKLIV	202	8	10	16	6930
ENV	IMQLTIV	650	8	10	16	6931
ENV	DITNLWLY	769	8	10	16	6932
ENV	DIRQAICNV	380	9	10	16	6933
ENV	LPCRKQIV	485	9	10	16	6934
ENV	MLQLTYWGI	651	9	10	16	6935
ENV	DFTNLWLY	769	9	10	16	6936
ENV	SOELKNSAV	911	9	10	16	6937
ENV	PIIYCTPAGF	260	10	10	16	6938
ENV	TLPCRKQIV	484	10	10	16	6939
ENV	IPHIYCTPAGF	259	11	10	16	6940
ENV	RYGQAMYAHH	498	11	10	16	6941
ENV	WMEWERIDNY	723	11	10	16	6942
ENV	ALDKWASLVNW	757	11	10	16	6943
ENV	SLKGLRLGW	889	9	11	39	6944
ENV	GIGAVFLGF	598	9	11	18	6945
ENV	KLWVTVY	44	8	11	17	6946
ENV	AVGIGAVE	595	8	11	17	6947
ENV	KLWVTVYTV	44	10	11	17	6948
ENV	AVGIGAVFLGF	595	11	11	17	6949
ENV	RIGPGQTF	357	8	11	17	6950
ENV	NITLPCR	482	8	11	17	6951
ENV	WQVVGQAM	496	8	11	17	6952
ENV	QIRCSSNI	512	8	11	17	6953
ENV	ALFYRLDVV	202	9	11	17	6954
ENV	GRCTNVSTV	283	9	11	17	6955
ENV	RIGPGQTFY	357	9	11	17	6956
ENV	WQVVGQAMY	496	9	11	17	6957
ENV	QIRCSSNI	511	9	11	17	6958
ENV	ALDKWASLV	757	9	11	17	6959
ENV	AVSLLNATAI	918	10	11	17	6960

Table XIV
IIIY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	NITLPCRIKQI	482	11	11	17	6961
ENV	VVEREKIRAVGI	588	11	11	17	6962
ENV	LLALDKWASLW	755	11	11	17	6963
ENV	NMWKNDMMV	107	8	12	19	6964
ENV	ALFYRLDIV	202	8	12	19	6965
ENV	RIKQIVNM	488	8	12	19	6966
ENV	KLICITTV	687	8	12	19	6967
ENV	WMIEWEREI	723	8	12	19	6968
ENV	ILKCNDDKKF	271	9	12	19	6969
ENV	RIKQIVNMW	488	9	12	19	6970
ENV	LICTTTVPW	688	9	12	19	6971
ENV	GQELKNSAI	911	9	12	19	6972
ENV	AILIIPRKI	946	9	12	19	6973
ENV	AILKCNDDKKF	270	10	12	19	6974
ENV	KLCTTTVPW	687	10	12	19	6975
ENV	NMTWMEWEREI	720	11	12	19	6976
ENV	IVCGLIGLIII	783	11	12	19	6977
ENV	ELYKYKYVVEI	560	10	13	21	6978
ENV	DPNPQEVV	91	8	13	20	6979
ENV	IILKLTWV	650	8	13	20	6980
ENV	NVPWNSSW	693	8	13	20	6981
ENV	EIWDNMTW	716	8	13	20	6982
ENV	SIRLVNGF	842	8	13	20	6983
ENV	SIRLVSGF	842	8	13	20	6984
ENV	RIKDLII	867	8	13	20	6985
ENV	ILIIIPRKI	947	8	13	20	6986
ENV	EIKNCSFNI	181	9	13	20	6987
ENV	AITQACTKV	244	9	13	20	6988
ENV	SLAEFEVVI	311	9	13	20	6989
ENV	QQIILKLTIV	648	9	13	20	6990
ENV	LLKLTWVGI	651	9	13	20	6991
ENV	AQQIILKLTIV	647	10	13	20	6992
ENV	QQIILKLTWV	648	10	13	20	6993
ENV	IILKLTWVGI	650	10	13	20	6994
ENV	EQELIELDKW	752	11	13	20	6995
ENV	VPTDFNIEVV	88	11	13	20	6996
ENV	VMISFNCGLIEF	412	11	13	20	6997
ENV	TITLPCRIKQI	482	11	13	20	6998
ENV	AQQIILKLTWV	647	11	13	20	6999
ENV	SLAEFEVV	311	8	14	22	7000
ENV	TITLPCRI	482	8	14	22	7001
ENV	SLCNATAI	920	8	14	22	7002
ENV	DPEIVMISF	428	9	14	22	7003
ENV	QAMVAPPI	501	9	14	22	7004
ENV	RIIFAVLSI	791	9	14	22	7005
ENV	AVAEGTDRV	928	9	14	22	7006
ENV	EQDLALDKW	752	10	14	22	7007
ENV	RIIFAVLSIV	791	10	14	22	7008
ENV	SLNATAIIV	920	10	14	22	7009
ENV	AVAEGTDRVI	928	10	14	22	7010

Table XIV
 HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	VITQACPKVSF	244	11	14	22	7011
ENV	GLRIFAVLSI	789	11	14	22	7012
ENV	AIAVAEGTDIRV	926	11	14	22	7013
ENV	RLINCNTSAI	236	10	15	24	7014
ENV	GLIGLRRII	786	8	15	23	7015
ENV	IIFAVLSI	792	8	15	23	7016
ENV	GHDRPEGI	822	8	15	23	7017
ENV	LINCNTSAI	237	9	15	23	7018
ENV	VITQACPKV	244	9	15	23	7019
ENV	GPCKNVSTV	283	9	15	23	7020
ENV	DIRQAICNI	380	9	15	23	7021
ENV	GLIGLRRII	786	9	15	23	7022
ENV	IIFAVLSI	792	9	15	23	7023
ENV	LLNATAIAV	921	9	15	23	7024
ENV	SVITQACPKV	243	10	15	23	7025
ENV	TLPCRIKQII	484	10	15	23	7026
ENV	NMWQEVGKAM	494	10	15	23	7027
ENV	AVAEGTDIRI	928	10	15	23	7028
ENV	NMWQEVGKAMY	494	11	15	23	7029
ENV	GLIGLRRII	786	11	15	23	7030
ENV	LGILRIIF	787	8	16	25	7031
ENV	VVQREKRAV	588	9	16	25	7032
ENV	AVAEGTDIRI	928	9	16	25	7033
ENV	RVVQREKRAV	587	10	16	25	7034
ENV	LIGLRRII	787	10	16	25	7035
ENV	LVSGFLALAW	845	10	16	25	7036
ENV	DLRNLCFSY	856	10	16	25	7037
ENV	LLNGSLAEIEV	307	11	16	25	7038
ENV	ELDKWASLWNW	757	11	16	25	7039
ENV	RLVSGFLALAW	844	11	16	25	7040
ENV	AIAVAEGTDIRI	926	11	16	25	7041
ENV	VQREKRAV	589	8	17	27	7042
ENV	IIMWQEV	492	8	17	27	7043
ENV	KLICTINV	687	8	17	27	7044
ENV	SLWNWFDI	763	8	17	27	7045
ENV	DLRNLCIF	856	8	17	27	7046
ENV	QIIMWQEV	491	9	17	27	7047
ENV	LICTINVPW	688	9	17	27	7048
ENV	RPNNNTRKSI	347	10	17	27	7049
ENV	KQIIMWQEV	490	10	17	27	7050
ENV	EIERPGGDM	544	10	17	27	7051
ENV	KLICTINVPW	687	10	17	27	7052
ENV	RIVFAVLSI	791	10	17	27	7053
ENV	GVAPTKAKRRV	573	11	17	27	7054
ENV	WQEVGKAM	496	8	18	28	7055
ENV	GLRIIFAV	789	8	18	28	7056
ENV	WQEVGKAMY	496	9	18	28	7057
ENV	ELDKWASLW	757	9	18	28	7058
ENV	IIFAVLSI	792	9	18	28	7059
ENV	YLRDQQLLGI	672	10	18	28	7060

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	LPCRKQIINM	485	11	18	28	7061
ENV	EVGKAMYAPPI	498	11	18	28	7062
ENV	YLRDQQLGIW	672	11	18	28	7063
ENV	LELDKWSLW	755	11	18	28	7064
ENV	CLFSYIIRLDF	861	11	18	28	7065
ENV	KLICITAV	687	8	19	30	7066
ENV	LICTTAVFW	688	9	19	30	7067
ENV	RIVFAVLSI	791	9	19	30	7068
ENV	KLICITAVFW	687	10	19	30	7069
ENV	GLRIVFAVLSI	789	11	19	30	7070
ENV	ELLELDKW	754	8	20	31	7071
ENV	IVFAVLSI	792	8	20	31	7072
ENV	LPCRKQII	485	9	20	31	7073
ENV	NMVEQMIEDI	112	10	20	31	7074
ENV	NMVEQMIEDII	112	11	20	31	7075
ENV	ILLALDKW	754	8	21	33	7076
ENV	ILEITTHSF	428	9	21	33	7077
ENV	VITDNPQEV	88	10	21	33	7078
ENV	LIGLRIVFAV	787	10	21	33	7079
ENV	CVPTDNPQEV	87	11	21	33	7080
ENV	GLIGLRIVFAV	786	11	21	33	7081
ENV	APTKAKRRV	575	9	22	34	7082
ENV	APTKAKRRV	575	10	22	34	7083
ENV	IVELLGRIGW	879	10	22	34	7084
ENV	PVWKEATTLE	54	11	22	34	7085
ENV	EQMIEDISLW	115	11	22	34	7086
ENV	TVQCTHIGIRPV	290	11	22	34	7087
ENV	RIVELLGRGW	878	11	22	34	7088
ENV	ELLGRGW	881	8	23	37	7089
ENV	MVEQMIEDI	113	9	23	36	7090
ENV	VVKTEPLGV	566	9	23	36	7091
ENV	MVEQMIEDII	113	10	23	36	7092
ENV	KVKTEPLGV	565	10	23	36	7093
ENV	EQMIEDII	115	8	24	38	7094
ENV	VVEREKIRAV	588	9	25	39	7095
ENV	VPTDNPQEI	88	10	25	39	7096
ENV	VQCTHIGIRPV	292	10	25	39	7097
ENV	RVEREKIRAV	587	10	25	39	7098
ENV	QQQNLLRAI	636	10	25	39	7099
ENV	CVPTDNPQEI	87	11	25	39	7100
ENV	VQCTHIGIRPV	292	11	25	39	7101
ENV	VQQQNLLRAI	635	11	25	39	7102
ENV	TLPCRKQI	484	9	26	41	7103
ENV	QQNLLRAI	637	9	26	41	7104
ENV	QQNLLRAI	637	9	26	41	7105
ENV	QQSNLLRAI	636	10	26	41	7106
ENV	PIIHYCAPAGF	259	11	26	41	7107
ENV	VQQSNLLRAI	635	11	26	41	7108
ENV	PIIHYCAPAGF	260	10	27	42	7109
ENV	YLRDQQLGI	672	10	27	42	7110

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	YKDDQQLGIW	672	11	27	42	7111
ENV	KVSFEPHLY	252	11	28	44	7112
ENV	TVQCTIGIKPV	290	11	28	44	7113
ENV	ELYKYKVKI	560	10	29	46	7114
ENV	LIGLRIVF	787	8	29	45	7115
ENV	GLRIVFAV	789	8	29	45	7116
ENV	GLIGLRIVF	786	9	29	45	7117
ENV	QMIEDIISLW	116	10	29	45	7118
ENV	RIKQINM	488	8	30	47	7119
ENV	TQACTPKVSF	247	9	30	47	7120
ENV	CPKVSFEP	250	9	30	47	7121
ENV	KVSFEP	252	9	30	47	7122
ENV	RIKQINM	488	9	30	47	7123
ENV	NMWKNNMVEQM	107	11	30	47	7124
ENV	CPKVSFEP	250	11	30	47	7125
ENV	IVGGLIGLRIV	783	11	30	47	7126
ENV	LPCKIKQI	485	8	31	48	7127
ENV	AVLSIVNRV	795	9	31	48	7128
ENV	VQCTIGIKPV	292	11	31	48	7129
ENV	KIFIMVGGI	778	11	31	48	7130
ENV	GLIGLRIV	786	8	32	50	7131
ENV	VQCTIGIKPV	292	10	32	50	7132
ENV	LQARVLAV	662	8	33	52	7133
ENV	RVLAVERY	665	8	33	52	7134
ENV	QLQARVLAV	661	9	33	52	7135
ENV	KQLQARVLAV	660	10	33	52	7136
ENV	LQARVLAVERY	662	11	33	52	7137
ENV	NLWVTYYGV	44	10	34	54	7138
ENV	NVTENFM	101	8	34	53	7139
ENV	NMWKNNMV	107	8	34	53	7140
ENV	IILLQLTVW	650	8	34	53	7141
ENV	NVTENFM	101	9	34	53	7142
ENV	QQILLQLTV	648	9	34	53	7143
ENV	LLQLTVWGI	651	9	34	53	7144
ENV	AQQILLQLTV	647	10	34	53	7145
ENV	QQILLQLTVW	648	10	34	53	7146
ENV	IILLQLTVWGI	650	10	34	53	7147
ENV	AQQILLQLTVW	647	11	34	53	7148
ENV	NLWVTYY	44	8	35	56	7149
ENV	IMIVGGI	781	8	35	56	7150
ENV	FIMIVGGI	780	9	35	55	7151
ENV	DLKSLCLFSY	856	10	35	55	7152
ENV	VQARQLLSGI	625	10	36	56	7153
ENV	SIVNRVQGY	798	10	36	56	7154
ENV	TMGAAITLV	615	11	36	56	7155
ENV	TVQARQLLSGI	624	11	36	56	7156
ENV	VQARQLLSGI	625	11	36	56	7157
ENV	MIVGGLIGLR	782	11	36	56	7158
ENV	DMRDNRSELY	552	11	37	58	7159
ENV	VLSIVNRV	796	8	38	59	7160

Table XIV
IIIY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	DLISLCLF	856	8	38	59	7161
ENV	IVNRVQGY	799	9	38	59	7162
ENV	RPGGDMRDNW	547	11	38	59	7163
ENV	YIKIFIMV	776	9	39	61	7164
ENV	GKQLQARV	658	9	40	63	7165
ENV	TLFCASDAKAY	64	11	40	63	7166
ENV	IVGGLIGLRI	783	10	42	66	7167
ENV	YIKIFIMI	776	8	43	67	7168
ENV	WLWYIKIFIM	773	10	43	67	7169
ENV	WLWYIKIFIMI	773	11	43	67	7170
ENV	LQLTVWGI	652	8	44	69	7171
ENV	SLWDQSLKPCV	123	11	47	75	7172
ENV	RVRQGYSPLSF	802	11	47	73	7173
ENV	RQGYSPLSF	804	9	48	75	7174
ENV	GIWGCSGKLI	680	10	48	75	7175
ENV	ROLLSGIV	628	8	49	77	7176
ENV	NVWATIACV	80	9	49	77	7177
ENV	WLWYIKIFI	773	9	49	77	7178
ENV	DQSLKPCV	126	8	50	78	7179
ENV	WLWYIKIF	773	8	50	78	7180
ENV	TVQCTHGI	290	8	51	80	7181
ENV	DQLLGIW	675	8	51	80	7182
ENV	NVSTVQCTHGI	287	11	51	80	7183
ENV	KPCVKLTPLCV	130	11	54	84	7184
ENV	TVYGVIV	48	8	55	86	7185
ENV	TVYVGVIVW	48	9	55	86	7186
ENV	CVKLTPLCV	132	9	55	86	7187
ENV	FLGAAGSTM	608	9	55	86	7188
ENV	WVTVYVGVIVW	46	10	55	86	7189
ENV	ELYKYKVV	46	11	55	86	7190
ENV	WVTVYGV	560	8	56	89	7191
GAG	PPESFRF	46	8	58	91	7192
GAG	EPIDKELY	510	8	01	33	7193
GAG	APPESFRF	537	8	01	25	7194
GAG	APPESFRF	509	9	01	33	7195
GAG	KQEPDKELY	535	10	01	33	7196
GAG	KQETIDKELY	535	10	01	25	7197
GAG	EPLTALRSLF	547	10	01	33	7198
GAG	PPLASLKSFL	547	10	01	33	7199
GAG	PPLSLKSFL	547	10	01	33	7200
GAG	EPTAPPAESF	506	10	01	33	7201
GAG	EPTAPPESF	506	10	01	50	7202
GAG	PPAESFRF	510	8	02	67	7203
GAG	APPAESFRF	509	9	02	67	7204
GAG	PPLASLKSFL	546	10	04	24	7205
GAG	YPLASLRSFL	545	10	07	15	7206
GAG	YPLASLKSFL	545	10	08	17	7207
GAG	NIMMQRGNF	407	9	10	17	7208
GAG	TPSQKQEP	527	9	10	17	7209
GAG	NPPIPVGDI	277	9	10	16	7210

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	NPPIPVGDIY	277	10	10	16	7211
GAG	QIGWMTSNPI	267	11	10	16	7212
GAG	KLDKWEKI	12	8	10	16	7213
GAG	GPVAIPQGM	242	8	10	16	7214
GAG	PIPIVGDI	278	8	10	16	7215
GAG	PPAESFGF	498	8	10	16	7216
GAG	PIPIVGDIY	278	9	10	16	7217
GAG	APPAESFGF	497	9	10	16	7218
GAG	ALSPRTLNAW	167	10	10	16	7219
GAG	ALSPRTLNAWV	167	11	10	16	7220
GAG	IPVGDIYKRWI	280	11	10	16	7221
GAG	VQNAIPJCKSI	347	11	10	16	7222
GAG	PIPIVGDIY	279	8	11	17	7223
GAG	SQEVKNWM	334	8	11	17	7224
GAG	IMMQSNF	408	8	11	17	7225
GAG	PQDLNMLNI	202	10	11	17	7226
GAG	IPVGDIYKRW	280	10	11	17	7227
GAG	EQASQEVKNW	331	10	11	17	7228
GAG	TPQDLNMLNI	201	11	11	17	7229
GAG	PQDLNMLNIV	202	11	11	17	7230
GAG	IVGGIIQAAMQM	211	11	11	17	7231
GAG	TLRAEQATQDV	327	11	11	17	7232
GAG	EQASQEVKNWM	331	11	11	17	7233
GAG	WISSKGRPGNF	474	11	11	17	7234
GAG	EPIDKELY	533	8	12	19	7235
GAG	KQEPIDKELY	531	10	12	19	7236
GAG	TPQDLNMM	201	8	12	19	7237
GAG	DLNMLNI	204	8	12	19	7238
GAG	TLQEQIAW	263	8	12	19	7239
GAG	TLYCVIIQKI	86	9	12	19	7240
GAG	DLNMLNIV	204	9	12	19	7241
GAG	IVGGIIQAAM	211	9	12	19	7242
GAG	TLQEQIAWM	263	9	12	19	7243
GAG	PLTSLKSLF	548	9	12	19	7244
GAG	PLTSLRSLF	548	9	12	19	7245
GAG	NIVGGIIQAAM	210	10	12	19	7246
GAG	TLRAEQASQEV	327	11	12	19	7247
GAG	TIMMQRGNF	407	9	13	22	7248
GAG	SPTSILDI	302	8	13	20	7249
GAG	RMYSPTSILDI	299	11	13	20	7250
GAG	LQEQIAWM	264	8	14	22	7251
GAG	RMYSPTSI	299	8	14	22	7252
GAG	VQNAQGMV	156	9	14	22	7253
GAG	IVQNAQGMV	155	10	14	22	7254
GAG	RVIIPVILAGPI	235	10	14	22	7255
GAG	IVRMYSPTSI	297	10	14	22	7256
GAG	PIVQNAQGMV	154	11	14	22	7257
GAG	KIVRMYSPTSI	296	11	14	22	7258
GAG	WISNRKGRPGNF	474	11	14	22	7259
GAG	KVSQNYPI	148	8	15	27	7260

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
GAG	KVSNYPV	148	9	15	27	7261
GAG	TQDVKNWM	334	8	15	23	7262
GAG	PPEESFRF	498	8	15	23	7263
GAG	ELRSLYNTV	76	9	15	23	7264
GAG	TLVCYIQR	86	9	15	23	7265
GAG	APPEESFRF	497	9	15	23	7266
GAG	PLSLKSLF	548	9	15	23	7267
GAG	VLSGGKLDV	7	10	15	23	7268
GAG	SLFNTVATLY	79	10	15	23	7269
GAG	LQQMVIQAI	159	10	15	23	7270
GAG	EQATQDVKNW	331	10	15	23	7271
GAG	EPTAPPEESF	494	10	15	23	7272
GAG	SVLSGGKLDV	6	11	15	23	7273
GAG	NLQQMVIQAI	158	11	15	23	7274
GAG	EQATQDVKNWM	331	11	15	23	7275
GAG	WMTSNPIH	270	8	16	25	7276
GAG	GPAATLEEM	362	9	16	25	7277
GAG	WMTSNPIPV	270	10	16	25	7278
GAG	GPAATLEEM	362	10	16	25	7279
GAG	LLETSEGCROI	52	11	16	25	7280
GAG	ALGPAATLEEM	360	11	16	25	7281
GAG	GPIPPGQM	242	8	17	27	7282
GAG	DIYKRWH	284	8	17	27	7283
GAG	PVGDYKRWH	281	10	17	27	7284
GAG	PVGDYKRWH	281	11	17	27	7285
GAG	ALGPGATLEEM	360	11	17	27	7286
GAG	QIGWMTNPIH	267	11	18	29	7287
GAG	KLDWEEKI	12	8	18	28	7288
GAG	TQEVKNWM	334	8	18	28	7289
GAG	PVGDIYKRW	281	9	18	28	7290
GAG	GPGATLEEM	362	9	18	28	7291
GAG	EQATQEVKNW	331	10	18	28	7292
GAG	GPGATLEEM	362	10	18	28	7293
GAG	EQATQEVKNWM	331	11	18	28	7294
GAG	GPIAGQM	242	8	19	30	7295
GAG	GPSIKARV	379	8	19	30	7296
GAG	DIKQGPKEPF	308	10	19	30	7297
GAG	IVWASRELERF	35	11	19	30	7298
GAG	GVGGPSIKARV	376	11	19	30	7299
GAG	WMTNPIH	270	8	20	31	7300
GAG	WMTNPIPV	270	10	20	31	7301
GAG	EPTAPPEESF	494	10	20	31	7302
GAG	YPIVNAQOGM	153	11	20	31	7303
GAG	VIEKAFSPEV	179	11	20	31	7304
GAG	VQNAQOGM	156	8	21	33	7305
GAG	KQGPKEPF	310	8	21	33	7306
GAG	IVQNAQOGM	155	9	21	33	7307
GAG	PIVQNAQOGM	154	10	21	33	7308
GAG	KQGPKEPRDY	310	11	21	33	7309
GAG	SVVSNQYPI	146	9	22	44	7310

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
GAG	SQVSQNYIIV	146	10	22	44	7311
GAG	WMTDTLLV	340	8	22	34	7312
GAG	SLYNTVATLY	79	10	22	34	7313
GAG	RLHIPVILAGPI	235	10	22	34	7314
GAG	WPSIKGRPGNF	474	11	23	36	7315
GAG	KVIEKAF	178	8	24	38	7316
GAG	WVKVIEKAF	176	10	24	38	7317
GAG	TLRAIQATQEV	327	11	24	38	7318
GAG	LVWASRELERF	35	11	25	39	7319
GAG	MQMLKETI	219	8	26	41	7320
GAG	AMQMLKETI	218	9	26	41	7321
GAG	QVSQNYPI	148	8	27	48	7322
GAG	QVSQNYPIV	148	9	27	48	7323
GAG	TLQEQIGW	263	8	27	42	7324
GAG	IMMQRGNF	408	8	27	42	7325
GAG	TLQEQIGWM	263	9	27	42	7326
GAG	QMVIIQAI	161	8	28	44	7327
GAG	KVVEEKAF	178	8	28	44	7328
GAG	WVKVVEEKAF	176	10	28	44	7329
GAG	VVEEKAFSPV	179	11	28	44	7330
GAG	EIPRDYVDIRFY	315	11	28	44	7331
GAG	VQNLCQGM	156	8	29	45	7332
GAG	LQEQIGWM	264	8	29	45	7333
GAG	IVQNLCQGM	155	9	29	45	7334
GAG	VQNLCQGMV	156	9	29	45	7335
GAG	PIVQNLCQGM	154	10	29	45	7336
GAG	IVQNLCQGMV	155	10	29	45	7337
GAG	AIPTLTNAW	167	10	29	45	7338
GAG	YHVNLCQGM	153	11	29	45	7339
GAG	PIVQNLCQGMV	154	11	29	45	7340
GAG	AIPTLTNAWV	167	11	29	45	7341
GAG	TLNAWVKVI	172	9	30	47	7342
GAG	TLNAWVKVV	172	9	31	48	7343
GAG	MQMLKDTI	219	8	33	52	7344
GAG	AMQMLKDTI	218	9	33	52	7345
GAG	VLAEMSQV	386	9	33	52	7346
GAG	RVLAEAMSQV	385	10	33	52	7347
GAG	NPIPVGEI	277	9	34	54	7348
GAG	NPIPVGEIY	277	10	34	54	7349
GAG	RLRGGKKKY	20	10	34	54	7350
GAG	IPVGEIYKRW	280	10	34	53	7351
GAG	IPVGEIYKRW	279	11	34	53	7352
GAG	IPVGEIYKRWI	280	11	34	53	7353
GAG	RIGGKKKY	22	8	35	53	7354
GAG	PIPVGEI	278	8	35	53	7355
GAG	PIPVGEIY	279	8	35	53	7356
GAG	PIPVGEIY	278	9	35	53	7357
GAG	EPFRDYVDRFF	315	9	35	53	7358
GAG	GFQHIKARV	379	11	36	56	7359
GAG	GVGGPGIHKARV	376	11	36	56	7360

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	WMETLLY	340	8	37	58	7361
GAG	IIPVHAGPI	237	8	38	59	7362
GAG	RMYSPPVSLDI	299	11	38	59	7363
GAG	EIKRWII	284	8	39	61	7364
GAG	PVGEIYKRWII	281	11	39	61	7365
GAG	KIVRMYSPPVSI	296	11	39	61	7366
GAG	RMYSPPVSI	299	8	40	63	7367
GAG	SPVSILDI	302	8	40	63	7368
GAG	PVGEIYKRW	281	9	40	63	7369
GAG	PVGEIYKRWI	281	10	40	63	7370
GAG	IVRMYSPPVSI	297	10	40	63	7371
GAG	TVATLYCV	83	8	41	64	7372
GAG	KIVRMYSPPV	296	9	41	64	7373
GAG	DIRGPKPEF	308	10	41	64	7374
GAG	PQDLNTMLNTV	202	11	41	64	7375
GAG	TIQDLNTM	201	8	42	66	7376
GAG	IVRMYSPPV	297	8	42	66	7377
GAG	ROGPKPEF	310	8	42	66	7378
GAG	DLNTMLNTV	204	9	42	66	7379
GAG	RQGPKPEFRDY	310	11	42	66	7380
GAG	QMREPRGSDI	248	10	44	69	7381
GAG	GQIREPRGSDI	247	11	44	69	7382
GAG	VQANPDKCTI	347	11	45	70	7383
GAG	TVGGIIQAAM	211	9	47	73	7384
GAG	TVGGIIQAAMQM	211	11	47	73	7385
GAG	TINEEALEW	225	9	53	83	7386
GAG	SPVEIIMF	186	8	55	86	7387
GAG	APRKKGCV	440	8	55	86	7388
GAG	SPRTLNAWVKV	169	11	55	86	7389
GAG	RQANFLGKI	465	9	56	88	7390
GAG	RQANFLGKIW	465	10	56	88	7391
GAG	IILGLNKIVRM	290	11	56	88	7392
GAG	SPRTLNAW	169	8	57	89	7393
GAG	IILGLNKI	290	8	57	89	7394
GAG	SPRTLNAWV	169	9	57	89	7395
GAG	WIILGLNKI	289	9	57	89	7396
GAG	IILGLNKIV	290	9	57	89	7397
GAG	WIILGLNKIV	289	10	57	89	7398
GAG	IILGLNKIVRM	291	10	57	89	7399
GAG	IILGLNKIVRMV	291	11	57	89	7400
GAG	IILGLNKIV	291	8	58	91	7401
GAG	EMMTACQGV	369	9	59	92	7402
GAG	GLNKIVRM	293	8	60	94	7403
GAG	MMTACQGV	370	8	60	94	7404
GAG	GLNKIVRMV	293	9	60	94	7405
GAG	TLNAWVKV	172	8	61	95	7406
GAG	GPKEPFRDY	312	9	63	98	7407
GAG	GPKEPFRDYV	312	10	63	98	7408
GAG	EPFRDYVDRF	315	10	63	98	7409
NEF	APTAAKGV	34	8	01	33	7410

Table XIV
III B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	APTAAGVGAV	34	11	01	33	7411
NEF	KQEPAAEGV	32	10	01	17	7412
NEF	QAPTAAKGV	32	10	01	17	7413
NEF	AOAEPAAAGV	33	10	01	17	7414
NEF	EPAADGVGAV	40	10	04	15	7415
NEF	VPLRPMTF	101	8	10	16	7416
NEF	IIPICQIGM	259	8	10	16	7417
NEF	QVPLRPMTF	100	9	10	16	7418
NEF	PQVPLRPMTF	99	10	10	16	7419
NEF	LLIIPICQIGM	257	10	10	16	7420
NEF	IIMARELIPEY	320	10	10	16	7421
NEF	RQVPLRPMTF	98	11	10	16	7422
NEF	CLLIIPMSQIGM	256	11	10	16	7423
NEF	IIMARELIPEYV	320	11	10	16	7424
NEF	WQNYTPGKGV	204	10	11	17	7425
NEF	VVDIPREV	230	8	11	17	7426
NEF	LVIIVDPREV	229	9	11	17	7427
NEF	KLVPVIDPREV	228	10	11	17	7428
NEF	PMTYKGAF	105	8	12	19	7429
NEF	IPMSQIGM	259	8	12	19	7430
NEF	RPMTYKGAF	104	9	12	19	7431
NEF	LLIIPMSQIGM	257	10	12	19	7432
NEF	PLAPMTYKGAF	102	11	12	19	7433
NEF	SQKRQDILDW	177	11	12	19	7434
NEF	WVYITQGF	191	8	13	20	7435
NEF	TPGPQTRF	208	8	13	20	7436
NEF	GIRYPLTF	213	8	13	20	7437
NEF	WVYITQGF	191	9	13	20	7438
NEF	DLWVYITQGF	188	10	13	20	7439
NEF	GPGRYPLTF	210	10	13	20	7440
NEF	GPGRYPLTF	210	10	13	20	7441
NEF	GIRYPLTFGW	213	10	13	20	7442
NEF	DLWVYITQGF	188	11	13	20	7443
NEF	DLEKIGAI	57	8	14	22	7444
NEF	WLEAQEEEV	79	10	15	24	7445
NEF	AQEEEVGFF	83	9	17	27	7446
NEF	AQEEEVGFFV	83	11	17	27	7447
NEF	TPGPQIRY	208	8	17	27	7448
NEF	FPLTFGWCF	217	9	17	27	7449
NEF	TQGFPPDWQNY	195	11	17	27	7450
NEF	WQNYTPGFI	204	10	18	29	7451
NEF	LIYSKKRQEI	174	10	18	28	7452
NEF	GLYSKKRQEI	173	11	18	28	7453
NEF	DILDWVY	185	8	20	31	7454
NEF	RQDILDWV	182	9	20	31	7455
NEF	RQDILDWVY	182	10	20	31	7456
NEF	WVYITQGY	191	8	21	33	7457
NEF	WVYITQGYF	191	9	21	33	7458
NEF	DLWVYITQGY	188	10	21	33	7459
NEF	DLWVYITQGYF	188	11	21	33	7460

Table XIV
IIIY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	TQGFPPDW	195	8	22	34	7461
NEF	YPLTFGWCF	217	9	24	38	7462
NEF	RQDILDW	182	8	25	39	7463
NEF	RQEILDWVY	182	10	32	50	7464
NEF	EILDWVY	185	8	33	52	7465
NEF	RQEILDWV	182	9	35	55	7466
NEF	PLTFGWCFKLV	219	11	35	55	7467
NEF	RPQVPLRPMTY	98	11	36	56	7468
NEF	TQGYFPDWQNY	195	11	36	56	7469
NEF	RQEILDW	182	8	37	58	7470
NEF	TQGYFPDW	195	8	37	58	7471
NEF	EVGFVPRQV	91	10	40	63	7472
NEF	PLTFGWCF	219	8	43	67	7473
NEF	PQVPLRPMTY	99	10	45	70	7474
NEF	VPLRPMTY	101	8	46	73	7475
NEF	QVPLRPMTY	100	9	46	72	7476
NEF	RIQVPLRPM	98	9	47	73	7477
NEF	PVRIQVPLRPM	95	11	47	73	7478
NEF	PQVPLRPM	99	8	56	88	7479
POL	SPTSRELQV	35	9	01	33	7480
POL	AISLSLPIQI	80	9	01	33	7481
POL	SPSSRELQV	38	9	01	50	7482
POL	GPERALSV	70	8	01	20	7483
POL	VPTFNFPQI	79	9	01	17	7484
POL	EPGEDRELSV	69	10	01	17	7485
POL	GORGQTVSLSF	69	11	01	17	7486
POL	PQGEAREF	9	8	10	16	7487
POL	FQGEAREF	8	9	10	16	7488
POL	LIEICGHKAI	150	10	10	16	7489
POL	AVOKIATESI	563	10	10	16	7490
POL	MLTQLGCTLNF	176	11	10	16	7491
POL	AVQKIATESIV	563	11	10	16	7492
POL	AVKAACWVAGI	877	11	10	16	7493
POL	IQTKELQKH	960	11	10	16	7494
POL	RIGHENY	238	8	11	17	7495
POL	YQLETEPI	619	8	11	17	7496
POL	AQEDIEKY	760	8	11	17	7497
POL	GIQEFEGI	886	8	11	17	7498
POL	KVPRRKV	1011	8	11	17	7499
POL	VPRRKVKI	1013	8	11	17	7500
POL	VPRRKVKI	1012	9	11	17	7501
POL	VPRRKVKII	1013	9	11	17	7502
POL	IKDYOKQM	1020	9	11	17	7503
POL	GIQEFEGIPY	886	10	11	17	7504
POL	KVPRRKVKI	1011	10	11	17	7505
POL	VPRRKVKII	1012	10	11	17	7506
POL	KIKDYGQM	1019	10	11	17	7507
POL	KISRIGPENPY	235	11	11	17	7508
POL	IPSTNNEIPGI	321	11	11	17	7509
POL	KLWYQLETEPI	616	11	11	17	7510

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SFQ ID NO.
POL	KVVPRRKVKII	1011	11	11	17	7511
POL	KQIKIQNF	967	9	12	19	7512
POL	IKIKQNFV	969	9	12	19	7513
POL	IKIKQNFVY	969	10	12	19	7514
POL	KQIKIQNFV	967	11	12	19	7515
POL	IKIKQNFVY	969	11	12	19	7516
POL	RPLVTVKI	95	8	12	19	7517
POL	EINLPKW	122	8	12	19	7518
POL	QIKIQNF	968	8	12	19	7519
POL	VIQNSEI	1003	8	12	19	7520
POL	RQILLRWGF	395	9	12	19	7521
POL	NQKTELIIAI	666	9	12	19	7522
POL	IIDIASDI	952	9	12	19	7523
POL	IVDIIATDI	952	9	12	19	7524
POL	VVIQNSEI	1002	9	12	19	7525
POL	IQDNSEIKV	1004	9	12	19	7526
POL	WQRPVTVKI	93	10	12	19	7527
POL	ROYDQPIEI	144	10	12	19	7528
POL	GQDQWYQIY	525	10	12	19	7529
POL	RMKGAIITNDV	548	10	12	19	7530
POL	NQKTELQAIY	666	10	12	19	7531
POL	RIDIASDI	951	10	12	19	7532
POL	RVIDIATDI	951	10	12	19	7533
POL	QIKIQNFV	968	10	12	19	7534
POL	AVVIQDNSEI	1000	10	12	19	7535
POL	VIQDNSEIKV	1003	10	12	19	7536
POL	IQDNSEIKV	1004	10	12	19	7537
POL	VLEEINLPKW	119	11	12	19	7538
POL	ELRQILLRWGF	393	11	12	19	7539
POL	INPKWTVQPIV	424	11	12	19	7540
POL	IQKQGDQWY	521	11	12	19	7541
POL	LQKIQIQNF	965	11	12	19	7542
POL	QIKIQNFVY	968	11	12	19	7543
POL	VVIQDNSEIKV	1002	11	12	19	7544
POL	VIQDNSEIKV	1003	11	12	19	7545
POL	ELQKQIKI	964	9	13	21	7546
POL	NLKTGKYARM	540	10	13	21	7547
POL	DINLPKW	122	8	13	20	7548
POL	RQYDQPI	144	8	13	20	7549
POL	QLPEKDSW	434	8	13	20	7550
POL	VLPEKDSW	434	8	13	20	7551
POL	LQKQIKI	965	8	13	20	7552
POL	QLPEKDSW	433	9	13	20	7553
POL	IVLPEKDSW	433	9	13	20	7554
POL	IQKQGDQW	521	9	13	20	7555
POL	GQDQWYQI	525	9	13	20	7556
POL	SPTRRELQW	29	10	13	20	7557
POL	KVROYDQPI	142	10	13	20	7558
POL	LIEIGCKAI	150	10	13	20	7559
POL	PIQLPEKDSW	432	10	13	20	7560

Table XIV
 IIIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PVLPEKDSW	432	10	13	20	7561
POL	QLPEKDSWT	434	10	13	20	7562
POL	VLPEKDSWT	434	10	13	20	7563
POL	EQKQGGQDW	528	10	13	20	7564
POL	EQAEILKTAV	919	10	13	20	7565
POL	VLEDINLPKAW	119	11	13	20	7566
POL	ILIEICGKKAI	149	11	13	20	7567
POL	QHQLPEKDSW	431	11	13	20	7568
POL	QIVLPEKDSW	431	11	13	20	7569
POL	QLPEKDSWT	433	11	13	20	7570
POL	IVLPEKDSWT	433	11	13	20	7571
POL	KQGQDQWTYQI	523	11	13	20	7572
POL	LIKKEKVLSW	717	11	13	20	7573
POL	KLGRWPVKTI	855	11	13	20	7574
POL	RPLVTIKI	95	8	14	22	7575
POL	KQNPDI	362	8	14	22	7576
POL	KIATESIV	566	8	14	22	7577
POL	YQLEKDP	619	8	14	22	7578
POL	SPTRRELQV	29	9	14	22	7579
POL	KQNPDI	362	9	14	22	7580
POL	VOKIATESI	564	9	14	22	7581
POL	KIATESIVI	566	9	14	22	7582
POL	WQKPLVTIKI	93	10	14	22	7583
POL	VOKIATESIV	564	10	14	22	7584
POL	KIATESIVI	566	10	14	22	7585
POL	TIITIDNGSNF	864	10	14	22	7586
POL	EPFRKQNPDI	358	11	14	22	7587
POL	KQNPDI	362	11	14	22	7588
POL	ELREIILK WGF	393	11	14	22	7589
POL	VOKIATESIVI	564	11	14	22	7590
POL	KLWYQLEKDP	616	11	14	22	7591
POL	LVEICTEM	221	8	15	24	7592
POL	KIKALVEL	217	8	15	23	7593
POL	TQLGCTLNF	178	9	15	23	7594
POL	ALVEICTEM	220	9	15	23	7595
POL	ELRQIILLRW	393	9	15	23	7596
POL	IQKQGGQW	521	9	15	23	7597
POL	KQGQDQWTY	523	9	15	23	7598
POL	IQKETWEAW	585	9	15	23	7599
POL	LVSAGIRKV	743	9	15	23	7600
POL	LPGRWPKMI	125	10	15	23	7601
POL	EQKQGGQW	520	10	15	23	7602
POL	PIQKETWEAW	584	10	15	23	7603
POL	IQKETWEAW	585	10	15	23	7604
POL	QVDKLVSAGI	739	10	15	23	7605
POL	KLVSAGIRKV	742	10	15	23	7606
POL	TQLGCTLNFPI	178	11	15	23	7607
POL	PLTEBKIKALV	212	11	15	23	7608
POL	IQKQGGQWTY	521	11	15	23	7609
POL	LPIQKETWEAW	583	11	15	23	7610

Table XIV
IIIY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PIQKETWEAWW	584	11	15	23	7611
POL	IILALQDSGLEV	675	11	15	23	7612
POL	EQVDKLVSAHI	738	11	15	23	7613
POL	LVSAGIRKVLV	743	11	15	23	7614
POL	QLGCTLNF	179	8	16	25	7615
POL	QLEKEPIV	620	8	16	25	7616
POL	AQEEHERY	760	8	16	25	7617
POL	LPGRWKPKM	125	9	16	25	7618
POL	YOLEKEPIV	619	9	16	25	7619
POL	IQEFGIPY	887	9	16	25	7620
POL	QLGCTLNFPI	179	10	16	25	7621
POL	EPFRKQNPDI	358	10	16	25	7622
POL	TPKFKLPI	578	8	17	27	7623
POL	NPDIVIQY	364	9	17	27	7625
POL	ELREIILKKW	393	9	17	27	7626
POL	NPDIVIQYM	364	10	17	27	7627
POL	MLTQIGCTLNF	176	11	17	27	7628
POL	NLKTGKYAKM	540	10	18	29	7629
POL	SVPLDKDF	306	8	18	28	7630
POL	DIVIQYM	366	8	18	28	7631
POL	TLWQRPLVTY	91	10	18	28	7632
POL	IIGRNMLTQI	171	10	18	28	7633
POL	VPLDKDFRKY	307	10	18	28	7634
POL	NIIGRNMLTQI	170	11	18	28	7635
POL	SVPLDKDFRKY	306	11	18	28	7636
POL	LLRGTRKALTEV	471	11	18	28	7637
POL	ELVNQIEQLI	708	11	18	28	7638
POL	AMASDFNLPI	773	11	18	28	7639
POL	PLWKGPAKLLW	985	11	18	28	7640
POL	PLDKDFRKY	308	9	19	30	7641
POL	WQRPLVTY	93	8	19	30	7642
POL	EICGIIKAI	152	8	19	30	7643
POL	LVNQHIEQLI	709	10	19	30	7644
POL	LVSQIEQLI	709	10	19	30	7645
POL	EICGIIKAIQTV	152	11	19	30	7646
POL	ELVSQIEQLI	708	11	19	30	7647
POL	QKEFGIPY	888	8	20	32	7648
POL	RQYDQILI	144	8	20	31	7649
POL	SQIEQLI	711	8	20	31	7650
POL	KLPIQKETW	582	9	20	31	7651
POL	KVRQYDQILI	142	10	20	31	7652
POL	RQYDQILIEI	144	10	20	31	7653
POL	DLEIGQIIRTKI	381	11	20	31	7654
POL	LIKKEKYYLAW	717	11	20	31	7655
POL	TVKAACWWAGI	877	11	20	31	7656
POL	KVIHTDNGSNF	863	11	21	33	7657
POL	WQRPLVTI	93	8	21	33	7658
POL	EIGQIIRTKI	383	9	21	33	7659
POL	EPVGAETI	624	9	21	33	7660
POL	TLWQRPLVTI	91	10	21	33	7660

Table XIV
 IIIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	IIGRNLLTOI	171	10	21	33	7661
POL	EPVGAETFY	624	10	21	33	7662
POL	NIIGRNLLTOI	170	11	21	33	7663
POL	LLTIGCTLNF	176	11	21	33	7664
POL	EPVGAETFY	624	11	21	33	7665
POL	DQWTYQY	527	8	22	34	7666
POL	GIKQIEFGI	886	8	22	34	7667
POL	GIKQIEFGIPY	886	10	22	34	7668
POL	LLRGAKALTDI	471	11	22	34	7669
POL	YLAWVPAIKGI	724	11	22	34	7670
POL	KLGRWPVKVI	855	11	22	34	7671
POL	NPEVIYQY	364	9	23	36	7672
POL	IIEGKVILV	819	9	23	36	7673
POL	KVILVAVIIV	823	9	23	36	7674
POL	NPEVIYQYM	364	10	23	36	7675
POL	EICGKKAIGTV	152	11	23	36	7676
POL	IIEGKVILVAV	819	11	23	36	7677
POL	EICGKKAI	152	8	24	38	7678
POL	NPYNTPIF	243	8	24	38	7679
POL	EIVYQYM	366	8	24	38	7680
POL	NQIEQLI	711	8	24	38	7681
POL	VILVAVIIV	824	8	24	38	7682
POL	TVKAACW	877	8	24	38	7683
POL	IVNIIGRNIM	168	9	24	38	7684
POL	TPVNIIGRNIM	167	10	24	38	7685
POL	GPENPYNTPI	240	10	24	38	7686
POL	NPYNTPIF	243	10	24	38	7687
POL	GQGQWYQIY	525	10	24	38	7688
POL	VHTDNGSNF	864	10	24	38	7689
POL	GPENPYNTPIF	240	11	24	38	7690
POL	LQDSGSEV	678	8	25	39	7691
POL	LLKLAGRW	853	8	25	39	7692
POL	KQGQWYQY	523	9	25	39	7693
POL	GQGQWYQI	525	9	25	39	7694
POL	ALQDSGSEV	677	9	25	39	7695
POL	FLKLAGRW	852	9	25	39	7696
POL	LQDSGSEVNI	678	10	25	39	7697
POL	LLKLAGRWIPV	853	10	25	39	7698
POL	KQGQWYQI	523	11	25	39	7699
POL	ALQDSGSEVNI	677	11	25	39	7700
POL	LQDSGSEVNI	678	11	25	39	7701
POL	AMASDFNLPIV	773	11	25	39	7702
POL	FLKLAGRWIPV	852	11	25	39	7703
POL	QLDCTIIEGKV	814	11	26	41	7704
POL	PIVAKEIV	782	8	26	41	7705
POL	EIGQIRAKI	383	9	26	41	7706
POL	RLPIQKETW	582	9	26	41	7707
POL	LYSSGIRKV	743	9	26	41	7708
POL	PIVAKEIV	781	9	26	41	7709
POL	DISKDLIAEI	512	10	26	41	7710

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	KLVSQIRKV	742	10	26	41	7711
POL	NLPPIVAKEI	779	10	26	41	7712
POL	LPIPIVAKEI	780	10	26	41	7713
POL	DLEIGQIRAKI	381	11	26	41	7714
POL	LVSSGIRKVLV	743	11	26	41	7715
POL	NLPPIVAKEIV	779	11	26	41	7716
POL	QIYAGIKV	458	8	27	43	7717
POL	QIYPGIKV	458	8	27	43	7718
POL	LODSGLEV	678	8	27	42	7719
POL	AQHEIEKY	760	8	27	42	7720
POL	PPIVAKEI	781	8	27	42	7721
POL	SQIYAGIKV	457	9	27	42	7722
POL	SOIYPGIKV	457	9	27	42	7723
POL	IQKETWETW	585	9	27	42	7724
POL	ALQDSGLEV	677	9	27	42	7725
POL	LPIPIVAKEI	780	9	27	42	7726
POL	PIQKETWETW	584	10	27	42	7727
POL	IQKETWETWW	585	10	27	42	7728
POL	LQDSGLEVNI	678	10	27	42	7729
POL	NLPPIVAKEI	779	10	27	42	7730
POL	LPIPIVAKEIV	780	10	27	42	7731
POL	LPIQKETWETW	583	11	27	42	7732
POL	PIQKETWETWW	584	11	27	42	7733
POL	YVTDGRQKVV	649	11	27	42	7734
POL	ALQDSGLEVNI	677	11	27	42	7735
POL	LQDSGLEVNI	678	11	27	42	7736
POL	NLPPIVAKEIV	779	11	27	42	7737
POL	KQKFGIPY	888	8	28	44	7738
POL	KIKALTEI	217	8	28	44	7739
POL	PIVGAETF	625	8	28	44	7740
POL	IVGAETFY	626	8	28	44	7741
POL	OLIKKEKV	716	8	28	44	7742
POL	PVVAKEIV	782	8	28	44	7743
POL	PIVGAETFY	625	9	28	44	7744
POL	IVGAETFYV	626	9	28	44	7745
POL	EQIKKEKV	715	9	28	44	7746
POL	OLIKKEKVY	716	9	28	44	7747
POL	LPIPIVAKEI	780	9	28	44	7748
POL	PIVVAKEIV	781	9	28	44	7749
POL	PIVGAETFYV	625	10	28	44	7750
POL	EQIKKEKVY	715	10	28	44	7751
POL	IIIQLIKKEKV	713	11	28	44	7752
POL	PIVVAKEI	781	8	29	45	7753
POL	IIDIIATDI	952	9	29	45	7754
POL	YVTDGRQKVV	649	10	29	45	7755
POL	QVQDKLVSSGI	739	10	29	45	7756
POL	RIDIATDI	951	10	29	45	7757
POL	EQVQDKLVSSGI	738	11	29	45	7758
POL	TIKFRLLI	578	8	30	47	7759
POL	IILVAIVIV	824	8	30	47	7760

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SI:Q ID NO.
POL	KILVAVIV	823	9	30	47	7761
POL	KLGRWPKV	855	10	30	47	7762
POL	GOWTYQIV	527	8	31	48	7763
POL	YQLEKEPI	619	8	31	48	7764
POL	QGETAYFI	846	8	31	48	7765
POL	ILEGKIIV	819	9	31	48	7766
POL	IPSINNETPGI	321	11	31	48	7767
POL	GVYYDPSKDLI	508	11	31	48	7768
POL	KLWYQLEKEPI	616	11	31	48	7769
POL	ILEGKIIVAV	819	11	31	48	7770
POL	KQLTEAVQKI	558	10	32	51	7771
POL	AVKAAACWW	877	8	32	50	7772
POL	SINNETPGI	323	9	32	50	7773
POL	FILKLGRW	852	9	32	50	7774
POL	IMEKEGKISKI	229	11	32	50	7775
POL	SINNETPGIRY	323	11	32	50	7776
POL	FILKLGRWIV	852	11	32	50	7777
POL	QLDCTILEGKI	814	11	33	52	7778
POL	DVKQLTEAV	556	9	33	52	7779
POL	ELQKQITKI	964	9	34	54	7780
POL	KQITKIQNF	967	9	34	54	7781
POL	KQITKIQNFV	967	11	34	54	7782
POL	ILKLGRW	853	8	34	53	7783
POL	QLTEAVQKI	559	9	34	53	7784
POL	ILKLGRWPKV	853	10	34	53	7785
POL	LQKQITKIQNF	965	11	34	53	7786
POL	RYYRDSRIPI	976	11	34	53	7787
POL	LIKKEKVV	717	8	35	55	7788
POL	QITKIQNF	968	8	35	55	7789
POL	NLPCKWKPKM	124	10	35	55	7790
POL	QITKIQNFV	968	10	35	55	7791
POL	NLPCKWKPKMI	124	11	35	55	7792
POL	QITKIQNFVY	968	11	35	55	7793
POL	PIWKGPAKLLW	985	11	35	55	7794
POL	KLGRAGVV	643	8	36	56	7795
POL	LQKQITKI	965	8	36	56	7796
POL	AFQSSMTKI	347	10	36	56	7797
POL	AQPKSESELV	700	11	36	56	7798
POL	VIQDNSDI	1003	11	37	58	7799
POL	VVIQDNSDI	1002	9	37	58	7800
POL	NPYNTPVFAI	243	10	37	58	7801
POL	QPDKSESELV	701	10	37	58	7802
POL	AVVIQDNSDI	1000	10	37	58	7803
POL	VVIQDNSDIK	1003	10	37	58	7804
POL	YLSWVPAIKGI	724	11	37	58	7805
POL	VVIQDNSDIK	1002	11	37	58	7806
POL	VVIQDNSDIKVV	1003	11	37	58	7807
POL	NPYNTPVF	243	8	38	59	7808
POL	FQSSMTKI	349	8	38	59	7809
POL	IQDNSDIK	1004	9	38	59	7810

Table XIV
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	GRNPNTPTV	240	10	38	59	7811
POL	IQDNDIKVV	1004	10	38	59	7812
POL	GRNPNTPTVF	240	11	38	59	7813
POL	ILKEPVIGVYY	498	11	38	59	7814
POL	LPGRWKPKM	125	9	39	61	7815
POL	LPGRWKPKMI	125	10	39	61	7816
POL	LPKXDSWTV	435	9	40	63	7817
POL	ILKEPVIGVY	498	10	40	63	7818
POL	ILKEPVIGVY	497	11	40	63	7819
POL	KVROYDQI	142	8	41	64	7820
POL	QIGCTLNF	179	8	41	64	7821
POL	EPVIGVYY	504	8	41	64	7822
POL	TOIGCTLNF	178	9	41	64	7823
POL	ILKEPVIGV	498	9	41	64	7824
POL	FIKVRQYDQI	140	10	41	64	7825
POL	QIGCTLNFPI	179	10	41	64	7826
POL	ILKEPVIGV	497	10	41	64	7827
POL	TOIGCTLNFPI	178	11	41	64	7828
POL	KISKIGPENPY	235	11	41	64	7829
POL	SIVWGTPTKF	571	11	41	64	7830
POL	EMEKEGKI	229	8	42	66	7831
POL	SPAFQSSM	345	9	42	66	7832
POL	NQKTELQAI	666	9	42	66	7833
POL	IVIQYMDILY	367	11	42	66	7834
POL	YQIQEFP	531	8	43	67	7835
POL	SMTKILEP	352	9	43	67	7836
POL	QMAQDDCV	1027	8	44	69	7837
POL	KQMAQDDCV	1026	9	44	69	7838
POL	IQTKELQKI	960	10	44	69	7839
POL	DIQTKELQKI	959	11	44	69	7840
POL	EPFKNLKTKGY	536	11	45	70	7841
POL	DQAEHLKTA V	919	10	46	72	7842
POL	LPIQKETW	583	8	47	73	7843
POL	VIWGTPTKF	573	9	47	73	7844
POL	QITLWQRPV	89	10	47	73	7845
POL	IVIWGKTPKF	572	10	47	73	7846
POL	POITLWQRPV	88	11	47	73	7847
POL	KLKPGMDGPKV	197	11	47	73	7848
POL	LVAVIIVASGYI	826	11	47	73	7849
POL	TLWQRPV	91	8	49	77	7850
POL	GLKKKKSIV	288	10	49	77	7851
POL	GIRKVLFDGI	747	11	49	77	7852
POL	KVLFDDGI	750	8	50	78	7853
POL	VPRRKAKII	1013	9	50	78	7854
POL	IRDYGKOM	1020	9	50	78	7855
POL	VVPRRKAKII	1012	10	50	78	7856
POL	KIIRDYGKOM	1019	10	50	78	7857
POL	HPAGLKKKKS V	285	11	50	78	7858
POL	KVPRRKAKII	1011	11	50	78	7859
POL	KIGPENPY	238	8	51	80	7860

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	VPRRKAKI	1013	8	51	80	7861
POL	KPCMDGPKV	199	9	51	80	7862
POL	VVPRKAKI	1012	9	51	80	7863
POL	GMDGPKVKQW	201	10	51	80	7864
POL	TIGIRYQYNV	328	10	51	80	7865
POL	VIVQYMDLKY	368	10	51	80	7866
POL	KVPRKAKI	1011	10	51	80	7867
POL	VLVGPTPVNII	162	11	51	80	7868
POL	VIVQYMDLKY	368	11	51	80	7869
POL	WIPEWFF	602	8	52	84	7870
POL	IONFRVY	972	8	52	84	7871
POL	GLKKKSV	288	8	52	81	7872
POL	TIGIRYQY	328	8	52	81	7873
POL	GIRYQYNV	330	8	52	81	7874
POL	KIONFRVY	971	8	52	81	7875
POL	KIONFRVY	971	9	52	81	7876
POL	LVGPTPVNII	163	10	52	81	7877
POL	WQATWIPEWFF	598	11	52	81	7878
POL	IIVASGYIEAEV	830	11	52	81	7879
POL	VLVGPTPV	162	8	53	83	7880
POL	COLKGEAM	795	8	53	83	7881
POL	SQGVVESM	899	8	53	83	7882
POL	TVLVGPTPV	161	9	53	83	7883
POL	AVIIVASGYI	828	9	53	83	7884
POL	SMNKELKI	905	9	53	83	7885
POL	VLVGPTPVNI	162	10	53	83	7886
POL	HPDKWTVPPI	424	10	53	83	7887
POL	ELELAENREI	489	10	53	83	7888
POL	LVAVIIVASGY	826	10	53	83	7889
POL	PQSQGVVESM	897	10	53	83	7890
POL	SMNKELKII	905	10	53	83	7891
POL	GIGGFIKIRQY	136	11	53	83	7892
POL	TVLVGPTPVNI	161	11	53	83	7893
POL	VLDVGDAYFSV	297	11	53	83	7894
POL	QLKGEAMIGQV	796	11	53	83	7895
POL	ILVAVIIVASGY	825	11	53	83	7896
POL	NPQSQGVVESM	896	11	53	83	7897
POL	FVNTPLV	608	8	54	86	7898
POL	FVNTPLVKKLW	608	11	54	86	7899
POL	GPTPVNII	165	8	54	84	7900
POL	LVGPTPVNI	163	9	54	84	7901
POL	DVGDAYFSV	299	9	54	84	7902
POL	WQATWIPEW	598	9	54	84	7903
POL	TVPVKKLPQM	193	10	54	84	7904
POL	FPSPITVPV	186	11	55	86	7905
POL	TQDFWEVQLGI	273	11	55	86	7906
POL	SPMETVPV	189	8	56	88	7907
POL	PVKLLKPGM	195	8	56	88	7908
POL	WPLTEEKI	211	8	56	88	7909
POL	FPSPITETV	186	9	56	88	7910

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	VPVCLKPGM	194	9	56	88	7911
POL	PISPIETPV	187	10	56	88	7912
POL	KQWPLTEKI	209	10	56	88	7913
POL	SVTVLDVGDAY	294	11	56	88	7914
POL	PISPIETV	187	8	57	89	7915
POL	ELAENKEI	491	8	57	89	7916
POL	TPPLVKLW	611	8	57	89	7917
POL	PPLVKLWY	612	8	57	89	7918
POL	QVIDCSPI	805	8	57	89	7919
POL	IILKTAVQM	923	8	57	89	7920
POL	ELNKRTQDF	268	9	57	89	7921
POL	TVLDVGDAY	296	9	57	89	7922
POL	TPPLVKLWY	611	9	57	89	7923
POL	GOVIXSPI	804	9	57	89	7924
POL	QVDCSPGIW	805	9	57	89	7925
POL	ELKKIIGQV	909	9	57	89	7926
POL	AIKKDSTKW	251	10	57	89	7927
POL	ELNKRTQIFW	268	10	57	89	7928
POL	TVLDVGDAYF	296	10	57	89	7929
POL	QVDCSPGIW	804	10	57	89	7930
POL	IILKTAVQMAY	923	10	57	89	7931
POL	IILKTAVQMAYF	923	11	57	89	7932
POL	GIGGYSAGERI	942	11	57	89	7933
POL	LPQGWKGSPI	338	11	58	92	7934
POL	YVGSDEL	377	8	58	91	7935
POL	DLVQSDLEI	375	10	58	91	7936
POL	IVTDSQYALGI	687	11	58	91	7937
POL	IPAEITGQETAY	841	11	58	91	7938
POL	FIINFKRKGII	913	11	58	91	7939
POL	SOYALGII	691	8	59	92	7940
POL	GIGGNEQV	713	8	59	92	7941
POL	AVIIVASGY	828	8	59	92	7942
POL	KLGRWIV	855	8	59	92	7943
POL	NIQSQGVV	896	8	59	92	7944
POL	PQGWKGSPI	339	10	59	92	7945
POL	EVNIVTDSQY	684	10	59	92	7946
POL	PQGWKGSPIF	339	11	59	92	7947
POL	IPYNIQSQGVV	893	11	59	92	7948
POL	KLLWKGEAVV	992	11	59	92	7949
POL	LLWKGEAVVI	993	11	59	92	7950
POL	KPKMIGGI	130	8	60	94	7951
POL	VLDVGDAY	297	8	60	94	7952
POL	AVQMAVFI	927	8	60	94	7953
POL	VLDVGDAYF	297	9	60	94	7954
POL	ELHPDKWTV	422	9	60	94	7955
POL	KLNWASQTY	452	9	60	94	7956
POL	QMAVFIIN	929	9	60	94	7957
POL	VQMAVFIIN	928	10	60	94	7958
POL	KLLWKGEAV	992	10	60	94	7959
POL	KPKMIGGIGF	130	11	60	94	7960

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	WMGYELIPDKW	418	11	60	94	7961
POL	LVGKLNWASQI	449	11	60	94	7962
POL	AVQMAVFIINF	927	11	60	94	7963
POL	TLNFFISH	183	9	61	97	7964
POL	YQYMDLY	370	8	61	95	7965
POL	KLNWASQI	452	8	61	95	7966
POL	YQYMDDLTV	370	9	61	95	7967
POL	TVNDIQKLV	442	9	61	95	7968
POL	LLWKGEAVV	993	10	61	95	7969
POL	ALLDTGADDTV	109	11	61	95	7970
POL	MIGGIGGF	133	8	62	97	7971
POL	KLVGKLNW	448	8	62	97	7972
POL	NIVTDSQY	686	8	62	97	7973
POL	KMIGGIGGF	132	9	62	97	7974
POL	MIGGIGGF	133	9	62	97	7975
POL	IQKEPFLW	410	9	62	97	7976
POL	LLWKGEAVV	993	9	62	97	7977
POL	KMIGGIGGF	132	10	62	97	7978
POL	IQKEPFLW	410	10	62	97	7979
POL	IQKLVGKLNW	446	10	62	97	7980
POL	MIGGIGGF	133	11	62	97	7981
POL	DIQKLVGKLNW	445	11	62	97	7982
POL	WVPAIKGI	727	8	63	98	7983
POL	EPFLWMGY	413	9	63	98	7984
POL	LLDTGADDTV	110	10	63	98	7985
POL	YQYNVLPQGW	333	10	63	98	7986
POL	IFYNPQSGV	893	10	63	98	7987
POL	GIPYNPQSGV	892	11	63	98	7988
POL	GIGGFIV	136	8	64	100	7989
POL	PPFLWMGY	414	8	64	100	7990
REV	PGTETGV	101	8	05	18	7991
REV	SQGTETGV	101	8	05	18	7992
REV	QPQGTETGV	100	9	05	18	7993
REV	CLGRPAEPV	67	9	10	16	7994
REV	TQGVGSPI	98	9	11	18	7995
REV	LKTVRLI	12	8	11	17	7996
REV	IQRQHISI	52	8	11	17	7997
REV	VPLQLPI	75	8	11	17	7998
REV	PVPLQLPI	74	8	11	17	7999
REV	EPVPLQLPI	73	10	11	17	8000
REV	AVRIKILY	17	9	13	20	8001
REV	ROARKNRNRW	39	11	16	25	8002
REV	IKILYQSNPY	20	11	18	28	8003
REV	KILYQSNPY	22	9	26	41	8004
REV	ILYQSNPY	23	8	27	42	8005
REV	ROARRNRNRW	39	11	38	59	8006
TAT	GPESKSKV	90	9	13	20	8007
TAT	EPVDPRLPEW	2	10	13	20	8008
TAT	FLNKGLGI	41	8	14	22	8009
TAT	PVDPRLPEW	3	9	14	22	8010

Table XIV
 HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
TAT	EPVDPNLEPW	2	10	14	22	8011
TAT	FLNKGGLGISY	41	10	14	22	8012
TAT	PVDPNLEPW	3	9	20	31	8013
VIF	ALIKPKKI	157	8	10	16	8014
VIF	PLGEARLVI	58	9	10	16	8015
VIF	QVDRMRINTW	12	10	10	16	8016
VIF	IIPLGDARLV	56	10	10	16	8017
VIF	IPLGEARLVI	57	10	10	16	8018
VIF	WQVDRMRINTW	11	11	10	16	8019
VIF	IIPLGEARLVI	56	11	10	16	8020
VIF	GVSIEVRLRRY	87	11	10	16	8021
VIF	QIDPLADQLI	102	11	10	16	8022
VIF	PLGDARLV	58	8	11	17	8023
VIF	IPLGDARLV	57	9	11	17	8024
VIF	SIEWRLRRY	89	9	11	17	8025
VIF	GLADQLIIMIIY	106	11	11	17	8026
VIF	RLVITYW	65	8	12	19	8027
VIF	LQTGERDW	74	8	12	19	8028
VIF	KIRTWNSLV	17	9	12	19	8029
VIF	GLQTGERDW	73	9	12	19	8030
VIF	IYWQVDRMKI	9	10	12	19	8031
VIF	QVDRMKIRTW	12	10	12	19	8032
VIF	WQVDRMKIRTW	11	11	12	19	8033
VIF	RMKIRTWNSLV	15	11	12	19	8034
VIF	WQVDRMKI	11	8	13	20	8035
VIF	IIPKISSEV	48	8	13	20	8036
VIF	IIPKISSEV	48	8	13	20	8037
VIF	DQLIIMIIY	109	8	13	20	8038
VIF	DQLIIMIIYF	109	9	13	20	8039
VIF	IIPKISSEVIII	48	10	13	20	8040
VIF	IIPKISSEVIII	48	10	13	20	8041
VIF	SVKKLTEDRW	174	10	13	20	8042
VIF	QLIILYYFDCF	110	11	13	20	8043
VIF	DQLIILYY	109	8	14	22	8044
VIF	QLIILYYF	110	8	14	22	8045
VIF	QLIIMIIYF	110	8	14	22	8046
VIF	IVSPRCEY	133	8	14	22	8047
VIF	DQLIILYYF	109	9	14	22	8048
VIF	QVDPGLADQLI	102	11	14	22	8049
VIF	QLIIMIIYDCF	110	11	14	22	8050
VIF	KISSEVIII	50	8	15	23	8051
VIF	RISSEVIII	50	8	15	23	8052
VIF	IIIMIIYDCF	113	8	15	23	8053
VIF	RIRTWKSIV	17	9	15	23	8054
VIF	RIRTWNSLV	17	9	15	23	8055
VIF	GLADQLIIM	106	9	15	23	8056
VIF	LIIMIIYDCF	111	10	15	23	8057
VIF	RMKIRTWKSIV	15	11	15	23	8058
VIF	RMKIRTWNSLV	15	11	15	23	8059
VIF	IILYYFDCF	113	8	16	25	8060

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SI:Q ID NO.
VIF	LIILYYFDCF	111	10	16	25	8061
VIF	LVKIHIMYI	24	8	19	30	8062
VIF	IIPKVSSEV	48	8	19	30	8063
VIF	PLGEARLV	58	8	19	30	8064
VIF	SLVKIHIMYI	23	9	19	30	8065
VIF	IPLGEARLV	57	9	19	30	8066
VIF	DPDLADQLI	104	9	19	30	8067
VIF	DPGLADQLI	104	9	19	30	8068
VIF	KIKPPLPSV	164	9	19	30	8069
VIF	IIPKVSSEV	48	10	19	30	8070
VIF	IIPLGEARLV	56	10	19	30	8071
VIF	KVSSEV	50	8	20	31	8072
VIF	LVKIHIMYV	24	8	21	33	8073
VIF	SLVKIHIMYV	23	9	21	33	8074
VIF	GLITIGERDW	73	9	22	34	8075
VIF	IILKIGVSI	83	8	25	39	8076
VIF	IILGIGVSI	83	10	25	39	8077
VIF	IILQGVSI	83	8	26	41	8078
VIF	QGVSI	85	8	26	41	8079
VIF	IILQGVSI	83	10	26	41	8080
VIF	SLQYLALALI	149	11	27	42	8081
VIF	YLALALI	132	8	28	44	8082
VIF	LQYLALALI	130	10	28	44	8083
VIF	QVDRMRITW	12	10	31	48	8084
VIF	WQVDRMRITW	11	11	31	48	8085
VIF	YQAGINKV	140	8	38	59	8086
VIF	QVMIVWQV	5	8	43	67	8087
VIF	WQVMIVWQV	5	9	43	67	8088
VIF	QVMIVWQVDRM	6	11	43	67	8089
VIF	MIVWQVDRM	8	11	43	67	8090
VIF	SLVKIHIMY	23	8	44	69	8091
VIF	MIVWQVDRM	7	10	44	69	8092
VIF	MIVWQVDRM	8	9	46	72	8093
VIF	IWQVDRM	9	10	47	73	8094
VIF	WQVDRM	11	8	48	75	8095
VIF	IWQVDRM	9	8	59	92	8096
VIF	RPWLHGLGQY	36	10	10	16	8097
VIF	QQLLFVIF	63	8	10	16	8098
VIF	LQQLLFVIF	64	9	10	16	8099
VIF	QQLLFVIFRI	66	9	10	16	8100
VIF	QQLLFVIFRI	65	10	10	16	8101
VIF	LQQLLFVIFRI	64	11	10	16	8102
VIF	KQEA	27	8	11	17	8103
VIF	WLIGLGOY	38	8	11	17	8104
VIF	RIGCRHSRIGI	74	11	11	19	8105
VIF	RPWLHGLGQHI	36	11	12	19	8106
VIF	LLFVIFRI	67	8	12	19	8107
VIF	RIGCRHSRI	74	9	12	19	8108
VIF	QGHYNTY	43	8	13	20	8109
VIF	AVRIHPRI	30	8	14	22	8110

Table XIV
IIIY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	GQYIYET	43	8	14	22	8111
VPR	AVRIIFRIW	30	9	14	22	8112
VPR	IIYNTYGDW	45	10	14	22	8113
VPR	YIVTYGDW	45	10	14	22	8114
VPR	ELKSEAVRIIF	25	10	15	23	8115
VPR	CQHSRIGI	77	9	16	25	8116
VPR	LLEELKSEAV	22	10	16	25	8117
VPR	ELLEELKNEAV	21	11	16	25	8118
VPR	ELLEELKSEAV	21	11	16	25	8119
VPR	GQIYIYET	43	8	17	27	8120
VPR	LLEELKNEAV	22	10	17	27	8121
VPR	ELKNEAVRIIF	25	10	17	27	8122
VPR	IIYTYGDW	45	10	17	27	8123
VPR	WLIIGLQII	38	9	20	31	8124
VPR	WLIIGLQIIY	38	10	20	31	8125
VPR	IIKILQXLLF	60	11	33	52	8126
VPR	GVEAIKI	56	8	34	53	8127
VPR	AVRIIFRPW	30	9	34	53	8128
VPR	KILQQLFIIF	62	11	34	53	8129
VPR	ILQQLFIIF	63	10	35	55	8130
VPR	RILQQLFI	62	9	36	56	8131
VPR	ILQQLFI	63	8	37	58	8132
VPR	PQREPYNEW	10	9	37	58	8133
VPR	GPQREPYNEW	9	10	37	58	8134
VPR	AIRILQQLF	59	11	38	59	8135
VPR	DQGPQREPY	7	9	41	64	8136
VPR	IIKILQQLF	60	10	41	64	8137
VPR	QQLFIIF	65	8	44	69	8138
VPR	LLFIIFRI	67	8	44	69	8139
VPR	LQQLFIIF	64	9	44	69	8140
VPR	QLLFIIFRI	66	9	44	69	8141
VPR	QQLLFIIFRI	65	10	44	69	8142
VPR	LQQLFIIFRI	64	11	44	69	8143
VPR	RILQQLF	62	8	45	70	8144
VPR	CQHSRIGI	77	8	45	70	8145
VPR	RIGCQHSRIGI	74	11	45	70	8146
VPR	RIGCQHSRI	74	9	47	73	8147
VPR	KVDYRIVI	7	8	01	33	8148
VPR	KVDYRLGV	7	8	01	33	8149
VPR	RUDYRLGV	7	8	01	33	8150
VPR	KVDYRIVV	7	9	01	33	8151
VPR	KVDYRIVIVAF	7	11	01	33	8152
VPR	GVEMGIHIAFW	91	10	01	50	8153
VPR	RIKEIRDDSDY	64	11	01	50	8154
VPR	RIREIRDDSDY	64	11	01	50	8155
VPR	LIIAIVVW	26	8	01	16	8156
VPR	DOEELSALV	79	9	11	18	8157
VPR	IIAIVVW	12	9	11	17	8158
VPR	EMGHIAFW	89	8	11	17	8159
VPR	IIAIVVW	12	8	12	19	8160

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPV	IVFIEYRKI	36	9	12	19	8161
VPV	VVWTVTFIEY	31	10	12	19	8162
VPV	IVVWTVTFIEY	30	11	12	19	8163
VPV	ILRQRKIDRLI	46	11	13	20	8164
VPV	AIIVVWTVTF	29	9	14	22	8165
VPV	KIDRLIDRI	52	9	14	22	8166
VPV	AIIVVWTVFI	29	10	14	22	8167
VPV	IVVWTVTF	30	8	15	23	8168
VPV	VVWTVTFI	31	8	15	23	8169
VPV	KILRQRKI	45	8	15	23	8170
VPV	IVVWTVFI	30	9	15	23	8171
VPV	RQRKIDRLI	48	9	17	27	8172
VPV	IIAIVVWTVI	27	10	20	31	8173
VPV	IIAIVVWTVI	27	9	23	36	8174
VPV	AIIVVWTVI	29	8	29	45	8175

Table XV
HIV A01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
ENV	IGSQQAFY	361	8	01	25		R176
ENV	GKDLWVTYY	42	9	01	33		R177
ENV	GKDLWVTYY	42	10	01	33		R178
ENV	NTSPISRVA	376	10	01	33		R179
ENV	GTAQSSRAA	375	11	01	33		R180
ENV	DSSNSTGNY	218	9	01	20		R181
ENV	TNSSYTNDY	458	10	01	17		R182
ENV	WFDITNLW	767	10	10	16		R183
ENV	WMEWEREDN	723	11	10	16		R184
ENV	EWEREIDNY	725	9	11	17		R185
ENV	NMWQFVGKA	494	11	15	23		R186
ENV	HSFNCRGFFY	434	11	16	25		R187
ENV	WQEVGKAMY	496	9	18	28		R188
ENV	VSEFPHIYY	253	10	28	44		R189
ENV	KVSEPHIYY	252	11	28	44		R190
ENV	SPEPHIYY	254	9	31	48		R191
ENV	LQARVLAVIER	662	11	33	52		R192
ENV	LSIVNRVROGY	797	11	34	53		R193
ENV	RSCLFSY	858	8	35	55		R194
ENV	LRSLCLFSY	857	9	35	55		R195
ENV	IISFNCGFFY	434	11	35	55		R196
ENV	DMRDNRWSEL	552	11	37	58		R197
ENV	MIRDNRWSELY	553	10	40	63		R198
ENV	CASDAKAY	67	8	42	66	0.0010	R199
ENV	FCASDAKAY	66	9	42	66		R200
ENV	WRSELYKY	557	8	54	84		R201
GAG	ETIDKOLY	537	8	01	25		R202
GAG	EKEEKGLY	538	8	01	25		R203
GAG	KQEPIDKELY	535	10	01	25		R204
GAG	KQETIDKOLY	535	10	01	25		R205
GAG	AADKGVSONY	130	10	01	50		R206
GAG	ASAQQDLKGG	392	11	01	50		R207
GAG	ATAQQDLKGG	392	11	01	50		R208
GAG	AADKGVSON	129	11	02	18		R209
GAG	EADKGVSONY	129	10	04	36		R210
GAG	GNSQVSONY	140	10	12	23		R211
GAG	KQEPIDKELY	531	10	12	19		R212
GAG	SEELKSLY	74	8	12	19		R213
GAG	GSEELKSLY	73	9	12	19		R214
GAG	TGSEELKSLY	72	10	12	19		R215
GAG	NSSQVSONY	144	9	14	31		R216
GAG	SSQVSONY	145	8	15	31		R217
GAG	ASLYNTVATL	78	11	29	45	0.0900	R218
GAG	FRDYVDRFY	317	9	29	45		R219
GAG	PKEPERDY	313	8	63	98		R220
NEF	IIMARELIPEY	320	10	10	16		R221
NEF	IIMARELIPEY	320	11	10	16		R222
NEF	ARELIHIPEY	322	9	11	17		R223
NEF	YTPGHICIN	207	9	17	27		R224
NEF	RQDILDWVY	182	10	20	31		R225

Table XV
HIV A01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
NEF	ARELIPEYY	322	9	21	33		8226
NEF	ARELIPEY	322	8	24	38		8227
NEF	RQEILDWVY	182	10	32	50		8228
POL	TWETWTDY	589	9	10	16		8229
POL	TWETWTEY	589	9	10	16		8230
POL	ETWETWTD	588	10	10	16		8231
POL	ETWETWTE	588	10	10	16		8232
POL	AQEDIIEKY	760	8	11	17		8233
POL	ISIRIGPENPY	236	10	11	17		8234
POL	KISIRIGPENPY	235	11	11	17		8235
POL	STNETPGIRY	323	11	11	17		8236
POL	KTELQAIY	668	8	12	19		8237
POL	GQDQWYQIY	525	10	12	19		8238
POL	DKAQEIERY	758	10	15	23		8239
POL	AQEEIERY	760	8	16	25		8240
POL	NPIVIYQY	364	9	17	27	0.0011	8241
POL	PLDKDFRY	308	9	19	30		8242
POL	QQEFIPY	888	8	20	32		8243
POL	NPIVIYQY	364	9	23	36		8244
POL	DKAQEIEKY	758	10	25	39		8245
POL	AQEEIEKY	760	8	27	42		8246
POL	KQEGIPY	888	8	28	44		8247
POL	NRETKLGKAG	639	11	28	44		8248
POL	ETKLKAGY	641	9	35	55	0.0010	8249
POL	ITKIQNFRVY	969	10	36	57	0.0010	8250
POL	ITKIQNFRVY	969	11	36	57	0.0110	8251
POL	LKEPVIQVY	502	10	39	61	0.0010	8252
POL	LKEPVIQVY	502	9	41	64	0.0007	8253
POL	RKAKIRDY	1016	9	41	64		8254
POL	KISKIGPENPY	235	11	41	64		8255
POL	ISKIGPENPY	236	10	42	66	0.0130	8256
POL	NNETPGIRY	325	9	51	80	0.0007	8257
POL	NNETPGIRYQY	325	11	51	80	0.0004	8258
POL	ETPGIRYQY	327	9	52	81	0.0052	8259
POL	LVAVIVASGY	826	10	53	83	0.0390	8260
POL	VTVLDVGDAY	295	10	56	88	0.0041	8261
POL	NTPLVLKLY	610	10	57	89	0.0041	8262
POL	PAETGOETAY	842	10	58	91	0.0130	8263
POL	PAETGOETAY	841	11	58	91		8264
POL	ETGOETAY	844	8	59	92		8265
POL	VLDVGDAY	297	8	60	94	0.0004	8266
POL	QKEPFLWMG	411	11	63	98		8267
VIF	GVSEWRLLR	87	11	10	16		8268
VIF	SEWRLLR	89	9	11	17		8269
VIF	VSEWRLLR	88	10	11	17		8270
VIF	GLADQLHIMH	106	11	11	17		8271
VIF	LADQLHIMH	107	10	13	20		8272
VIF	IVSPRCEY	133	8	14	22		8273
VIF	LADQLHILY	107	10	14	22		8274
VIF	LADQLHILY	107	9	15	23		8275

Table XV
HIV A01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
VIF	KSLVKIIMY	22	9	18	28		8276
VIF	WKSIVKIIIM	21	10	18	28		8277
VIF	NSLVKIIIMY	22	9	24	38		8278
VIF	WNSLVKIIIM	21	10	24	38		8279
VPR	PEDQIQREPY	5	11	37	58		8280
VPU	WTIVFIY	34	8	12	19		8281

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	GIGPGQTF	360	8	01	33		8282
ENV	SIGSGOAF	360	8	01	33		8283
ENV	IGPGQTFY	361	8	01	25		8284
ENV	IGSQAFY	361	8	01	25		8285
ENV	GTAGNSSR	375	8	01	33		8286
ENV	TAGNSSRA	376	8	01	33		8287
ENV	KLREIRQF	405	8	01	25		8288
ENV	ADNLWTVVY	42	9	01	33		8289
ENV	GIGPGQTFY	360	9	01	33		8290
ENV	SIGSGQAFY	360	9	01	33		8291
ENV	IGPGQTFYA	361	9	01	25		8292
ENV	GTAGNSSRA	375	9	01	33		8293
ENV	NTSPRSYA	376	9	01	33		8294
ENV	TAGNSSRAA	376	9	01	33		8295
ENV	ADNLWTVVY	42	10	01	33		8296
ENV	EGKNEINDY	217	10	01	33		8297
ENV	GIGPGQTFYA	360	10	01	33		8298
ENV	GTAGNSSRAA	375	10	01	33		8299
ENV	NTSPRSVAY	376	10	01	33		8300
ENV	TAGNSSRAAY	376	10	01	33		8301
ENV	FGLGALFLGF	597	10	01	33		8302
ENV	VGLGAVFLGF	597	10	01	33		8303
ENV	GTAGNSSRAA	375	11	01	33		8304
ENV	KLREIROFENK	405	11	01	25		8305
ENV	QLYATVYA	34	8	01	50		8306
ENV	INIITPII	584	8	01	50		8307
ENV	VISTRTHIR	584	8	01	50		8308
ENV	STRTHIREK	586	8	01	50		8309
ENV	NANITPCR	478	9	01	50		8310
ENV	INIITPIIR	584	9	01	50		8311
ENV	ISTRTHIREK	585	9	01	50		8312
ENV	NIITPIREK	586	9	01	50		8313
ENV	STRTHIREK	586	9	01	50		8314
ENV	ISTRTHIREK	585	10	01	50		8315
ENV	NIITPIREK	586	10	01	50		8316
ENV	STRTHIREK	586	10	01	50		8317
ENV	ISTRTHIREK	585	10	01	50		8318
ENV	ITEGNITLQCR	478	11	01	50		8319
ENV	NANITPCR	478	11	01	50		8320
ENV	INIITPIREK	584	11	01	50		8321
ENV	VISTRTHIREK	584	11	01	50		8322
ENV	ISTRTHIREK	585	11	01	50		8323
ENV	NIITPIREK	586	11	01	50		8324
ENV	VTSTGNSA	161	8	01	20		8325
ENV	DSSNSTGNY	218	9	01	20		8326
ENV	STNGTETF	537	8	01	17		8327
ENV	STNGTETF	537	9	01	17		8328
ENV	NDTENNTET	537	10	01	17		8329
ENV	NTEINKTETF	537	10	01	17		8330
ENV	NTTGNTTETF	537	10	01	17		8331

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
ENV	NDTENNTETFR	537	11	01	17		8332
ENV	NTETNKTETFR	537	11	01	17		8333
ENV	NTTGNITETFR	537	11	01	17		8334
ENV	NGSENGTETFR	537	10	02	33		8335
ENV	NGSENGTETFR	537	11	02	33		8336
ENV	GSENGTETFR	538	9	02	18		8337
ENV	GSENGTETFR	538	10	02	18		8338
ENV	TIGAMFLGF	599	9	03	27		8339
ENV	NDITLPCR	477	9	03	20		8340
ENV	NDITLPCR	477	11	03	20		8341
ENV	MLGAMFLGF	599	9	04	36		8342
ENV	RGWEALKY	895	8	06	19		8343
ENV	KGRLGWEGIL	891	11	08	27		8344
ENV	LGWEGLKY	895	8	09	29		8345
ENV	RLGWEGILKY	894	9	09	29		8346
ENV	GLRLGWEGILK	892	11	09	29		8347
ENV	LGRRGWEGALK	883	10	09	15		8348
ENV	LLGRRGWEGAL	882	11	09	15		8349
ENV	ELGRRGWEGAL	881	10	10	16		8350
ENV	ELGRRGWEGAL	881	10	10	16		8351
ENV	ELGRRGWEGAL	881	10	10	16		8352
ENV	ELGRRGWEGAL	881	10	10	16		8353
ENV	ELGRRGWEGAL	881	10	10	16		8354
ENV	ELGRRGWEGAL	881	10	10	16		8355
ENV	ELGRRGWEGAL	881	10	10	16		8356
ENV	ELGRRGWEGAL	881	10	10	16		8357
ENV	ELGRRGWEGAL	881	10	10	16		8358
ENV	ELGRRGWEGAL	881	10	10	16		8359
ENV	ELGRRGWEGAL	881	10	10	16		8360
ENV	ELGRRGWEGAL	881	10	10	16		8361
ENV	ELGRRGWEGAL	881	10	10	16		8362
ENV	ELGRRGWEGAL	881	10	10	16		8363
ENV	ELGRRGWEGAL	881	10	10	16		8364
ENV	ELGRRGWEGAL	881	10	10	16		8365
ENV	ELGRRGWEGAL	881	10	10	16		8366
ENV	ELGRRGWEGAL	881	10	10	16		8367
ENV	ELGRRGWEGAL	881	10	10	16		8368
ENV	ELGRRGWEGAL	881	10	10	16		8369
ENV	ELGRRGWEGAL	881	10	10	16		8370
ENV	ELGRRGWEGAL	881	10	10	16		8371
ENV	ELGRRGWEGAL	881	10	10	16		8372
ENV	ELGRRGWEGAL	881	10	10	16		8373
ENV	ELGRRGWEGAL	881	10	10	16		8374
ENV	ELGRRGWEGAL	881	10	10	16		8375
ENV	ELGRRGWEGAL	881	10	10	16		8376
ENV	ELGRRGWEGAL	881	10	10	16		8377
ENV	ELGRRGWEGAL	881	10	10	16		8378
ENV	ELGRRGWEGAL	881	10	10	16		8379
ENV	ELGRRGWEGAL	881	10	10	16		8380
ENV	ELGRRGWEGAL	881	10	10	16		8381

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
ENV	EGIEEGGER	828	10	10	16		8382
ENV	PIIYCTPAGFA	260	11	10	16		8383
ENV	GFALKCNDKK	268	11	10	16		8384
ENV	FAILKNDKKF	269	11	10	16		8385
ENV	GDIIGDIRQAI	371	11	10	16		8386
ENV	NVPWNSSWSN	693	11	10	16		8387
ENV	WMEWERGIDN	723	11	10	16		8388
ENV	NSAVSLLNAT	916	11	10	16		8389
ENV	IAIAVAEGTDR	925	11	10	16		8390
ENV	RGWEALKY	886	8	11	18		8391
ENV	GIGAVFLGF	598	9	11	18		8392
ENV	KLWTVVY	44	8	11	17		8393
ENV	AVGIGAVF	595	8	11	17		8394
ENV	RAVGIGAVF	594	9	11	17		8395
ENV	AVGIGAVFLGF	595	11	11	17		8396
ENV	TIITQACPK	244	8	11	17		8397
ENV	YCTPAGFA	263	8	11	17		8398
ENV	RIGMQTF	357	8	11	17		8399
ENV	IQPGQTFY	358	8	11	17		8400
ENV	LFLGFLGA	603	8	11	17		8401
ENV	LAVERYLR	667	8	11	17		8402
ENV	NLCFSYII	859	8	11	17		8403
ENV	SAVSLINA	917	8	11	17		8404
ENV	VSLNATA	919	8	11	17		8405
ENV	LQMLMCSA	27	9	11	17		8406
ENV	RIGMQTFY	357	9	11	17		8407
ENV	ITTHSFNCR	431	9	11	17		8408
ENV	NITLPCRK	482	9	11	17		8409
ENV	ALFLGFLGA	602	9	11	17		8410
ENV	LFLGFLGAA	603	9	11	17		8411
ENV	VLAVERYLR	666	9	11	17		8412
ENV	ISNLWYIK	770	9	11	17		8413
ENV	NLCFSYIIR	859	9	11	17		8414
ENV	AVSLLNATA	918	9	11	17		8415
ENV	GDIIGDIRQA	371	10	11	17		8416
ENV	EITTHSFNCR	430	10	11	17		8417
ENV	VGIGAVFLGF	596	10	11	17		8418
ENV	GALFLGFLGA	601	10	11	17		8419
ENV	ALFLGFLGAA	602	10	11	17		8420
ENV	SAVSLNATA	917	10	11	17		8421
ENV	VSLNATAIA	919	10	11	17		8422
ENV	YATGDIIGDIR	368	11	11	17		8423
ENV	GALFLGFLGAA	601	11	11	17		8424
ENV	ISNLWYIKIF	770	11	11	17		8425
ENV	DLRNLCFSYII	856	11	11	17		8426
ENV	NLCFSYIIRL	859	11	11	17		8427
ENV	AVSLLNATAIA	918	11	11	17		8428
ENV	PTRIQQLERA	951	11	11	17		8429
ENV	TGDIIGDIR	370	9	12	19		8430
ENV	DIIGDIRQA	372	9	12	19		8431

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0.001	SEQ ID NO.
ENV	EAQIILLK	646	8	12	19		8432
ENV	GMLMCSA	28	8	12	19		8433
ENV	ILKCNKK	271	8	12	19		8434
ENV	TTTSHNCR	432	8	12	19		8435
ENV	IGAVFLGF	600	8	12	19		8436
ENV	MTWMEWER	721	8	12	19		8437
ENV	GGENDRR	834	8	12	19		8438
ENV	AILKCNKK	270	9	12	19		8439
ENV	ILKCNKKF	271	9	12	19		8440
ENV	LAEEVVIR	312	9	12	19	0.00002	8441
ENV	AMFLGLGA	602	9	12	19		8442
ENV	NMTWMEWER	720	9	12	19		8443
ENV	GIEEGGER	829	9	12	19		8444
ENV	EGGERDRR	833	9	12	19		8445
ENV	RSIRLVNGF	841	9	12	19		8446
ENV	WQIELKNSA	910	9	12	19		8447
ENV	WSQIELKNSA	910	9	12	19		8448
ENV	KITLFCASDA	60	10	12	19		8449
ENV	AILKCNKKF	270	10	12	19		8450
ENV	SLAEVVIR	311	10	12	19		8451
ENV	ATGDIIGDIR	369	10	12	19		8452
ENV	IINMWQEVGK	492	10	12	19		8453
ENV	GAMFLGFLGA	601	10	12	19		8454
ENV	AMFLGFLGAA	602	10	12	19		8455
ENV	AIEAQHLLK	644	10	12	19		8456
ENV	QDLLALDKWA	753	10	12	19		8457
ENV	SIRLVSGFLA	842	10	12	19		8458
ENV	LLQYWSQELK	906	10	12	19		8459
ENV	AIIIIIPRRIR	946	10	12	19		8460
ENV	PTRIROGLER	951	10	12	19		8461
ENV	KITLFCASDA	60	11	12	19		8462
ENV	GSLAEVVIR	310	11	12	19		8463
ENV	TTTSHNCRGE	432	11	12	19		8464
ENV	QIINMWQEVG	491	11	12	19		8465
ENV	IINMWQEVGK	492	11	12	19		8466
ENV	GAMFLGFLGA	601	11	12	19		8467
ENV	ITKWLWYKIF	770	11	12	19		8468
ENV	GIEEGGERDR	829	11	12	19		8469
ENV	RSIRLVSGFLA	841	11	12	19		8470
ENV	NLLQYWSQEL	905	11	12	19		8471
ENV	RAIIIIIPRRIR	945	11	12	19		8472
ENV	NTSVITQA	241	8	13	20		8473
ENV	SVEINCTR	340	8	13	20		8474
ENV	GDIIGDIR	371	8	13	20		8475
ENV	MFLGFLGA	603	8	13	20		8476
ENV	KLTWVGK	653	8	13	20		8477
ENV	SIRLVNGF	842	8	13	20		8478
ENV	SIRLVSGF	842	8	13	20		8479
ENV	RLVNGFLA	844	8	13	20		8480
ENV	RAIIIIIPRRIR	945	8	13	20		8481

Table XVI
 HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	AILIIPRR	946	8	13	20		8482
ENV	KAKRRVVOR	579	9	13	20		8483
ENV	MFLGFLGAA	603	9	13	20	0.0002	8484
ENV	RSIRLVSGF	841	9	13	20		8485
ENV	RAILIIIPRR	945	9	13	20		8486
ENV	ILIIIPRIIR	947	9	13	20		8487
ENV	SGGDPEIVMII	425	10	13	20		8488
ENV	LLKLTIVGK	651	10	13	20		8489
ENV	NTSVITQACPK	241	11	13	20		8490
ENV	CTNVSTVQCT	285	11	13	20		8491
ENV	SSGGDLEITTH	424	11	13	20		8492
ENV	SSGGDPEIVMII	424	11	13	20		8493
ENV	VMIISFNCGE	432	11	13	20		8494
ENV	PTKAKRRVQ	576	11	13	20		8495
ENV	KAKRRVVORE	579	11	13	20		8496
ENV	HLLKLTIVGK	650	11	13	20		8497
ENV	VGGUGLRIIF	784	11	13	20		8498
ENV	SLLNATAIAVA	920	11	13	20		8499
ENV	TGEIGDIR	370	9	14	23		8500
ENV	NTSAITQA	241	8	14	22		8501
ENV	AUTOACPK	244	8	14	22		8502
ENV	GDPEIVMII	427	8	14	22		8503
ENV	QDLLALDK	753	8	14	22		8504
ENV	NATAIAVA	923	8	14	22		8505
ENV	SAITQACPK	243	9	14	22		8506
ENV	FAILKCNCK	269	9	14	22		8507
ENV	GDDPEIVMII	426	9	14	22	0.0002	8508
ENV	TITLPCRIK	482	9	14	22		8509
ENV	SLLNATAIA	920	9	14	22		8510
ENV	NENTSAITQA	239	10	14	22		8511
ENV	TSAITQACPK	242	10	14	22		8512
ENV	TSVITQACPK	242	10	14	22		8513
ENV	GFAILKCNCK	268	10	14	22		8514
ENV	GDPEIVMISF	427	10	14	22		8515
ENV	IFAVLSIVNR	793	10	14	22		8516
ENV	LLNATAIAVA	921	10	14	22		8517
ENV	NTSAITQACPK	241	11	14	22		8518
ENV	VITQACPKVSF	244	11	14	22		8519
ENV	AGFAILKCNCK	267	11	14	22		8520
ENV	GGDPEIVMISF	426	11	14	22		8521
ENV	ITNLWLYIKIF	770	11	14	22		8522
ENV	IIFAVLSIVNR	792	11	15	24		8523
ENV	KIEPLGVPTK	568	11	15	24		8524
ENV	FDPIPIIY	255	8	15	23		8525
ENV	PAGYAILK	266	8	15	23		8526
ENV	NMWQEVGK	494	8	15	23		8527
ENV	LLNATAIA	921	8	15	23		8528
ENV	NMWQEVGKA	494	9	15	23		8529
ENV	DLALDKWA	754	9	15	23		8530
ENV	ITNLWLYIK	770	9	15	23		8531

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	SEQ ID NO.
ENV	GLGLRIIF	786	9	15	23		8532
ENV	DDLNLCLF	855	9	15	23		8533
ENV	SGDLEITTI	425	10	15	23		8534
ENV	IFRPGGDMR	545	10	15	23		8535
ENV	GLGLRIIF	785	10	15	23		8536
ENV	GLGLRIIFA	786	10	15	23		8537
ENV	WDDLRLNCLF	854	10	15	23		8538
ENV	NMWQEVGKA	494	11	15	23		8539
ENV	EIRPGGDMR	544	11	15	23		8540
ENV	GLGLRIIFA	785	11	15	23		8541
ENV	DDLRLNCLFSY	855	11	15	23		8542
ENV	SFNCRGFE	437	8	16	25		8543
ENV	LIGLRIIF	787	8	16	25		8544
ENV	VSGFLALA	846	8	16	25		8545
ENV	IISNCRGIEF	434	9	16	25		8546
ENV	SFNCRGIEFF	437	9	16	25		8547
ENV	ITKWLWYIK	770	9	16	25		8548
ENV	LIGLRIIFA	787	9	16	25		8549
ENV	LVSGLALA	845	9	16	25		8550
ENV	IISNCRGIEFE	434	10	16	25		8551
ENV	SFNCRGIEFFY	437	10	16	25		8552
ENV	RLVSGFLALA	844	10	16	25		8553
ENV	DLRLNCLFSY	856	10	16	25		8554
ENV	TTIISNCGGE	432	11	16	25		8555
ENV	IISNCRGIEFFY	434	11	16	25		8556
ENV	RLINCNTSA	236	9	17	27		8557
ENV	KAYDTEVII	72	8	17	27		8558
ENV	LINCNTSA	237	8	17	27		8559
ENV	VITQACPK	244	8	17	27		8560
ENV	RVVQREKR	587	8	17	27	0.0003	8561
ENV	VVQREKRA	588	8	17	27		8562
ENV	IGLRIIFA	788	8	17	27		8563
ENV	DLRLNCLF	856	8	17	27		8564
ENV	SVITQACPK	243	9	17	27		8565
ENV	VAPTKAKRR	574	9	17	27	0.0002	8566
ENV	RVVQREKRA	587	9	17	27		8567
ENV	DAKAYDTEVII	70	10	17	27		8568
ENV	YDTEVINVWA	74	10	17	27		8569
ENV	GVAPTAKARR	573	10	17	27		8570
ENV	VFAVLSIVNR	703	10	17	27		8571
ENV	SDAKAYDTEV	69	11	17	27		8572
ENV	NCTEIVINWAT	75	11	17	27		8573
ENV	NCTRPNINNR	344	11	17	27		8574
ENV	LGVAPTAKAR	572	11	17	27		8575
ENV	IVFAVLSIVNR	792	11	17	27		8576
ENV	PHIYCTPA	260	8	18	28		8577
ENV	EVGKAMYA	498	8	18	28		8578
ENV	DTEVINVWA	75	9	18	28		8579
ENV	VLAVERYLK	666	9	18	28		8580
ENV	ELLELDKWA	754	9	18	28		8581

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
ENV	KIEPLGVA	568	8	23	37		8632
ENV	LGVAPTKA	572	8	23	36		8633
ENV	TVQCTIIGIR	290	9	23	36	0.0018	8634
ENV	PLGVAPTKA	571	9	23	36		8635
ENV	STVQCTIIGIR	289	10	23	36		8636
ENV	VVKIEPLGVA	566	10	23	36		8637
ENV	QSNLLRAIEA	638	10	23	36		8638
ENV	ATTLFCASD	59	11	23	36		8639
ENV	VSTVQCTIIGIR	288	11	23	36		8640
ENV	KVKIEPLGVA	565	11	23	36		8641
ENV	ATTLFCA	59	8	24	38		8642
ENV	EATTLFCA	58	9	24	38		8643
ENV	TTLFCASDA	60	10	24	38		8644
ENV	TFRPGGDMR	545	10	24	38		8645
ENV	ALAWDILR	851	8	25	39		8646
ENV	LALAWDDL	850	9	25	39		8647
ENV	IVQQNNLLR	634	10	25	39	0.0024	8648
ENV	FLALAWDDL	849	10	25	39		8649
ENV	GIVQQNNLLR	633	11	25	39		8650
ENV	IVQQNNLLRA	634	11	25	39		8651
ENV	GFLALAWDDL	848	11	25	39		8652
ENV	ITLPCRIK	483	8	26	41		8653
ENV	PLGVAPTK	571	8	26	41		8654
ENV	LAVERYLK	667	8	26	41		8655
ENV	IVQQSNLLR	634	10	26	41		8656
ENV	GIVQQSNLLR	633	11	26	41		8657
ENV	IVQQSNLLRA	634	11	26	41		8658
ENV	LDKWASLWN	758	11	26	41		8659
ENV	IIGIRQAI	377	9	27	44		8660
ENV	ESQNOQEK	743	8	27	42		8661
ENV	PIIYCAPAGF	260	10	27	42		8662
ENV	PIIYCAPAGFA	260	11	27	42		8663
ENV	VGGLGLRIVF	784	11	27	42		8664
ENV	IIGIRQAI	378	8	28	44		8665
ENV	YCAPAGFA	263	8	28	44		8666
ENV	TVQCTIIGIK	290	9	28	44	0.0021	8667
ENV	CTRPNNNR	345	9	28	44		8668
ENV	ASITLTQA	619	9	28	44		8669
ENV	VSEPIPIHY	253	10	28	44		8670
ENV	STVQCTIIGIK	289	10	28	44		8671
ENV	AASITLTQA	618	10	28	44		8672
ENV	ASITLTQAR	619	10	28	44		8673
ENV	KVSEPIPIHY	252	11	28	44		8674
ENV	YCAPAGFAILK	263	11	28	44		8675
ENV	VSTVQCTIIGIK	288	11	28	44		8676
ENV	GAASITLTQA	617	11	28	44		8677
ENV	AASITLTQAR	618	11	28	44		8678
ENV	LIGLRIVF	787	8	29	45		8679
ENV	VSEPIPIH	253	9	29	45		8680
ENV	GLIGLRIVF	786	9	29	45		8681

Table XVI
 HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	FSYIURLDF	863	9	18	28		8582
ENV	PIPIIVCTPA	258	10	18	28		8583
ENV	RVLAVERYLK	665	10	18	28		8584
ENV	LFSYIURLDF	862	10	18	28		8585
ENV	CFESYIURLDF	861	11	18	28		8586
ENV	NCRGIEFFY	439	8	19	30		8587
ENV	GVAPTAK	573	8	19	30		8588
ENV	VAPTKAKR	574	8	19	30		8589
ENV	VFLGFLGA	603	8	19	30		8590
ENV	LLALDKWA	755	8	19	30		8591
ENV	LGVAPTAK	572	9	19	30		8592
ENV	GVAPTAKR	573	9	19	30		8593
ENV	AVFLGFLGA	602	9	19	30		8594
ENV	VFLGFLGAA	603	9	19	30		8595
ENV	SGKLICTTA	685	9	19	30		8596
ENV	PLGVAPTAK	571	10	19	30		8597
ENV	LGVAPTAKR	572	10	19	30		8598
ENV	GAVFLGFLGA	601	10	19	30		8599
ENV	AVFLGFLGAA	602	10	19	30		8600
ENV	CSGKLICTTA	684	10	19	30		8601
ENV	SSNIGLLLTR	516	11	19	30		8602
ENV	PLGVAPTAK	571	11	19	30		8603
ENV	GAVFLGFLGA	601	11	19	30		8604
ENV	GCSGKLICTTA	683	11	19	30		8605
ENV	AILKCNDK	270	8	20	31		8606
ENV	RLVSGFLA	844	8	20	31		8607
ENV	ETFRPGGDM	544	11	20	31		8608
ENV	LIEESQSQEK	740	11	20	31		8609
ENV	GDLEITTI	427	8	21	33		8610
ENV	YCNTSGLF	446	8	21	33		8611
ENV	LLELDKWA	755	8	21	33		8612
ENV	GGDLITTH	426	9	21	33		8613
ENV	DLEITTHSF	428	9	21	33		8614
ENV	LIGLRVFA	787	9	21	33		8615
ENV	GDLEITTHSF	427	10	21	33		8616
ENV	FFYCNISGLF	444	10	21	33		8617
ENV	GLIGLRVFA	786	10	21	33		8618
ENV	SFPIPIIYCA	234	11	21	33		8619
ENV	GGDLITTHSF	426	11	21	33		8620
ENV	FFYCNISGLF	443	11	21	33		8621
ENV	GGLIGLRVFA	785	11	21	33		8622
ENV	TAIAVAECTDR	925	11	21	33		8623
ENV	IGLRVFA	788	8	22	34		8624
ENV	RIVELLGR	878	8	22	34		8625
ENV	IVELLGRR	879	8	22	34	0.0550	8626
ENV	NCTRPNNTR	344	9	22	34		8627
ENV	CTRPNNTTRK	345	10	22	34		8628
ENV	PWVKEATITL	54	10	22	34		8629
ENV	TTTLFCASDA	60	11	22	34		8630
ENV							8631

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ°D101	SEQ ID NO.
ENV	ITQACPKVSF	245	10	29	45		8682
ENV	KVSEPIPIII	252	10	29	45		8683
ENV	CAPAGFAILK	264	10	29	45		8684
ENV	GGLIGLRIVF	785	10	29	45		8685
ENV	RSELYKYKVV	558	11	29	45		8686
ENV	IIGDIRQA	377	8	30	49		8687
ENV	WASLWNWF	761	8	30	47		8688
ENV	AVLSIVNR	795	8	31	48		8689
ENV	AVAEGTDIR	928	8	31	48		8690
ENV	VTFNFMWK	102	9	31	48		8691
ENV	SFEPIPIIY	254	9	31	48		8692
ENV	FAVLSIVNR	794	9	31	48		8693
ENV	SLCLFSYIIR	859	9	31	48		8694
ENV	IAVAEGTDR	927	9	31	48		8695
ENV	NYTFNFMW	101	10	31	48	0.0004	8696
ENV	AVLSIVNRVR	795	10	31	48		8697
ENV	RSCLFSYIIR	858	10	31	48		8698
ENV	AIAVAEGTDR	926	10	31	48		8699
ENV	FAVLSIVNRVR	794	11	31	48		8700
ENV	IDLRSLCLFSY	855	11	31	48		8701
ENV	SLCLFSYIIRLR	859	11	31	48		8702
ENV	ELYKYKVKV	560	9	32	51		8703
ENV	RVVEREKR	587	8	32	50		8704
ENV	VVEREKRA	588	8	32	50		8705
ENV	SITLTVOA	620	8	32	50		8706
ENV	ITLTVOAR	621	8	32	50		8707
ENV	SLCLFSYII	859	8	32	50		8708
ENV	RVVEREKRA	587	9	32	50		8709
ENV	SITLTVOAR	620	9	32	50		8710
ENV	RSCLFSYII	858	9	32	50		8711
ENV	DLRSLCLFSYII	856	11	32	50		8712
ENV	SFEPIPIII	254	8	33	52		8713
ENV	RVLAVERY	665	8	33	52	0.0009	8714
ENV	QARVLAVR	663	9	33	52		8715
ENV	DDLRSCLF	855	9	33	52		8716
ENV	QARVLAVERY	663	10	33	52		8717
ENV	WDLRLSCLF	854	10	33	52		8718
ENV	QLQARVLAVE	661	11	33	52		8719
ENV	IMVGGGLGLR	781	11	34	54		8720
ENV	GVPIVWKEA	52	8	34	53		8721
ENV	YGPIVWKEA	51	9	34	53		8722
ENV	RIRQLERA	953	9	34	53		8723
ENV	LLQLTVWGIR	651	10	34	53	0.0055	8724
ENV	ILLQLTVWGI	650	11	34	53		8725
ENV	LSIVNRVROGY	797	11	34	53		8726
ENV	NLWVTYVY	44	8	35	56		8727
ENV	NCGGEFFY	439	8	35	55		8728
ENV	RSCLFSY	858	8	35	55		8729
ENV	EVINNVWATH	77	9	35	55		8730
ENV	SFNCGGEFF	437	9	35	55		8731

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SIQ ID NO.
ENV	NITGLLLTR	519	9	35	55	0.0004	8732
ENV	EVINWATHA	77	10	35	55		8733
ENV	IISFNCGGEFF	434	10	35	55		8734
ENV	SFNCGGEFF	437	10	35	55		8735
ENV	DLRSLCLFSY	856	10	35	55		8736
ENV	IISFNCGGEFF	434	11	35	55		8737
ENV	SFNCGGEF	437	8	36	56		8738
ENV	IISFNCGGEF	434	9	36	56		8739
ENV	PIIIYCAPA	258	10	36	56		8740
ENV	GGGDMRDNW	549	10	36	56		8741
ENV	MVGLIGLR	782	10	36	56		8742
ENV	SIVNRVROGY	798	10	36	56	0.0008	8743
ENV	PGGDMRDN	548	11	36	56		8744
ENV	PIIIYCAPA	260	8	37	58		8745
ENV	ITGLLLTR	520	8	37	58		8746
ENV	IMRDINWRSIEL	552	11	37	58		8747
ENV	PAGFAILK	266	8	38	59		8748
ENV	LSIVNRVR	797	8	38	59		8749
ENV	DLRSLCLF	856	8	38	59		8750
ENV	VLSIVNRVR	796	9	38	59		8751
ENV	IVNIVROGY	799	9	38	59		8752
ENV	IISLWDQSLK	121	10	38	59	0.0410	8753
ENV	DIISLWDQSLK	120	11	38	59		8754
ENV	GDMRDNR	551	8	39	61		8755
ENV	GGDMRDNR	550	9	39	61		8756
ENV	QACPKVSF	248	8	40	63		8757
ENV	PIIIYCA	258	8	40	63		8758
ENV	RDNWRSLEY	554	9	40	63	0.0003	8759
ENV	RDNWRSLEYK	554	10	40	63	0.0008	8760
ENV	TLFCASDAKA	64	11	40	63		8761
ENV	RDNWRSLEYK	554	11	40	63		8762
ENV	GIKQLOARVLA	658	11	40	63		8763
ENV	QLOARVLA	661	8	41	64		8764
ENV	TVYYGVVVK	48	10	41	64	3.8000	8765
ENV	VTYYGVVW	47	11	41	64	0.8600	8766
ENV	CASDAKAY	67	8	42	66		8767
ENV	LCLFSYLR	860	8	42	66		8768
ENV	FCASDAKAY	66	9	42	66		8769
ENV	IVGGLIGLR	783	9	42	66		8770
ENV	CLFSYIHLR	861	9	42	66		8771
ENV	LFCASDAKAY	65	10	42	66	0.0004	8772
ENV	GAAGSTMGA	610	10	42	66		8773
ENV	LCLFSYIHLR	860	10	42	66		8774
ENV	LGAAGSTMGA	609	11	42	66		8775
ENV	VGGLIGLR	784	8	43	67		8776
ENV	QLTVWGK	653	8	44	69		8777
ENV	LFSYIHLR	862	8	44	69		8778
ENV	RIRQLER	953	8	44	69		8779
ENV	TLFCASDAK	61	11	44	69		8780
ENV	AAGSTMGA	611	9	45	70		8781

Table XVI
 IIIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	TLFCASDAKA	64	10	46	72		8782
ENV	SLWDQSLK	123	8	47	75		8783
ENV	ISLWDQSLK	122	9	47	73	0.0048	8784
ENV	WDQSLKPCVK	125	10	47	73		8785
ENV	RVRQGYSPLSF	802	11	47	73		8786
ENV	QSLKPCVK	127	8	48	75		8787
ENV	FLGLGAA	604	8	48	75		8788
ENV	QQYSPLSF	805	8	48	75		8789
ENV	TVWGKQLQA	655	11	48	75		8790
ENV	GKQLQAR	658	8	49	77	0.0004	8791
ENV	WGKQLQAR	657	9	49	77		8792
ENV	TVWGKQLQA	655	10	49	77		8793
ENV	LTWVGKQLQ	654	11	49	77		8794
ENV	FCASDAKA	66	8	50	78		8795
ENV	AGSTMGA	612	8	50	78		8796
ENV	WLWYKIF	773	8	50	78		8797
ENV	LFCASDAKA	65	9	50	78		8798
ENV	LGIWGCSGK	679	9	50	78	0.0097	8799
ENV	TLFCASDAK	61	10	50	78	0.0920	8800
ENV	LLGIWGCSGK	678	10	50	78	0.1200	8801
ENV	NLLRAIEAQH	640	11	50	78		8802
ENV	QLLGIWGCSG	677	11	50	78		8803
ENV	VSTVQCTH	288	8	51	80		8804
ENV	NLLRAIEA	640	8	51	80		8805
ENV	RAIEAQH	643	8	51	80		8806
ENV	WGKQLQA	657	8	51	80		8807
ENV	NVSTVQCTH	287	9	51	80		8808
ENV	LLRAIEAQH	641	10	51	80		8809
ENV	GIWGCSGK	680	8	52	81		8810
ENV	TLFCASDA	61	9	52	81		8811
ENV	TLFCASDAK	64	9	52	81	0.0930	8812
ENV	TLFCASDA	64	8	54	84		8813
ENV	RSELYKYK	558	8	54	84		8814
ENV	LLNGSLA	306	8	55	86		8815
ENV	QLLNGSLA	305	9	55	86		8816
ENV	GAAAGSTMGA	610	9	55	86		8817
ENV	LGAAGSTMGA	609	10	55	86		8818
ENV	STQLLNGSLA	303	11	55	86		8819
ENV	FLGAAGSTMG	608	11	55	86		8820
ENV	LFCASDAK	65	8	57	89		8821
ENV	AAGSTMGA	611	8	58	91		8822
GAG	EDTSARQA	133	8	01	33		8823
GAG	AAAIMMQK	405	8	01	25		8824
GAG	SATIMMQR	405	8	01	25		8825
GAG	TAPPPESF	508	8	01	33		8826
GAG	KDKDKELY	535	8	01	25		8827
GAG	ETIDKDLV	537	8	01	25		8828
GAG	NSATIMMQR	404	9	01	33		8829
GAG	PTAPPPESF	507	9	01	33		8830
GAG	TAPPPESFR	508	9	01	33		8831

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	NGKQANFLGK	461	10	01	25		8832
GAG	NGRQANFLGK	461	10	01	25		8833
GAG	PTAPPESFR	507	10	01	33		8834
GAG	TAPPESFR	508	10	01	33		8835
GAG	TIDKDLPLA	538	10	01	25		8836
GAG	AAIMQKSN	405	11	01	25		8837
GAG	SATIMQRGN	405	11	01	25		8838
GAG	NGKQANFLGK	461	11	01	25		8839
GAG	NGRQANFLGK	461	11	01	25		8840
GAG	PTAPPESFR	507	11	01	33		8841
GAG	KDKKELYPL	535	11	01	25		8842
GAG	ETIDKDLPLA	537	11	01	25		8843
GAG	PAADKEK	123	8	01	50		8844
GAG	ASAQDLK	392	8	01	50		8845
GAG	ATAQDLK	392	8	01	50		8846
GAG	PAEPTAPP	492	9	01	50		8847
GAG	AADKGVSONY	130	10	01	50		8848
GAG	SAQDLKGGY	393	10	01	50		8849
GAG	TAQDLKGGY	393	10	01	50		8850
GAG	GTRPGNYVQR	480	10	01	50		8851
GAG	ITSLPKQEQK	526	10	01	50		8852
GAG	PAADKEDIS	123	11	01	50		8853
GAG	GANSHVGDY	276	11	01	50		8854
GAG	ASQDLKGG	392	11	01	50		8855
GAG	ATAQDLKGG	392	11	01	50		8856
GAG	ETSLPKQEQK	525	11	01	50		8857
GAG	YTAVFMQR	405	8	02	50		8858
GAG	TAPPESF	508	8	02	67		8859
GAG	PTAPPESF	507	9	02	67		8860
GAG	TAPPESFR	508	9	02	67		8861
GAG	PTAPPESFR	507	10	02	67		8862
GAG	TAPPESFR	508	10	02	67		8863
GAG	PTAPPESFR	507	11	02	67		8864
GAG	EGRQANFLGK	462	11	02	67		8865
GAG	AADKGVSONY	129	11	02	100		8866
GAG	EADKGVSONY	129	11	02	18		8867
GAG	AAIMQK	400	10	04	36		8868
GAG	AAIMQKSNF	406	8	04	19		8869
GAG	AAIMQKSNF	406	10	06	15		8870
GAG	AAIMQKSNF	406	11	06	15		8871
GAG	KTKCFNCGK	421	10	08	16		8872
GAG	NIMMQRGNF	407	9	10	17		8873
GAG	GARASILR	2	8	10	16		8874
GAG	PGNFQSR	483	8	10	16		8875
GAG	MGARASILR	1	9	10	16		8876
GAG	KIWSSKGR	472	9	10	16		8877
GAG	TGNSSQVSON	139	11	10	16		8878
GAG	NFLGKIWFSSK	468	11	10	16		8879
GAG	NFLQNRPEPTA	485	11	10	16		8880
GAG	PVATQDMR	243	8	10	16		8881

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
GAG	MMQKSFK	409	8	10	16		8882
GAG	MMQRGNFK	409	8	10	16		8883
GAG	KLIDKWEKIR	12	9	10	16		8884
GAG	GGKKYKLLK	24	9	10	16	0.0001	8885
GAG	RDTEALDK	97	9	10	16		8886
GAG	ALSPRTLNA	167	9	10	16		8887
GAG	IMMQKSFK	408	9	10	16		8888
GAG	LQKIWPSSK	470	9	10	16		8889
GAG	PGKKKYKLLK	23	10	10	16		8890
GAG	GGKKKYKLLKII	24	10	10	16		8891
GAG	QALSPRTLNA	166	10	10	16		8892
GAG	AGPVATPGMR	241	10	10	16		8893
GAG	GASLEEMMTA	364	10	10	16		8894
GAG	FLGIWPSK	469	10	10	16		8895
GAG	FLQNRPEPTA	486	10	10	16		8896
GAG	TAPPALSFQF	496	10	10	16		8897
GAG	KLIDKWEKIRL	12	11	10	16		8898
GAG	PGKKKYKLLK	23	11	10	16		8899
GAG	LQKIWPSSKGR	470	11	10	16		8900
GAG	PTAPPAISFGF	495	11	11	16		8901
GAG	ATIMMQRGNF	406	10	11	28		8902
GAG	ATIMMQRGNF	406	11	11	28		8903
GAG	PSQKQEMDK	528	10	11	18		8904
GAG	SSKGRPGNF	476	9	11	18		8905
GAG	TTSTLQEQIA	260	10	11	17		8906
GAG	DVKDTKEA	95	8	11	17		8907
GAG	PIPVGDIY	279	8	11	17		8908
GAG	SLEEMMTA	366	8	11	17		8909
GAG	MSQVTNSA	391	8	11	17		8910
GAG	IMMQKSFK	408	8	11	17		8911
GAG	IDVRDTKEA	94	9	11	17		8912
GAG	ASLEEMMTA	365	9	11	17		8913
GAG	AMSQVTNSA	390	9	11	17		8914
GAG	TIKCFNCGK	422	9	11	17		8915
GAG	TVKCFNCGK	422	9	11	17		8916
GAG	LAMSQVTNSA	389	10	11	17		8917
GAG	PSSKGRPGNF	475	10	11	17		8918
GAG	GTTSTLQEQIA	259	11	11	17		8919
GAG	TIMMQRGNF	407	10	12	21		8920
GAG	QTGSELR	71	8	12	19		8921
GAG	KSKKKAQQA	112	10	12	19		8922
GAG	KSKKKAQQA	112	11	12	19		8923
GAG	PGKKKYK	23	8	12	19		8924
GAG	TLYCVIQQ	86	8	12	19		8925
GAG	DTKEALEK	98	8	12	19		8926
GAG	MLNIVGGII	208	8	12	19		8927
GAG	NIVGGIIQA	210	8	12	19		8928
GAG	IVGGIIQA	211	8	12	19		8929
GAG	STLQEQIA	262	8	12	19		8930
GAG	PTSILDIR	303	8	12	19		8931

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.301$	SEQ ID NO.
GAG	LTSLSLF	549	8	12	19		8932
GAG	GSSELSLY	73	9	12	19		8933
GAG	ATLYCVIHK	85	9	12	19		8934
GAG	KD'KEALEK	97	9	12	19		8935
GAG	MMLNIVGGII	207	9	12	19		8936
GAG	NIYGGHQA	210	9	12	19		8937
GAG	TSTLQEQIA	261	9	12	19		8938
GAG	PLTSLKSLF	548	9	12	19		8939
GAG	PLTSLRSLF	548	9	12	19		8940
GAG	TGSELSRSLY	72	10	12	19		8941
GAG	VATLYCVIHK	84	10	12	19		8942
GAG	NAQGMVHQA	158	10	12	19		8943
GAG	NMMLNIVGGII	206	10	12	19		8944
GAG	MLNIVGGHQA	208	10	12	19		8945
GAG	YSPISLDIR	301	10	12	19		8946
GAG	RAEQASQIEVK	329	10	12	19		8947
GAG	RLRIGURKKY	20	11	12	19		8948
GAG	TVATLYCVIHK	83	11	12	19		8949
GAG	MMLNIVGGII	207	11	12	19		8950
GAG	MLNIVGGHQA	208	11	12	19		8951
GAG	TSLDIRQCPK	304	11	12	19		8952
GAG	TIMMQRGNE	407	9	13	22		8953
GAG	PGNFQNR	483	8	13	21		8954
GAG	IARNCRAPR	434	9	13	21		8955
GAG	KIWI'NSKGR	472	9	13	21		8956
GAG	NCKEGIIAR	427	10	13	21		8957
GAG	IARNCRAPRK	434	10	13	21		8958
GAG	IARNCRAPRKK	434	11	13	21		8959
GAG	NFLGKIWI'NSK	468	11	13	21		8960
GAG	KGRPGNFQNR	478	11	13	21		8961
GAG	KLKIIIVWA	31	8	13	20		8962
GAG	RIEYKDTK	93	8	13	20		8963
GAG	HIARNCIA	433	8	13	20		8964
GAG	LTSLSLSLF	349	8	13	20		8965
GAG	IVKFCNCGK	422	9	13	20		8966
GAG	CGKEGIIAR	428	9	13	20		8967
GAG	EGIIARNCR	431	9	13	20		8968
GAG	LGIKIWI'NSK	470	9	13	20		8969
GAG	KLKIIIVWASR	31	10	13	20		8970
GAG	RIEYKDTKEA	93	10	13	20		8971
GAG	TILRALGPGA	356	10	13	20		8972
GAG	EGIIARNCR	431	10	13	20		8973
GAG	HIARNCRAPR	433	10	13	20		8974
GAG	FLGKIWI'NSK	469	10	13	20		8975
GAG	EYKDTKEALD	95	11	13	20		8976
GAG	FSPEVIMFTA	185	11	13	20		8977
GAG	AAEWDRVIIPV	220	11	13	20		8978
GAG	KTILRALGPGA	355	11	13	20		8979
GAG	HIARNCRAPRK	433	11	13	20		8980
GAG	LGIKIWI'NSKG	470	11	13	20		8981

Table XVI
 HIV Δ93 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	NSSQVSQNY	144	9	14	31		8982
GAG	KSRRKAQQA	112	9	14	22		8983
GAG	NCGRGIIAK	427	10	14	22		8984
GAG	IAKNCRAPRKK	434	11	14	22		8985
GAG	EVIPMETA	188	8	14	22		8986
GAG	RGIRNRQK	412	9	14	22		8987
GAG	CGKIGIIAK	428	9	14	22		8988
GAG	EGHIAKNCR	431	9	14	22		8989
GAG	EGHIAKNCR	431	10	14	22		8990
GAG	PSNKGIRPGNF	475	10	14	22		8991
GAG	TAPEESFR	496	10	14	22		8992
GAG	TVATLYCVIIQ	83	11	14	22		8993
GAG	IVQNAQQQMV	155	11	14	22		8994
GAG	PTAPPEESFR	495	11	14	22		8995
GAG	SSQVSQNY	145	8	15	31		8996
GAG	VSQNYHIVQNA	149	11	15	26		8997
GAG	RSLYNTVATL	78	11	15	24		8998
GAG	TLVCVHOR	86	8	15	23		8999
GAG	FTALSEGA	193	8	15	23		9000
GAG	AAEWDRVII	230	8	15	23		9001
GAG	WDRVIPIVII	233	8	15	23		9002
GAG	RGNFRQK	412	8	15	23		9003
GAG	TAPEESF	496	8	15	23		9004
GAG	LASLKSFL	349	8	15	23		9005
GAG	VLSGGKLLDA	7	9	15	23		9006
GAG	LENTVATLY	80	9	15	23	0.0150	9007
GAG	ATLYCVHOR	85	9	15	23		9008
GAG	MFTALSEGA	192	9	15	23		9009
GAG	EAAEWDRVII	229	9	15	23		9010
GAG	WDRVIPIVII	233	9	15	23		9011
GAG	PTAPPEESF	495	9	15	23		9012
GAG	TAPEESFR	496	9	15	23		9013
GAG	PLASLKSFL	548	9	15	23		9014
GAG	SVLSGGKLLDA	6	10	15	23		9015
GAG	SGGKLDWEEK	9	10	15	23		9016
GAG	ELKSLYNTVA	76	10	15	23		9017
GAG	SLFNTVATLY	79	10	15	23		9018
GAG	VATLYCVHOR	84	10	15	23		9019
GAG	KIEEQNKSK	105	10	15	23		9020
GAG	PMFTALSEGA	191	10	15	23		9021
GAG	RAEQATQDVK	329	10	15	23		9022
GAG	PTAPPEESFR	495	10	15	23		9023
GAG	ASVLSGGKLLD	5	11	15	23		9024
GAG	LSGGKLDWEE	8	11	15	23		9025
GAG	PGLLETSEGR	50	11	15	23		9026
GAG	KIEEQNKSKK	105	11	15	23		9027
GAG	RLIPIVIAAGPIA	235	11	15	23		9028
GAG	MMQRGNFRN	409	11	15	23		9029
GAG	IAKNCRAPRK	434	10	16	25		9030
GAG	LSGGKLLDA	8	8	16	25		9031

Table XVI
 IIIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	LDAWEKIR	13	8	16	25		9032
GAG	NAQQMVII	158	8	16	25		9033
GAG	PVSILDIK	303	8	16	25		9034
GAG	ILKALGPA	357	8	16	25		9035
GAG	KLDAWEKIR	12	9	16	25		9036
GAG	GGKKKYRLK	24	9	16	25		9037
GAG	TILKALGPA	356	9	16	25		9038
GAG	ILKALGPA	357	9	16	25	0.0003	9039
GAG	VLAEMSQA	386	9	16	25		9040
GAG	LDWEKIRLR	13	10	16	25		9041
GAG	PGKKKYRLK	23	10	16	25		9042
GAG	GGKKKYRLKII	24	10	16	25		9043
GAG	GLLETSEGR	51	10	16	25		9044
GAG	YSPVILDIK	301	10	16	25		9045
GAG	KTILKALGPA	355	10	16	25	0.0045	9046
GAG	TILKALGPA	356	10	16	25		9047
GAG	AATLEEMMTA	364	10	16	25		9048
GAG	RVLAEAMSOA	385	10	16	25		9049
GAG	GGKLDWEKI	10	11	16	25		9050
GAG	KLDAWEKIRL	12	11	16	25		9051
GAG	PGKKKYRLK	23	11	16	25		9052
GAG	VSILDIKQGPX	304	11	16	25		9053
GAG	KTILKALGPA	355	11	16	25		9054
GAG	PAATLEEMMT	363	11	16	25		9055
GAG	IIAKNCRAPRK	433	11	16	25		9056
GAG	LAEAMSOA	387	8	17	27		9057
GAG	RLKILYWA	31	8	17	27		9058
GAG	LSPTLTNA	168	8	17	27		9059
GAG	PIPIQMR	243	8	17	27		9060
GAG	GGKLDWEK	10	9	17	27		9061
GAG	DAWEKIRLR	14	9	17	27		9062
GAG	LLETSEGR	52	9	17	27		9063
GAG	RLKILYWASR	31	10	17	27		9064
GAG	LDKIEEQNK	103	10	17	27		9065
GAG	AGPIPPQMR	241	10	17	27		9066
GAG	ALDKIEEQNK	102	11	17	27		9067
GAG	LSPTLTNAWV	168	11	17	27		9068
GAG	IIAGPIPPQMR	240	11	17	27		9069
GAG	PIPPQMRPR	243	11	17	27		9070
GAG	PGATLEEMMT	363	11	17	27		9071
GAG	RSLYNTVA	78	8	18	29	0.0009	9072
GAG	IAKNCRAPR	434	9	18	29		9073
GAG	LDWEKIR	13	8	18	28		9074
GAG	PVGDIYKR	281	8	18	28		9075
GAG	PDCKTILR	352	8	18	28		9076
GAG	DCKTILRA	353	8	18	28		9077
GAG	IIAKNCR	433	8	18	28		9078
GAG	PDCKTILRA	352	9	18	28		9079
GAG	ILRALGPGA	357	9	18	28		9080
GAG	LDWEKIRLR	13	10	18	28		9081

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^0301	SEQ ID NO.
GAG	SILDIKQGP	305	10	18	28		9082
GAG	IIAKNCRAPR	433	10	18	28		9083
GAG	IIAGIIAPQM	240	11	18	28		9084
GAG	NANPDKTILR	349	11	18	28		9085
GAG	LARNCRAPRK	434	11	19	30		9086
GAG	PVIAGPIA	238	8	19	30		9087
GAG	PIAPQM	243	8	19	30		9088
GAG	LDIKQGP	307	8	19	30		9089
GAG	ILDIKQGP	306	9	19	30		9090
GAG	PSIIKARVLA	380	9	19	30		9091
GAG	AGIIAPQM	241	10	19	30		9092
GAG	IAPQMREPR	244	10	19	30		9093
GAG	DIKQGPKEFF	308	10	19	30		9094
GAG	RLRPGKKKY	20	11	19	30		9095
GAG	IVWASRELERF	35	11	19	30		9096
GAG	PIAPQMREPR	243	11	19	30		9097
GAG	LDIKQGPKEFF	307	11	19	30		9098
GAG	DIKQGPKEPR	308	11	19	30		9099
GAG	GGPSIIKARVL	378	11	19	30		9100
GAG	PSIIKARVLA	380	11	19	30		9101
GAG	LARNCRAPR	434	9	20	32		9102
GAG	LARNCRAPRK	434	10	20	32		9103
GAG	PGCKKYYR	23	8	20	31		9104
GAG	TAPPAESF	496	8	20	31		9105
GAG	IMMQRGNFR	408	9	20	31		9106
GAG	PTAPPAESF	495	9	20	31	0.0099	9107
GAG	IVWASRELER	35	10	20	31		9108
GAG	ILARNCRAPR	433	10	20	31		9109
GAG	IIWASRELER	34	11	20	31		9110
GAG	ILARNCRAPR	433	11	20	31		9111
GAG	ILARNCR	433	8	21	33		9112
GAG	EGIIILANCR	431	9	21	33		9113
GAG	NLQGMVITQA	158	10	21	33		9114
GAG	EGIIILANCR	431	10	21	33		9115
GAG	QSKPPTAPPA	488	11	21	33		9116
GAG	KIIVPSIIKGR	472	9	22	35	0.0770	9117
GAG	EVDITKEA	95	8	22	34		9118
GAG	ETINEEAA	224	8	22	34		9119
GAG	DTLLVQNA	343	8	22	34		9120
GAG	GGPSIIKAR	378	8	22	34		9121
GAG	TDITLLVQNA	342	9	22	34		9122
GAG	VGGPSIIKAR	377	9	22	34		9123
GAG	SLYNTVATLY	79	10	22	34		9124
GAG	MLKETINEEA	221	10	22	34		9125
GAG	MTDITLLVQNA	341	10	22	34		9126
GAG	VGGPSIIKAR	376	10	22	34		9127
GAG	QMLKETINEEA	220	11	22	34		9128
GAG	MLKETINEEAA	221	11	22	34		9129
GAG	WMTDITLLVQ	340	11	22	34		9130
GAG	QGVGGPSIIKA	375	11	22	34		9131

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	LGIWPSIIKG	470	11	22	34		9132
GAG	NFLGIWPSIIK	468	11	23	37		9133
GAG	KIEEQNK	105	8	23	36		9134
GAG	QGVGGPSII	375	8	23	36		9135
GAG	GVGGPSIIK	376	8	23	36		9136
GAG	VGGPSIIKA	377	8	23	36		9137
GAG	MMQRGNFR	409	8	23	36		9138
GAG	QGVGGPSIIK	375	9	23	36		9139
GAG	GVGGPSIIKA	376	9	23	36		9140
GAG	LGIWPSIIK	470	9	23	36		9141
GAG	ACQGVGGPSII	373	10	23	36		9142
GAG	QGVGGPSIIKA	375	10	23	36		9143
GAG	FLGIWPSIIK	469	10	23	36		9144
GAG	PSIIKGIKGNF	475	10	23	36	0.02100	9145
GAG	TACQGVGGPS	372	11	23	36		9146
GAG	ACQGVGGPSII	373	11	23	36		9147
GAG	NCCKEGIIAR	427	10	24	38		9148
GAG	KVIEEKAF	178	8	24	38		9149
GAG	COKEGIIAR	428	9	24	38		9150
GAG	WVKVIEEKAF	176	10	24	38		9151
GAG	YSIVSILDIR	301	10	24	38		9152
GAG	NFLGIWPSII	468	10	25	40		9153
GAG	PSILDIR	303	8	25	39		9154
GAG	LGIWPSII	470	8	25	39		9155
GAG	KDTKEALDK	97	9	25	39		9156
GAG	WVKVIEEKA	176	9	25	39		9157
GAG	FLGIWPSII	469	9	25	39		9158
GAG	LVWASRELER	35	11	25	39		9159
GAG	NAWVKVIEEK	174	11	25	39		9160
GAG	VSILDIRQPK	304	11	25	39		9161
GAG	LVWASRELER	35	10	26	41		9162
GAG	ILVWASRELE	34	11	26	41		9163
GAG	CFNCGKEGIIA	425	11	26	41		9164
GAG	NCCKEGIIA	427	9	27	43		9165
GAG	NCCKEGIIIA	427	9	27	43		9166
GAG	RFFKTLRA	323	8	27	42		9167
GAG	IMMQKGNF	408	8	27	42		9168
GAG	CKKEGIIA	428	8	27	42		9169
GAG	CKKEGIIA	428	8	27	42		9170
GAG	MVIQAIISPR	163	9	27	42	0.1800	9171
GAG	VDRFFKTLR	321	9	27	42		9172
GAG	QMVIIQAIISPR	162	10	27	42	0.0260	9173
GAG	YVDRFFKTLR	320	10	27	42		9174
GAG	VDRFFKTLR	321	10	27	42		9175
GAG	FFKTLRAEQA	324	10	27	42		9176
GAG	RAEQATQEVK	329	10	27	42		9177
GAG	NAWVKVIEEK	174	11	27	42		9178
GAG	YVDRFFKTLR	320	11	27	42		9179
GAG	RFFKTLRAEQ	323	11	27	42		9180
GAG	RFYKTLRAEQ	323	11	27	42		9181

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	NANPCKTILK	349	11	27	42		9182
GAG	CFNCGEIGIL	425	11	27	42		9183
GAG	KGRIGNFLOS	478	11	28	44		9184
GAG	NFLOSREPTA	485	11	28	44		9185
GAG	KVVEEKAF	178	8	28	44		9186
GAG	RFYKTLRA	323	8	28	44		9187
GAG	PDCKTILK	352	8	28	44		9188
GAG	DKTILKA	353	8	28	44		9189
GAG	WVKVVEEKA	176	9	28	44		9190
GAG	VDRFYKTLR	321	9	28	44		9191
GAG	PDCKTILKA	352	9	28	44		9192
GAG	WVKVVEEKAF	176	10	28	44		9193
GAG	PFRDYVDRFY	316	10	28	44		9194
GAG	YVDRFYKTLR	320	10	28	44		9195
GAG	VDRFYKTLRA	321	10	28	44	0.0003	9196
GAG	GATLEEMMTA	364	10	28	44		9197
GAG	FLOSREPTA	486	10	28	44		9198
GAG	PFRDYVDRFY	316	11	28	44		9199
GAG	YVDRFYKTLR	320	11	28	44		9200
GAG	GARASVLSGG	2	11	29	46		9201
GAG	ASVLSGGK	5	8	29	45		9202
GAG	NLQGMVH	158	8	29	45		9203
GAG	WVKVVEEK	176	8	29	45	0.0005	9204
GAG	WDRLLIPVH	233	8	29	45		9205
GAG	RDYVDRFY	318	8	29	45		9206
GAG	RASVLSGGK	4	9	29	45	0.0050	9207
GAG	ASPRTLNA	167	9	29	45		9208
GAG	WDRLLIPVHA	233	9	29	45		9209
GAG	RDYVDRFYK	318	9	29	45	0.0007	9210
GAG	QASPRTLNA	166	10	29	45		9211
GAG	NAWKVVEEK	174	10	29	45		9212
GAG	IVQNLSQQMV	155	11	29	45		9213
GAG	AAEWDRLIPV	230	11	29	45		9214
GAG	PGNVLQSR	483	8	30	48		9215
GAG	NAWKVVEEK	174	10	30	47	0.0004	9216
GAG	KIRLRPGKKK	18	11	30	47		9217
GAG	WVKVVEEK	176	8	31	48	0.0003	9218
GAG	MLKDTINEEA	221	10	32	50		9219
GAG	QMLKDTINEEA	220	11	32	50		9220
GAG	MLKDTINEEA	221	11	32	50		9221
GAG	DTINEEA	223	8	33	52		9222
GAG	DTINEEA	224	8	33	52		9223
GAG	RDYVDRFFK	223	9	33	52		9224
GAG	PFRDYVDRFF	318	9	33	52		9225
GAG	RLRPGKKK	166	11	33	52		9226
GAG	RLRPGKKKY	20	9	34	53		9227
GAG	RLRPGKKKY	20	10	34	53		9228
GAG	PIPVGEIYK	279	10	34	53	0.0003	9229
GAG	PIPVGEIY	279	8	35	55		9230
GAG	RDYVDRFF	318	8	35	55		9231

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0J0I	SEQ ID NO.
GAG	PIPVGIIYK	279	9	35	55	0.0002	9232
GAG	PGHKARVLA	380	9	35	55		9233
GAG	IFRIDYVDRFF	316	10	35	55		9234
GAG	WMITELLVQN	340	11	35	55		9235
GAG	GGPIHKARVL	378	11	35	55		9236
GAG	PGHKARVLAIE	380	11	35	55		9237
GAG	DTKEALDK	98	8	36	56	0.0003	9238
GAG	ISPTLNA	168	8	36	56		9239
GAG	QGVGGPGII	375	8	36	56		9240
GAG	QSKPEPTA	488	8	36	56		9241
GAG	QGVGGPGIHK	375	9	36	56	0.0004	9242
GAG	MTETLLVQNA	341	10	36	56		9243
GAG	ACQGVGGPGII	373	10	36	56		9244
GAG	QGVGGPGIHK	375	10	36	56		9245
GAG	ISPTLNAAV	168	11	36	56		9246
GAG	TACQGVGGPG	372	11	36	56	0.0001	9247
GAG	ACQGVGGPGII	373	11	36	56		9248
GAG	QGVGGPGIHK	375	11	36	56		9249
GAG	QGMVITQA	160	8	37	58		9250
GAG	ETLLVQNA	143	8	37	58		9251
GAG	GVGGIHK	376	8	37	58	0.0012	9252
GAG	VGGIHK	377	8	37	58		9253
GAG	GGIHKAR	378	8	37	58		9254
GAG	VGGIHK	376	9	37	58		9255
GAG	VGGIHKAR	377	9	37	58		9256
GAG	VGGIHKAR	376	10	37	58	0.0003	9257
GAG	AAEWDRLLI	230	8	39	61		9258
GAG	EAIEWDRLLI	229	9	39	61		9259
GAG	PVGEIYKR	281	8	40	63	0.0003	9260
GAG	TVATLYCVII	83	9	40	63		9261
GAG	NTVATLYCVII	82	10	40	63		9262
GAG	SILDIRQGP	305	10	40	63	0.3100	9263
GAG	FSPEVIMFSA	185	11	40	63		9264
GAG	DIRQGPKEIF	308	10	41	64		9265
GAG	LDIRQGPKEIF	307	11	41	64		9266
GAG	DIRQGPKEIFR	308	11	41	64		9267
GAG	VATLYCVII	84	8	42	66		9268
GAG	LDIRQGP	307	8	42	66		9269
GAG	ILDIRQGP	306	9	42	66	0.0420	9270
GAG	NTMLNTVGGH	206	10	42	66		9271
GAG	TMLNTVGGII	207	9	43	67		9272
GAG	TMLNTVGGIIQ	207	11	43	67		9273
GAG	KGCWKCGK	444	8	44	69		9274
GAG	KIRLRPGK	18	9	44	69		9275
GAG	ASRELERFA	38	9	44	69		9276
GAG	KIRLRPGKK	18	10	44	69	1.9000	9277
GAG	WASRELERFA	37	10	44	69		9278
GAG	QMRLEPRGSDIA	248	11	44	69		9279
GAG	KGCWKCGKEG	444	11	44	69		9280
GAG	FSALSEGA	193	8	45	70		9281

Table XVI
 IIIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SI:Q ID NO.
GAG	PGQMRPR	246	8	45	70		9282
GAG	MFSALSEGA	192	9	45	70		9283
GAG	CKEGHQMK	449	9	45	70		9284
GAG	PMFSALSEGA	191	10	45	70		9285
GAG	KCGKEGHQMK	448	10	45	70		9286
GAG	ASRELERF	38	8	46	72		9287
GAG	EVIPMFSA	188	8	46	72		9288
GAG	TLIEEMMTA	366	8	46	72		9289
GAG	WASRELERF	37	9	46	72		9290
GAG	ATLEEMMTA	365	9	46	72	0.0003	9291
GAG	MLNTVGGII	208	8	47	73		9292
GAG	NTVGGIIQA	210	8	47	73		9293
GAG	TVGGIIQAA	211	8	47	73		9294
GAG	NTVGGIIQAA	210	9	47	73		9295
GAG	MLNTVGGIIQA	208	10	47	73		9296
GAG	MLNTVGGIIQA	208	11	47	73	0.0005	9297
GAG	WASRELER	37	8	48	75		9298
GAG	GCWCKGKEGII	445	10	48	75		9299
GAG	RLRPGGKK	20	8	49	77		9300
GAG	QMKDCTER	455	8	49	77		9301
GAG	QMKDCTERQA	455	10	49	77		9302
GAG	EGHIQMKDCTE	452	11	49	77		9303
GAG	AFSPEVPMF	184	10	50	78		9304
GAG	KAFSPEVPMF	183	11	50	78	0.0007	9305
GAG	RAPRKGCWK	439	10	51	80		9306
GAG	KDCTERQA	457	8	52	83		9307
GAG	KDCTERQANF	457	10	52	83		9308
GAG	CTERQANFLG	459	11	52	83		9309
GAG	CTERQANF	458	9	52	81		9310
GAG	NCRAPRKK	437	8	53	84		9311
GAG	TINEAAAEWD	225	11	53	83		9312
GAG	KTLRAEQA	326	8	54	84		9313
GAG	FSPEVPMF	185	9	54	84		9314
GAG	CTERQANF	459	8	55	87		9315
GAG	WIIILGINK	289	8	57	89		9316
GAG	KARVLAEA	383	8	57	89		9317
GAG	CFNCGKEGII	425	9	57	89		9318
GAG	ILGLNKIVR	290	10	57	89	0.0003	9319
GAG	KCFNCGKEGII	424	10	57	89		9320
GAG	WIIILGINKIVR	289	11	57	89		9321
GAG	ILGLNKIVRMY	291	11	57	89		9322
GAG	ILGLNKIVR	291	9	58	91	0.0008	9323
GAG	LGLNKIVRMY	292	10	58	91	0.0004	9324
GAG	LLVQNPDC	345	11	58	91		9325
GAG	LGLNKIVR	292	8	59	92		9326
GAG	LVQNPDPCK	346	10	59	92	0.0002	9327
GAG	GLNKIVRMY	293	9	60	94	0.0100	9328
GAG	QAAMQMLK	216	8	61	95		9329
GAG	GHIQAAMQM	213	11	61	95		9330
GAG	RTLNAWVK	171	8	63	98	0.0410	9331

Table XVI
 IIIY A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SIQ ID NO.
GAG	QGPKPEPR	311	8	63	98		9332
GAG	PFDDYVDR	316	8	63	98		9333
GAG	QGIKPEPRDY	311	9	63	98		9334
NEF	QAEPAAAGVG	34	10	01	33	0.0004	9335
NEF	RAQAEPAA	32	8	01	17		9336
NEF	RAQAEPAAA	32	9	01	17		9337
NEF	QTEPAAYGVG	32	11	01	17		9338
NEF	RAEPADGVG	32	11	01	17		9339
NEF	RTEPAAYGVG	32	11	01	17		9340
NEF	QTEPAAYGVG	33	11	01	17		9341
NEF	QAPTAAKGVG	33	11	01	17		9342
NEF	AADGVGAVSR	42	10	09	15		9343
NEF	SSVGWPA	8	8	09	15		9344
NEF	VGWPAIRER	11	9	10	17		9345
NEF	AAECVGAA	42	8	10	16		9346
NEF	FDSRLAFH	310	8	10	16		9347
NEF	FDSRLAFHII	310	9	10	16		9348
NEF	DSRLAFHII	311	8	10	16		9349
NEF	AVSQDLK	48	8	10	16		9350
NEF	PLIWMTFK	102	8	10	16		9351
NEF	KGAFDLSF	109	8	10	16		9352
NEF	GAFDLSFF	110	8	10	16		9353
NEF	GAVSQDLK	47	9	10	16		9354
NEF	QVILRPMTF	100	9	10	16		9355
NEF	KGAFDLSFF	109	9	10	16		9356
NEF	GLEGLYSK	125	9	10	16		9357
NEF	MARELIPEY	321	9	10	16		9358
NEF	VGAVSQDLK	46	10	10	16		9359
NEF	QVILRPMTFK	100	10	10	16		9360
NEF	GAFDLSFLK	110	10	10	16		9361
NEF	GGLKGLYSK	124	10	10	16		9362
NEF	CFKLVPVDP	226	10	10	16		9363
NEF	IMARELIPEY	320	10	10	16		9364
NEF	MARELIPEY	321	10	10	16		9365
NEF	GVGAVSQDLK	45	11	10	16		9366
NEF	KGAFDLSFLK	109	11	10	16		9367
NEF	KGGLGLYSK	122	11	10	16		9368
NEF	WCFKLVPVDP	225	11	10	16		9369
NEF	IMARELIPEY	320	11	10	16		9370
NEF	MARELIPEY	321	11	10	16		9371
NEF	AVSRDLEK	48	8	11	16		9372
NEF	VSRDLEKII	49	8	11	17		9373
NEF	KLVPVDP	228	8	11	17		9374
NEF	GAVSRDLEK	47	9	11	17	0.0002	9375
NEF	AVSRDLEKII	48	9	11	17		9376
NEF	VGAVSRDLEK	46	10	11	17		9377
NEF	GAVSRDLEK	47	10	11	17		9378
NEF	VSRDLEKII	49	10	11	17		9379
NEF	NSLLIIPICQH	255	10	11	17		9380
NEF							9381

Table XVI
 HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Antigenic Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.001$	SEQ ID NO.
NEF	GVGAVSRDLE	45	11	11	17		9182
NEF	VGAVSRDLEK	46	11	11	17		9183
NEF	AVSRDLEKIG	48	11	11	17		9184
NEF	AATNADCA	70	8	12	22		9185
NEF	ATNADCAWLE	71	11	12	22		9186
NEF	EGENNCLLII	251	9	12	19		9187
NEF	PMYKGA	105	8	12	19		9188
NEF	YTPGVR	207	8	12	19		9189
NEF	TAATNADCA	69	9	12	19		9190
NEF	DLDLWVYII	185	9	12	19		9191
NEF	NTAATNADCA	68	10	12	19		9192
NEF	QDLDLWVYII	184	10	12	19		9193
NEF	ITSSNTAATNA	64	11	12	19		9194
NEF	PLRPMYKGA	102	11	12	19		9195
NEF	PGRYPLTF	211	9	13	21		9196
NEF	PGTRPPLTF	211	9	13	21		9197
NEF	EGENNSLLII	251	9	13	21		9198
NEF	WVYITQGF	191	8	13	20		9199
NEF	GIRYPLTF	213	8	13	20		9400
NEF	GTRPPLTF	213	8	13	20		9401
NEF	SSNTAATNA	66	9	13	20		9402
NEF	WVYITQGF	191	9	13	20		9403
NEF	YTPGTRF	207	9	13	20		9404
NEF	TSSNTAATNA	65	10	13	20		9405
NEF	VDLSIFLKEK	112	10	13	20		9406
NEF	DLWVYITQGF	188	10	13	20		9407
NEF	AVDLSIFLKEK	111	11	13	20		9408
NEF	LDLWVYITQGF	187	11	13	20		9409
NEF	DLWVYITQGF	188	11	13	20		9410
NEF	PGRGYPLTF	209	11	13	20		9411
NEF	PGRGTRPPLTF	209	11	13	20		9412
NEF	VDLSIFLK	112	8	14	22		9413
NEF	DGLIYSKK	172	8	14	22		9414
NEF	ELIPEFYK	324	8	14	22	0.0003	9415
NEF	ATSSNTAA	63	9	14	22	0.0740	9416
NEF	AVDLSIFLK	111	9	14	22		9417
NEF	DGLIYSKK	171	9	14	22		9418
NEF	DGLIYSKKR	172	9	14	22		9419
NEF	SLIIPICQII	256	9	14	22		9420
NEF	GAITSSNTAA	62	10	14	22		9421
NEF	GLDGLIYSKK	125	10	14	22		9422
NEF	LDGLIYSKKR	171	10	14	22		9423
NEF	IIGAITSSNTAA	61	11	14	22		9424
NEF	GGDGLIYSKK	124	11	14	22		9425
NEF	GLDGLIYSKKR	125	11	14	22		9426
NEF	PAADGVGA	41	8	15	23		9427
NEF	ITSSNTAA	64	8	15	23		9428
NEF	CLLIIPMSQII	256	9	15	23		9429
NEF	NCLLIIPMSQII	255	10	15	23		9430
NEF	EAQEEEEVGF	82	10	16	25		9431

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ ⁰³⁰¹	SIQ ID NO.
NEF	ADLEKIQA	51	8	16	25		9432
NEF	LDGLIYSK	171	8	16	25		9433
NEF	GLDGLIYSK	125	9	16	25		9434
NEF	GGIINGLIYSK	124	10	16	25		9435
NEF	KGGLDGLIYSK	122	11	16	25		9436
NEF	RFPLTFGWCF	216	10	17	27		9437
NEF	RFPLTFGWCF	216	11	17	27		9438
NEF	ADCAWLEA	74	8	17	27		9439
NEF	FFPDWQNY	199	8	17	27		9440
NEF	LLHPMSQH	257	8	17	27		9441
NEF	NADCAWLEA	73	9	17	27		9442
NEF	GFHFDWQNY	198	9	17	27		9443
NEF	YTFGTGIRY	207	9	17	27		9444
NEF	FDSFLKEK	112	10	17	27		9445
NEF	QGFHFDWQNY	196	10	17	27		9446
NEF	AFDLSFLKEK	111	11	17	27		9447
NEF	FDSFLK	112	8	18	28		9448
NEF	LLHPICQH	257	8	18	28		9449
NEF	AFDLSFLK	111	9	18	28		9450
NEF	GGLEGLIY	124	9	19	30		9451
NEF	KGLEGLIY	122	9	19	30		9452
NEF	DLDLWVY	185	8	20	31		9453
NEF	YTFGTGIR	207	8	20	31		9454
NEF	QDLDLWVY	184	9	20	31		9455
NEF	PLRPMTYKAA	102	10	20	31		9456
NEF	QVPLRPMTYK	100	11	20	31		9457
NEF	PAEGVGGA	41	8	21	33		9458
NEF	GGLDGLIY	124	8	21	33		9459
NEF	WVYITQGY	191	8	21	33		9460
NEF	YTFGTGIR	207	8	21	33		9461
NEF	PLRPMTYKA	102	9	21	33		9462
NEF	KGGLDGLIY	122	9	21	33		9463
NEF	WVYITQGYF	191	9	21	33		9464
NEF	DLWVYITQGY	188	10	21	33		9465
NEF	LDLWVYITQGY	187	11	21	33		9466
NEF	DLWVYITQGY	188	11	21	33		9467
NEF	LSFFLKEK	114	8	22	34		9468
NEF	ELIPEYYK	324	8	22	34		9469
NEF	DLFFLKEK	113	9	22	34		9470
NEF	EILDWVYII	185	9	22	34		9471
NEF	GLIYSKKR	173	8	23	36		9472
NEF	PLRPMTYKGA	102	10	23	36		9473
NEF	ATSSNTA	63	8	27	42		9474
NEF	LSHFLKEK	114	8	27	42		9475
NEF	GAITSSNTA	62	9	27	42		9476
NEF	DLSHFLKEK	113	9	27	42		9477
NEF	IIGAITSSNTA	61	10	27	42		9478
NEF	EILDWVY	185	8	33	52		9479
NEF	IILDWVYII	186	8	34	53		9480
NEF	YFPDWQNY	199	8	36	56		9481

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Coverage (%)	A*0301	SEQ ID NO.
NEF	QGYEPDWQNY	196	10	36	56	0.0004	9482
NEF	LTFGWCCK	221	8	39	61		9483
NEF	PLTFGWCFK	219	9	39	61		9484
NEF	PLTFGWCF	219	8	43	67		9485
NEF	QVPLRPMITY	100	9	46	72		9486
NEF	QVPLRPMITYK	100	10	46	72		9487
NEF	I'VKPQVPLR	95	9	48	75	0.6100	9488
NEF	GFPRVQVPLR	93	11	48	75		9489
NEF	PLRPMITYK	102	8	49	77	0.0010	9490
POL	STNSPTSR	32	8	01	33		9491
POL	RANSPTSR	35	8	01	33		9492
POL	STNSPTSR	31	9	01	33		9493
POL	PTSRLEQVR	36	9	01	33		9494
POL	QTRANSPSSR	33	10	01	33		9495
POL	QTRANSPITR	35	10	01	33		9496
POL	NSPTSRLEQVR	34	11	01	33		9497
POL	RANSPTTR	37	8	01	50		9498
POL	PSRLEQVR	39	9	01	50		9499
POL	PSRANSTSR	24	10	01	50		9500
POL	NSPSSRLEQVR	37	11	01	50		9501
POL	NSPTTRLEQV	39	11	01	50		9502
POL	ADRQGVSF	71	9	01	20		9503
POL	DURQGVSF	71	9	01	20		9504
POL	GADRGVSVF	70	10	01	20		9505
POL	GIDRQGVSVF	70	10	01	20		9506
POL	ADRQGVSVNF	71	11	01	20		9507
POL	DDRQGVSVSF	71	11	01	20		9508
POL	AGADRGVSVF	69	11	01	17		9509
POL	AGDDRQGVSV	69	11	01	17		9510
POL	GTTLNFPQTF	79	11	01	17		9511
POL	NLAFQGEA	5	9	10	16		9512
POL	NLAFQGEAR	5	10	10	16		9513
POL	KTGRYAKMRT	342	11	10	16		9514
POL	ILIEICGH	149	8	10	16		9515
POL	ILIEICGH	150	8	10	16		9516
POL	YAKMRTAI	346	8	10	16		9517
POL	LIIEICGH	150	9	10	16		9518
POL	RSALTNDVK	350	9	10	16		9519
POL	AFQGEAREF	7	10	10	16		9520
POL	LIEALLDTGA	106	10	10	16		9521
POL	TGKYAKMRTA	343	10	10	16		9522
POL	ETWETWTD	588	10	10	16		9523
POL	ETWETWTE	588	10	10	16		9524
POL	ETWETWYQ	591	10	10	16		9525
POL	VSLDTTNNQK	659	10	10	16		9526
POL	LAFFQGEAREF	6	11	10	16		9527
POL	QLIEALLDTGA	105	11	10	16		9528
POL	MLTQLGCTLN	176	11	10	16		9529
POL	TGKYAKMRTA	343	11	10	16		9530
POL	VVSLDTTNNQ	658	11	10	16		9531

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	SI:Q ID NO.
POL	QTKELQKQIK	961	11	10	16		9532
POL	QTRANSPTRR	21	10	11	18		9533
POL	LDGHDKAQEDII	754	11	11	17		9534
POL	IGGFIKVK	137	8	11	17		9535
POL	RIGPENPY	238	8	11	17		9536
POL	VIPLTEEA	481	8	11	17		9537
POL	TAUTNDVK	551	8	11	17		9538
POL	QLTEVVQK	559	8	11	17		9539
POL	IDKAQEDII	757	8	11	17		9540
POL	WAGIQEF	884	8	11	17		9541
POL	VVPRKVK	1012	8	11	17		9542
POL	KIKDYGK	1019	8	11	17		9543
POL	GIGGFIKVK	136	9	11	17		9544
POL	EVIPLTEEA	480	9	11	17		9545
POL	SLDITTNQK	660	9	11	17		9546
POL	GIDKAQEDII	756	9	11	17		9547
POL	KVPIRKVK	1011	9	11	17		9548
POL	GGIGFIKVK	135	10	11	17		9549
POL	ISRIKENPY	236	10	11	17		9550
POL	STNNEIPGIR	323	10	11	17		9551
POL	ESWTVNDIQK	439	10	11	17		9552
POL	ETNOKTELI	663	10	11	17		9553
POL	DGIDKAQEDII	755	10	11	17		9554
POL	GSNFTSTTVK	870	10	11	17		9555
POL	GIQKEFGIPY	886	10	11	17		9556
POL	SDIQIKLEK	958	10	11	17		9557
POL	IKDYGKQMA	1020	10	11	17		9558
POL	IGGIGGFIKVK	134	11	11	17		9559
POL	KISRIKENPY	235	11	11	17		9560
POL	PSTNNEIPGIR	322	11	11	17		9561
POL	STNNEIPGIRY	323	11	11	17		9562
POL	LTEVIPLTEEA	478	11	11	17		9563
POL	VVSLTETTNQ	658	11	11	17		9564
POL	ETNOKTELI	663	11	11	17		9565
POL	NGSNFTSTTV	869	11	11	17		9566
POL	GSNFTSTTVK	870	11	11	17		9567
POL	ACWWAGIQQE	881	11	11	17		9568
POL	AGIQKEFGIPY	885	11	11	17		9569
POL	IDIASDIQTK	953	11	11	17		9570
POL	VDIATDIQTK	953	11	11	17		9571
POL	ASDIQTKELQK	957	11	11	17		9572
POL	NSEIKVVRPK	1007	11	11	17		9573
POL	KIKDYGKQMA	1019	11	11	17		9574
POL	NSLSEAGA	60	8	12	20		9575
POL	QTRANSPTSR	21	10	12	19		9576
POL	IKIQNER	969	8	12	19		9577
POL	QYFGKVK	458	9	12	19		9578
POL	QDQWTYQIY	526	9	12	19		9579
POL	IKIQNERVY	969	10	12	19		9580
POL	ASQYFGKVK	456	11	12	19		9581

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ°0301	SEQ ID NO.
POL	IIKIQNFRVYY	969	11	12	19		9582
POL	LAFPOGEA	6	8	12	19		9583
POL	LAFPOGKA	6	8	12	19		9584
POL	AFPOGEAR	7	8	12	19		9585
POL	KTELQATY	668	8	12	19		9586
POL	ELQAIYLA	670	8	12	19		9587
POL	QIKIQNF	968	8	12	19		9588
POL	KDYGKQMA	1022	8	12	19		9589
POL	LAFPOGEAR	6	9	12	19		9590
POL	GINLPKWK	122	9	12	19		9591
POL	TTNOKTELII	664	9	12	19		9592
POL	QIKIQNFR	968	9	12	19		9593
POL	VIQDNSEIK	1003	9	12	19		9594
POL	NSEIKVVPR	1007	9	12	19		9595
POL	VLEINLPK	119	10	12	19		9596
POL	TTNOKTELIIA	664	10	12	19		9597
POL	KTELQAIYLA	668	10	12	19		9598
POL	VVIQDNSEIK	1002	10	12	19		9599
POL	NSEIKVVPRR	1007	10	12	19		9600
POL	TVLEINLPK	118	11	12	19		9601
POL	ELNLPKWKPK	122	11	12	19		9602
POL	ELRQIILLRWG	393	11	12	19		9603
POL	QGQDQWYYQI	524	11	12	19		9604
POL	RMKGATITNDV	548	11	12	19		9605
POL	IIKIQNFRVY	968	11	12	19		9606
POL	AVVIQDNSEIK	1000	11	12	19		9607
POL	QDNSEIKVVPR	1005	11	12	19		9608
POL	ELQKQIK	964	8	13	21		9609
POL	EFSSQTRA	16	9	13	21		9610
POL	KTGKYARMR	542	9	13	21		9611
POL	NLKTGKYARM	540	11	13	21		9612
POL	KTGKYARMRG	542	11	13	21		9613
POL	EDINLPK	121	8	13	20		9614
POL	IVPLTEEA	481	8	13	20		9615
POL	TGKYARMR	543	8	13	20		9616
POL	YARMRGAI	546	8	13	20		9617
POL	IGQVREQA	914	8	13	20		9618
POL	QVREQAEH	916	8	13	20		9619
POL	DINLPKWK	122	9	13	20		9620
POL	LIEICGKKA	150	9	13	20		9621
POL	DIVPLTEEA	480	9	13	20		9622
POL	IGQVREQA	913	9	13	20		9623
POL	VLEDINLPK	119	10	13	20		9624
POL	EDINLPKWK	121	10	13	20		9625
POL	ILIEICGKKA	149	10	13	20		9626
POL	RAKIEELREH	388	10	13	20		9627
POL	TVQHVLPK	429	10	13	20		9628
POL	TDIVPLTEEA	479	10	13	20	0.1600	9629
POL	TGKYARMRGA	543	10	13	20		9630
POL	AGRWPVKTHI	857	10	13	20		9631

Table XVI
 IIIY A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0.101	SIQ ID NO.
POL	KIQGVREQA	912	10	13	20		9632
POL	IQGVREQAEEH	914	10	13	20		9633
POL	QVREQAEEHLK	916	10	13	20		9634
POL	EIKVVRKKA	1009	10	13	20		9635
POL	TLWQRLVTV	91	11	13	20		9636
POL	LVTIKIGGQLK	97	11	13	20		9637
POL	TVLEDINLFGK	118	11	13	20		9638
POL	DINLPGKWKJ	122	11	13	20		9639
POL	QILIECGKKA	148	11	13	20		9640
POL	KIEELREHLLK	390	11	13	20		9641
POL	WTQRIVLPEK	428	11	13	20		9642
POL	LTDIVPLTEEA	478	11	13	20	0.0011	9643
POL	TGKYARMRGA	543	11	13	20		9644
POL	LAGRWPKTI	856	11	13	20		9645
POL	IIGQVREQAEEH	913	11	13	20		9646
POL	DSRDPLWKGH	981	11	13	20		9647
POL	EIKVVRKKA	1009	11	13	20		9648
POL	EPSEQTR	16	8	14	22		9649
POL	QYRGKVR	458	9	14	22		9650
POL	ASQYFGIKVR	456	11	14	22		9651
POL	IATESIVWKG	567	11	14	22		9652
POL	ILIECGK	149	8	14	22		9653
POL	LIIECGKK	150	8	14	22		9654
POL	NFTSTTVK	872	8	14	22		9655
POL	FSTTVKA	873	8	14	22		9656
POL	TSITVKA	874	8	14	22		9657
POL	IASDIQTK	956	8	14	22		9658
POL	DSRDPLWK	981	8	14	22		9659
POL	QILIECGK	148	9	14	22		9660
POL	ILIECGKK	149	9	14	22		9661
POL	NFTSTTVKA	872	9	14	22		9662
POL	FSTTVKAA	873	9	14	22	0.0003	9663
POL	IASDIQTK	955	9	14	22		9664
POL	RDSRDPLWK	980	9	14	22		9665
POL	KDPLWKIPA	983	9	14	22		9666
POL	QILIECGKK	148	10	14	22		9667
POL	RTKIELRQH	388	10	14	22		9668
POL	PGIKVRLQCK	461	10	14	22		9669
POL	THITDNGSNF	864	10	14	22		9670
POL	NFTSTTVKAA	872	10	14	22		9671
POL	TTVKAACWW	876	10	14	22	0.0006	9672
POL	AGERIVDIA	948	10	14	22		9673
POL	DHASDIQTK	954	10	14	22		9674
POL	RDPLWKGPAK	983	10	14	22		9675
POL	FSFQITLWQR	85	11	14	22		9676
POL	YDQILIECGK	146	11	14	22		9677
POL	ELREILLKWG	393	11	14	22		9678
POL	KTPKFKLPQK	577	11	14	22		9679
POL	GIDKAOEEHER	756	11	14	22		9680
POL	STTVKACW	875	11	14	22		9681

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	SAGERIVDIIA	947	11	14	22		9682
POL	QTRANSPTIR	21	9	15	24		9683
POL	LVEICTEMEK	221	10	15	24	0.0002	9684
POL	FVIEDLAF	1	8	15	23		9685
POL	FSSEQTRA	17	8	15	23		9686
POL	ELRQIILLR	393	8	15	23		9687
POL	OGODOWTY	524	8	15	23		9688
POL	KTELQAIH	668	8	15	23		9689
POL	AGIRKLVLF	746	8	15	23		9690
POL	PIQKETWEA	584	9	15	23		9691
POL	SAGIRKVLV	745	9	15	23		9692
POL	EIKVVPFRK	1009	9	15	23		9693
POL	LTQLGCTLNF	177	10	15	23		9694
POL	KTELQAIHLA	668	10	15	23		9695
POL	LGIIQAQPIR	695	10	15	23		9696
POL	VDKLVASGIR	740	10	15	23		9697
POL	VSAGIRKVLV	744	10	15	23		9698
POL	IDKAQEIER	757	10	15	23		9699
POL	ALVEICTEMEK	220	11	15	23		9700
POL	KIELRQIILLR	390	11	15	23		9701
POL	ALGIQAQPIR	694	11	15	23		9702
POL	LVNQIEQLIK	709	11	15	23		9703
POL	QVDKLVASGIR	739	11	15	23		9704
POL	VDKLVASGIRK	740	11	15	23		9705
POL	LVSAGIRKVLV	743	11	15	23		9706
POL	IDKAQEIER	757	11	15	23		9707
POL	KAQEIER	759	8	16	25		9708
POL	NLAFQGEA	5	9	16	25		9709
POL	KAQEIER	759	9	16	25		9710
POL	NLAFQGEAR	5	10	16	25		9711
POL	KAQEIER	759	10	16	25		9712
POL	NLAFQGEA	6	8	16	25		9713
POL	AFQGEAR	7	8	16	25		9714
POL	RANSPTIR	36	8	16	25		9715
POL	QLGCTLNF	179	8	16	25		9716
POL	SAITNDVK	551	8	16	25		9717
POL	ELQAIHLA	670	8	16	25		9718
POL	IIOAQPIR	697	8	16	25		9719
POL	QVDKLVSA	739	8	16	25		9720
POL	KLVASGIR	742	8	16	25		9721
POL	LVSAGIRK	743	8	16	25	0.0091	9722
POL	EIKVVPFR	1009	8	16	25		9723
POL	NLAFQGEAR	6	9	16	25		9724
POL	GLIQAQPIR	696	9	16	25		9725
POL	KLVASGIRK	742	9	16	25	0.1300	9726
POL	QLEKEPIVGA	620	10	16	25		9727
POL	RANSPTIR	26	8	17	27		9728
POL	KIELRQII	390	8	17	27		9729
POL	ELREHLK	393	8	17	27		9730
POL	WGKTPKFK	575	8	17	27		9731

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0.001	SEQ ID NO.
POL	TIKIGQLK	99	9	17	27		9732
POL	VTIKIGQLK	98	10	17	27	0.2700	9733
POL	TVQMQLPEK	429	10	17	27	0.0370	9734
POL	VIWGTPEK	573	10	17	27		9735
POL	TLWQPLVTI	91	11	17	27		9736
POL	TIKIGQLKEA	99	11	17	27		9737
POL	MLTQIGCTLNF	176	11	17	27		9738
POL	WTVQPIQLPEK	428	11	17	27		9739
POL	IVWGTPEK	572	11	17	27		9740
POL	ETTNQKTELQ	663	11	17	27		9741
POL	KDFRKYTAF	311	9	18	29		9742
POL	YFSVPLDKDF	304	10	18	29		9743
POL	YFSVPLDKDF	304	11	18	29		9744
POL	NLRTGKYAKM	540	11	18	29		9745
POL	SVPLDKDF	306	8	18	28		9746
POL	PDIVIQY	365	8	18	28		9747
POL	FSPVLDKDF	305	9	18	28		9748
POL	SVPLDKDF	306	9	18	28		9749
POL	FSPVLDKDF	305	10	18	28		9750
POL	SVPLDKDF	306	10	18	28		9751
POL	AGIKVKQLCK	461	10	18	28		9752
POL	FSPVLDKDF	305	11	18	28		9753
POL	SVPLDKDF	306	11	18	28		9754
POL	LDKDFRYTA	309	11	18	28		9755
POL	YAGIKVKQLCK	460	11	18	28		9756
POL	LVSQIEQLIK	709	11	18	28		9757
POL	PLDKDFRK	308	8	19	30		9758
POL	KDFRYTA	311	8	19	30		9759
POL	PLDKDFRY	308	9	19	30		9760
POL	KTKYAKMR	542	9	19	30		9761
POL	PLDKDFRY	308	11	19	30		9762
POL	LDKDFRY	309	8	19	30		9763
POL	KIELREII	390	8	19	30		9764
POL	TGKYAKMR	543	8	19	30		9765
POL	GAITNDVK	551	8	19	30		9766
POL	LTDITNOK	661	8	19	30		9767
POL	PLWKGPAK	985	8	19	30		9768
POL	GKVRQLCK	462	9	19	30		9769
POL	RGAITNDVK	550	9	19	30		9770
POL	LDKDFRYTA	309	10	19	30		9771
POL	KVRQLCKLR	464	10	19	30		9772
POL	ATESIVWIK	568	10	19	30		9773
POL	VSQIEQLIK	710	10	19	30	0.0007	9774
POL	MAGIDCVASR	1028	10	19	30		9775
POL	VSQIEQLIK	710	11	19	30		9776
POL	QLIKKEKYYLA	716	11	19	30		9777
POL	QMAGDDCVAS	1027	11	19	30		9778
POL	QYAGIKVK	458	9	20	32		9779
POL	KVYLAWVPA	722	9	20	32	0.0750	9780
POL	KVYLAWVPAII	722	10	20	32	0.0280	9781

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
POL	KAACWWAGIK	879	10	20	32	0.0300	9782
POL	ASQIYAGIKVK	436	11	20	32		9783
POL	KVYLAWVPAIL	722	11	20	32	8.6000	9784
POL	KFKLHQK	580	8	20	31		9785
POL	GDIDCVASR	1030	8	20	31		9786
POL	AGDDCVASR	1029	9	20	31		9787
POL	VSLTETTNQK	659	10	20	31		9788
POL	LIKKEKVYLA	717	10	20	31		9789
POL	LLKLGRWFPV	853	11	20	31		9790
POL	YFSVPLDK	304	8	21	33		9791
POL	KVIITDNGSNF	863	11	21	33		9792
POL	ACWWAGIK	881	8	21	33		9793
POL	WAGIKQEF	884	8	21	33		9794
POL	SLTETTNQK	660	9	21	33		9795
POL	AACWWAGIK	880	9	21	33	0.0130	9796
POL	DAYFSVPLDK	302	10	21	33		9797
POL	DLEIGQIRTK	381	10	21	33		9798
POL	QLCKLLHGTG	467	10	21	33		9799
POL	SDFNLPIVA	776	10	21	33		9800
POL	LLTQIGCTLNF	176	11	21	33		9801
POL	IFAIRKKDSTK	249	11	21	33		9802
POL	GDVYFSVPLD	301	11	21	33		9803
POL	SDLEIGQIRTK	380	11	21	33		9804
POL	QLCKLLHGTG	467	11	21	33		9805
POL	ASDFNLPIVA	775	11	21	33		9806
POL	SDFNLPIPAK	776	11	21	33		9807
POL	ACWWAGIKQIE	881	11	21	33		9808
POL	AGIKQIEFGIPY	885	11	21	33		9809
POL	EDFRKYYTA	311	8	22	35		9810
POL	EDFRKYYTAF	311	9	22	35		9811
POL	EIGQIRTK	383	8	22	34		9812
POL	RTKIELR	388	8	22	34		9813
POL	YLAWVPAIL	724	8	22	34		9814
POL	LAWVPAIK	725	8	22	34		9815
POL	YLAWVPAIK	724	9	22	34	0.0770	9816
POL	NFMQITLWQR	86	10	22	34		9817
POL	MTKILEFRK	353	10	22	34	0.0150	9818
POL	KVILVAVIVA	823	10	22	34		9819
POL	AGRWPVKVHI	857	10	22	34		9820
POL	GIKQIEFGIPY	886	10	22	34	0.0002	9821
POL	SMTKILEFRK	352	11	22	34		9822
POL	KTPKFLPIQK	577	11	22	34		9823
POL	LAQRWPKVKI	856	11	22	34		9824
POL	KVYLSWVPA	722	9	23	37		9825
POL	KVYLSWVPAIL	722	10	23	37		9826
POL	KVYLSWVPAIL	722	11	23	37		9827
POL	KILEFRK	355	8	23	36		9828
POL	EGKVLVA	821	8	23	36		9829
POL	KVILVAVH	823	8	23	36		9830
POL	KIGGQLKEA	101	9	23	36		9831

Table XVI
HIV Δ93 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	SEQ ID NO.
POL	DFNLPPIVA	777	9	23	36		9832
POL	VILVAVIVA	824	9	23	36		9833
POL	TVKACQWVA	877	9	23	36		9834
POL	SFIQTLWOR	86	10	23	36		9835
POL	DFNLPPIVAK	777	10	23	36		9836
POL	ILIEGKVILVA	819	10	23	36		9837
POL	EGKVILVAVII	821	10	23	36		9838
POL	LLKWGFTTPD	398	11	23	36		9839
POL	LLRWGFTTPD	398	11	23	36		9840
POL	IDIATDIQTK	953	11	23	36		9841
POL	KLLRGTKA	470	8	24	38		9842
POL	NTPIFAIK	246	8	24	38		9843
POL	GDDCVAGR	1030	8	24	38		9844
POL	NTPIFAIKK	246	9	24	38		9845
POL	LCKLLRGTK	468	9	24	38	0.0004	9846
POL	AGDIDCVAGR	1029	9	24	38		9847
POL	NTPIFAIKK	246	10	24	38		9848
POL	LCKLLRGTKA	468	10	24	38		9849
POL	VIIITDGSNF	864	10	24	38		9850
POL	MAGIDICVAGR	1028	10	24	38		9851
POL	QLCKLLRGAK	467	11	24	38		9852
POL	QGGQWYTYQI	524	11	24	38		9853
POL	KLCKAGYVTD	643	11	24	38		9854
POL	TAYFLKLAG	849	11	24	38		9855
POL	QAGDDCVAG	1027	11	24	38		9856
POL	KLLRGAKA	470	8	25	40		9857
POL	QGGWYTYQIY	526	9	25	40		9858
POL	IGGQLKEA	102	8	25	39	0.0004	9859
POL	PIFAIKK	248	8	25	39		9860
POL	QGGQWYTY	524	8	25	39		9861
POL	FLLKLAGR	852	8	25	39		9862
POL	QLCKLLRGA	467	9	25	39		9863
POL	PIVAKEIVA	782	9	25	39		9864
POL	YFLKLAGR	851	9	25	39		9865
POL	QLCKLLRGAK	467	10	25	39		9866
POL	LCKLLRGAKA	468	10	25	39		9867
POL	LKGAGYVTD	644	10	25	39		9868
POL	IDKAQEIEIK	757	10	25	39		9869
POL	SDFNLPVVA	776	10	25	39		9870
POL	PSKIDIAEIQK	513	11	25	39		9871
POL	DTTNQKTELQ	663	11	25	39		9872
POL	GIDKAQEIEIK	756	11	25	39		9873
POL	IDKAQEIEIEKY	757	11	25	39		9874
POL	ASDFNLPVVA	775	11	25	39		9875
POL	SDFNLPVVAK	776	11	25	39		9876
POL	RAKIEELR	388	8	26	41		9877
POL	LCKLLRGA	468	8	26	41		9878
POL	KFRLPIQK	580	8	26	41		9879
POL	NLPPIVAK	779	8	26	41		9880
POL	IVAKEIVA	783	8	26	41		9881

Table XVI
 IIIY A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consistency (%)	A*0301	SEQ ID NO.
POL	LCKLLRGAK	468	9	26	41		9882
POL	LTEAVQKIA	560	9	26	41		9883
POL	SSGIRKVLV	745	9	26	41		9884
POL	DFNLPIVVA	777	9	26	41		9885
POL	QLTEAVQKIA	559	10	26	41		9886
POL	VSSGIRKVLV	744	10	26	41		9887
POL	DFNLPIVVA	777	10	26	41		9888
POL	GSNFTSAVK	870	10	26	41		9889
POL	LVSSGIRKVLV	743	11	26	41		9890
POL	TGQETAYFL	845	11	26	41		9891
POL	NGSFTSAAV	869	11	26	41		9892
POL	GSNFTSAVK	870	11	26	41		9893
POL	KAQEEHEK	759	8	27	43	0.0013	9894
POL	ASQIYAGIK	456	9	27	43		9895
POL	KAQEEHEKY	759	9	27	43		9896
POL	KAQEEHEKYII	759	10	27	43		9897
POL	EICTEMEK	223	8	27	42		9898
POL	EIGQIRAK	383	8	27	42		9899
POL	LVSSGIRK	743	8	27	42		9900
POL	SGIRKVLV	746	8	27	42		9901
POL	NLPIVVA	779	8	27	42		9902
POL	ETAYFLK	848	8	27	42	0.0037	9903
POL	TSAAVKAA	874	8	27	42		9904
POL	KLVSIGIRK	742	9	27	42		9905
POL	TAYFLKLA	849	9	27	42	0.0027	9906
POL	FTSAAVKAA	873	9	27	42		9907
POL	DLEIGQIRAK	381	10	27	42		9908
POL	KLNWASQIYA	452	10	27	42	0.0052	9909
POL	WASQIYAGIK	455	10	27	42		9910
POL	KVQLCKLLR	464	10	27	42		9911
POL	ETAYFLKLA	848	10	27	42		9912
POL	FTSAAVKAA	872	10	27	42		9913
POL	EICTEMEKECK	223	11	27	42		9914
POL	SDLEIGQIRAK	380	11	27	42		9915
POL	VDKLVSIGIRK	740	11	27	42		9916
POL	ASQIYPGIK	456	9	28	44		9917
POL	KDLAEIQK	515	9	28	44		9918
POL	NLKTGKYAK	540	9	28	44		9919
POL	DLAEIQK	516	8	28	44		9920
POL	PVGAETP	625	8	28	44		9921
POL	IVGAETP	626	8	28	44		9922
POL	GSNFTSAA	870	8	28	44		9923
POL	NFTSAAVK	872	8	28	44		9924
POL	FTSAAVKA	873	8	28	44		9925
POL	CTEMEKECK	223	9	28	44	0.0002	9926
POL	DLEIGQIRA	381	9	28	44		9927
POL	GIKVKQLCK	462	9	28	44		9928
POL	PVGAETP	625	9	28	44		9929
POL	QLIKKEKVV	716	9	28	44		9930
POL	PVVAKEIVA	782	9	28	44		9931

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	NGSNFTSAA	869	9	28	44		9932
POL	NFTSAAVKA	872	9	28	44		9933
POL	ICTEMKECK	224	10	28	44		9934
POL	SDLEIGQIRA	380	10	28	44		9935
POL	WASQTPQIK	455	10	28	44		9936
POL	AAVKAACWW	876	10	28	44		9937
POL	GSDLEIGQIRA	379	11	28	44		9938
POL	VGAEIFYVDG	627	11	28	44		9939
POL	TDNGSNFTSA	867	11	28	44		9940
POL	SAAVKAACW	875	11	28	44		9941
POL	NLKTCKYAR	540	9	29	46	0.0008	9942
POL	KLVSSGIR	742	8	29	45		9943
POL	VIWGRTPKFR	573	10	29	45		9944
POL	VDKLYSSGIR	740	10	29	45		9945
POL	PLTHAELELA	483	11	29	45		9946
POL	VIWGRTPKFR	572	11	29	45		9947
POL	QVDKLYSSGIR	739	11	29	45		9948
POL	WGKTPKFR	575	8	30	47		9949
POL	LTEFTNQK	661	8	30	47		9950
POL	ILVAVIIVA	824	9	30	47		9951
POL	AAARETKLCK	637	10	30	47	0.0007	9952
POL	IEQLKKEK	713	10	30	47	0.0004	9953
POL	KILVAVIIVA	823	10	30	47		9954
POL	GAANRETKLG	636	11	30	47		9955
POL	AAARETKLCK	637	11	30	47		9956
POL	QIEQLKKEK	712	11	30	47		9957
POL	ILKLGRWV	853	11	30	47		9958
POL	VVAKEIVA	783	8	31	48		9959
POL	EGKILVA	821	8	31	48		9960
POL	KILVAVII	823	8	31	48		9961
POL	ETAYFILK	848	8	31	48		9962
POL	YFILKLGR	851	9	31	48		9963
POL	ILEGKILVA	819	10	31	48		9964
POL	EGKILVAVII	821	10	31	48		9965
POL	ETAYFILKLA	848	10	31	48		9966
POL	PSINNETPGIR	322	11	31	48		9967
POL	TGQETAYFILK	845	11	31	48		9968
POL	TAYFILKLGR	849	11	31	48		9969
POL	FILKLGR	852	8	32	50		9970
POL	NDVKQLTEA	555	9	32	50		9971
POL	TAYFILKLA	849	9	32	50		9972
POL	AVKAACWWA	877	9	32	50		9973
POL	SINNETGIR	323	10	32	50		9974
POL	SINNETTGIR	323	11	32	50		9975
POL	SSMTKILEPFR	351	11	32	50		9976
POL	IITNDVKQLTE	553	11	32	50		9977
POL	IISNWRAMAS	768	11	32	50		9978
POL	QTKELQKQITK	961	11	32	50		9979
POL	DVKQLTEA	556	8	33	52	0.0050	9980
POL	NGSNFTSA	869	8	33	52		9981

Table XVI
 IIIY A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	EMKEFGKISK	229	10	33	52	0.0004	9982
POL	SSMTKILEPF	351	10	33	52	0.0004	9983
POL	TDNGSNFTSA	867	10	33	52		9984
POL	QSSMTKILEPF	350	11	33	52	0.0048	9985
POL	DVKQLTEAVQ	556	11	33	52		9986
POL	HTDNGSNFTS	866	11	33	52		9987
POL	YDFSKDLIA	511	9	34	53		9988
POL	DIIATDIQTK	954	10	34	53	0.0056	9989
POL	QLKEALLDTG	105	11	34	53		9990
POL	ELOKQTK	964	8	35	56		9991
POL	LIKKEKY	717	8	35	55		9992
POL	QITKIQNF	968	8	35	55		9993
POL	DSRDPWIK	981	8	35	55		9994
POL	ETKLGKAGY	641	9	35	55		9995
POL	IIATDIQTK	955	9	35	55	0.0250	9996
POL	QITKIQNFR	968	9	35	55	0.0021	9997
POL	RDSIDPIWK	980	9	35	55		9998
POL	TDIQTKELOK	958	10	35	55	0.0017	9999
POL	RDPWIKGP	983	10	35	55		10000
POL	ATDIQTKELQK	957	11	35	55	0.0051	10001
POL	QITKIQNFRVY	968	11	35	55		10002
POL	DSKDPWIKGP	981	11	35	55		10003
POL	SDIKVVPRIKKA	1008	11	35	55		10004
POL	ITKIQNFR	969	8	36	57		10005
POL	ITKIQNFRVY	969	10	36	57	0.0016	10006
POL	ITKIQNFRVY	969	11	36	57		10007
POL	IATDIQTK	956	8	36	56		10008
POL	PIWKGPAK	985	8	36	56		10009
POL	NLPKGWKPK	124	9	36	56		10010
POL	AFQSSMTK	347	9	36	56	1.0000	10011
POL	PAIFQSSMTK	346	10	36	56	0.0760	10012
POL	LTEGALELA	484	10	36	56		10013
POL	VFAIKKKDSTK	249	11	36	56		10014
POL	NTVFAIK	246	8	37	58	0.0003	10015
POL	PVFAIKKK	248	8	37	58	0.0003	10016
POL	QLTEAVOK	559	8	37	58		10017
POL	QIEQLIK	712	8	37	58		10018
POL	IEQLIKK	713	8	37	58		10019
POL	YLSWVPAIL	724	8	37	58		10020
POL	LSWVPAILK	725	8	37	58		10021
POL	NTVFAIKK	246	9	37	58	0.0330	10022
POL	QIEQLIKK	712	9	37	58	0.0091	10023
POL	YLSWVPAILK	724	9	37	58		10024
POL	RDPWIKGPA	983	9	37	58		10025
POL	VIQDNSDIK	1003	9	37	58	0.0049	10026
POL	NTVFAIKKK	246	10	37	58	0.0006	10027
POL	VVIQDNSDIK	1002	10	37	58	0.0005	10028
POL	AVVIQDNSDIK	1000	11	37	58	0.0004	10029
POL	IFQSSMTK	348	8	38	59	0.0055	10030
POL	ILKEPVIIGVY	498	11	38	59		10031

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SEQ ID NO.
POL	LDGDKAQEEII	754	11	39	62		10032
POL	HSNWRAMA	768	8	39	61		10033
POL	AGYVTDGR	647	9	39	61		10034
POL	YVTDGRGR	649	9	39	61	0.0011	10035
POL	KAGYVTDGR	646	10	39	61		10036
POL	LGIIQAQPDK	695	10	39	61	0.0007	10037
POL	DGIQKAQEEII	755	10	39	61		10038
POL	DIKVVPRKA	1009	10	39	61		10039
POL	PVIGVYDFPS	505	11	39	61		10040
POL	AGYVTDGRQ	647	11	39	61		10041
POL	ALGIQAQPDK	694	11	39	61		10042
POL	DIKVVPRKAK	1009	11	39	61		10043
POL	VDRIHQK	650	8	40	63	0.0090	10044
POL	IIQAQPDK	697	8	40	63		10045
POL	GIQAQPDK	696	9	40	63	0.0009	10046
POL	GIDKAQEEII	756	9	40	63		10047
POL	NSDIKVVPR	1007	9	40	63		10048
POL	ILKEPVIGVY	498	10	40	63		10049
POL	NSDIKVVPRR	1007	10	40	63	0.0007	10050
POL	HLKEPVIGVY	497	11	40	63		10051
POL	WTYQIQEPE	529	11	40	63	0.9200	10052
POL	QIQQEPFNK	532	11	40	63	0.2800	10053
POL	SAGERIDIIA	947	11	40	63		10054
POL	QNSDIKVVPR	1005	11	40	63		10055
POL	NSDIKVVPRK	1007	11	40	63		10056
POL	ESIVWGKTPK	570	11	41	65		10057
POL	FFRENLA	1	8	41	64		10058
POL	QIGCTLNF	179	8	41	64	0.0010	10059
POL	QIQQEPK	532	8	41	64		10060
POL	IDKAQEEII	757	8	41	64		10061
POL	KAKIRDY	1017	8	41	64		10062
POL	LTQIGCTLNF	177	10	41	64	0.0081	10063
POL	AGERIDIIA	948	10	41	64		10064
POL	KAKIRDYK	1017	10	41	64	0.0048	10065
POL	KISKIGPENPY	235	11	41	64		10066
POL	SIVWGTTPKF	571	11	41	64		10067
POL	DFRKYTAF	312	8	42	66		10068
POL	KAGYVTD	646	8	42	66		10069
POL	ISKIGPENPY	236	10	42	66	0.0004	10070
POL	SMTKILEPFR	352	10	42	66		10071
POL	WTYQIQEPE	529	10	42	66		10072
POL	SIVWGTTPK	571	10	42	66	0.0004	10073
POL	TTNQKTELQA	664	10	42	66		10074
POL	IVIQYMDLLY	367	11	42	66		10075
POL	VVPRKAKIIR	1012	11	42	66		10076
POL	QVYYDFSK	508	8	43	67		10077
POL	SCDKCQLK	791	8	43	67		10078
POL	SMTKILEPFR	352	9	43	67	0.0004	10079
POL	MTKILEPFR	353	9	43	67	0.0008	10080
POL	HGVYYDFSK	507	9	43	67	0.0004	10081

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SEQ ID NO.
POL	ASCDKCOLK	790	9	43	67	0.0027	10082
POL	DSWTVDNIQK	439	10	43	67	0.0007	10083
POL	TFYVIGAANR	631	10	43	67	0.0003	10084
POL	VASCDKCOLK	789	10	43	67	0.0004	10085
POL	KIQQVRDQA	912	10	43	67		10086
POL	KDSWTVDNIQ	438	11	43	67		10087
POL	ETFYVIGAAN	630	11	43	67		10088
POL	IVASCDKCOLK	788	11	43	67		10089
POL	SDCKCKQLKGE	791	11	43	67	0.0970	10090
POL	MTKILIEPF	353	8	44	69		10091
POL	IGQVRDQA	914	8	44	69		10092
POL	SDIKVVPK	1008	8	44	69		10093
POL	MAGDDCVA	1028	8	44	69		10094
POL	IIGQVRDQA	913	9	44	69		10095
POL	SDIKVVPK	1008	9	44	69	0.0002	10096
POL	QNIAGIDDCVA	1027	9	44	69	0.0003	10097
POL	VDAANRETK	634	10	44	69		10098
POL	IGQVRDQAEH	914	10	44	69		10099
POL	QVRDQAEHLK	916	10	44	69	0.0089	10100
POL	SDIKVVPK	1008	10	44	69	0.0004	10101
POL	PFKNLKTGKY	537	11	44	69		10102
POL	GAETFYVDGA	628	11	44	69		10103
POL	YVDGAANRET	633	11	44	69		10104
POL	IIGQVRDQAEH	913	11	44	69		10105
POL	VAKETVASCOK	784	11	45	71		10106
POL	GAANRETK	636	8	45	70		10107
POL	EIVASCOK	787	8	45	70		10108
POL	DGAANRETK	635	9	45	70		10109
POL	PFKNLKTGKY	537	10	45	70	0.0004	10110
POL	RIQAEHLKTA	918	10	45	70		10111
POL	PLVKLWYQLE	613	11	45	70		10112
POL	ELKEPVII	497	8	46	72		10113
POL	KLWYQLEK	616	8	46	72		10114
POL	RDQAEHLK	918	8	46	72		10115
POL	PFKNLKTGK	537	9	46	72		10116
POL	DIQTKELQK	959	9	46	72	0.0009	10117
POL	LVKLWYQLEK	614	10	46	72	0.0560	10118
POL	KVKQWPLTEE	207	11	46	72	0.0750	10119
POL	VIWGTTPKF	573	9	47	73		10120
POL	VIWGTTPKF	572	10	47	73		10121
POL	VIWGTTPK	573	8	48	75		10122
POL	QVRDQAEH	916	8	48	75		10123
POL	DIKVVPRR	1009	8	48	75		10124
POL	VIWGTTPK	572	9	48	75	0.0850	10125
POL	DIKVVPRRK	1009	9	48	75	0.0002	10126
POL	GAETFYVDGA	628	10	48	75		10127
POL	KVLFIDGIDK	750	10	48	75	0.3600	10128
POL	CDKQLKGEAII	792	10	48	75		10129
POL	KCQLKGEAII	794	10	48	75		10130
POL	VVESMNKELK	902	10	48	75		10131

Table XVI
 IIIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SI:Q ID NO.
POL	KVLELDGIDKA	750	11	48	75		10132
POL	GVVESMNKEL	901	11	48	75		10133
POL	VVESMNKELK	902	11	48	75		10134
POL	GVVESMNK	901	8	49	77		10135
POL	RDYKGOMA	1022	8	49	77		10136
POL	QGVVESMNK	900	9	49	77		10137
POL	KLKPGMDGPK	197	10	49	77		10138
POL	IRDYKGOMA	1020	10	49	77	0.39(8)	10139
POL	OSQGVVESMN	898	11	49	77		10140
POL	KIIRDYCKQMA	1019	11	49	77		10141
POL	ESIVWKG	570	8	50	79		10142
POL	YVDGAANR	633	8	50	78	0.0003	10143
POL	LAGRWPK	856	8	50	78		10144
POL	KIIRDYCK	1019	8	50	78		10145
POL	KLAGRWPVK	855	9	50	78	2.7(8)0	10146
POL	GMDGPKVK	201	8	51	80	0.0007	10147
POL	KIGPENPY	238	8	51	80		10148
POL	FTTPDKKII	403	8	51	80		10149
POL	TFYVDGAA	631	8	51	80		10150
POL	ITDNGSNF	866	8	51	80		10151
POL	PGMDGPKVK	200	9	51	80	0.0004	10152
POL	GFTTPDKKII	402	9	51	80		10153
POL	ETFYVDGAA	630	9	51	80	0.0380	10154
POL	VFLDGIDK	751	9	51	80	0.0007	10155
POL	VYQYMDDL	368	10	51	80		10156
POL	WGFTTPDKKII	401	10	51	80		10157
POL	FTTPDKKIIQK	403	10	51	80	0.0002	10158
POL	VFLDGIDKA	751	10	51	80	0.0004	10159
POL	KSVTVLDVGD	293	11	51	80		10160
POL	GFTTPDKKIIQ	402	11	51	80		10161
POL	QATWIPWEIF	599	10	52	83	0.0004	10162
POL	PAGLNKKK	286	8	52	81		10163
POL	SDLEIGQH	380	8	52	81		10164
POL	DLEIGQH	381	8	52	81		10165
POL	WGFTTPDK	401	8	52	81		10166
POL	GFTTPDKK	402	8	52	81		10167
POL	KCQLKGIA	794	8	52	81		10168
POL	VASGYIEA	831	8	52	81		10169
POL	KIQNFRVY	971	8	52	81		10170
POL	KVPRRKA	1011	8	52	81		10171
POL	VPRRKA	1012	8	52	81	0.0027	10172
POL	ETPGIRYQY	327	9	52	81		10173
POL	GSDLEIGQH	379	9	52	81		10174
POL	SDLEIGQH	380	9	52	81	0.0003	10175
POL	WGFTTPDKK	401	9	52	81	0.0004	10176
POL	ATWIPWEIF	600	9	52	81		10177
POL	HVASGYIEA	830	9	52	81	0.0003	10178
POL	KIQNFRVY	971	9	52	81	0.1200	10179
POL	KVPRRKA	1011	9	52	81	0.0290	10180
POL	VGSDLEIGQH	378	10	52	81		10181

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	GSDLEIGQIR	379	10	52	81		10182
POL	KIQNFVYVYR	971	10	52	81	0.0320	10183
POL	NERVYVYRISR	974	10	52	81		10184
POL	IGGIGGFVKR	134	11	52	81		10185
POL	VGPTPVNIIGR	164	11	52	81		10186
POL	YVGSDEIGQII	377	11	52	81		10187
POL	VGSDLEIGQIR	378	11	52	81		10188
POL	AVIVASGYIEA	828	11	52	81		10189
POL	SGYIEAEVIPA	833	11	52	81		10190
POL	GIPIIPAGLKKK	282	11	53	84		10191
POL	IGGFVKR	137	8	53	83		10192
POL	GFIKVRQY	139	8	53	83		10193
POL	PIETVPVK	190	8	53	83		10194
POL	ETVPVKLK	192	8	53	83	0.0049	10195
POL	ELELAENR	489	8	53	83		10196
POL	QLKGIEAMII	796	8	53	83		10197
POL	ISMNKELK	904	8	53	83		10198
POL	SMNKELKK	905	8	53	83		10199
POL	GIGGFVKR	136	9	53	83	0.0008	10200
POL	GGFIKVRQY	138	9	53	83	0.0004	10201
POL	YIEAEVIPA	835	9	53	83	0.0003	10202
POL	ISMNKELK	904	9	53	83		10203
POL	GIGGFVKR	135	10	53	83	0.0004	10204
POL	IGGFVKVRQY	137	10	53	83	0.0004	10205
POL	ISPIETVPVK	188	10	53	83	0.0003	10206
POL	PIETVPVKLK	190	10	53	83	0.0002	10207
POL	EAELELAENR	487	10	53	83		10208
POL	LVAVIIVASGY	826	10	53	83		10209
POL	GIGGFVKVRQY	136	11	53	83		10210
POL	PISPIETVPVK	187	11	53	83		10211
POL	ILVAVIIVASGY	825	11	53	83		10212
POL	FVNTPLVK	608	9	54	86	0.0120	10213
POL	GIPIIPAGLKK	282	10	54	86	0.0110	10214
POL	LGPIIPAGLKK	281	11	54	86		10215
POL	ILVAVIIVA	825	8	54	84		10216
POL	PTTPVNIIGR	166	9	54	84	0.0008	10217
POL	PLTEEKIK	212	9	54	84		10218
POL	LAENREIK	492	9	54	84	0.0002	10219
POL	EVQLGIPIPA	278	10	54	84		10220
POL	ELAENREIK	491	10	54	84	0.0002	10221
POL	EFVNTPLVK	607	10	54	84		10222
POL	PLTEEKIK	212	8	55	86		10223
POL	ETFYVDGA	630	8	55	86		10224
POL	LFLDGIDK	752	8	55	86		10225
POL	FLDGIDKA	753	8	55	86		10226
POL	LFLDGIDKA	752	9	55	86		10227
POL	QLGIPIPA	280	8	56	89		10228
POL	GIPIIPAGLK	282	9	56	89	0.2300	10229
POL	KGIGGYSA	940	9	56	89		10230
POL	LGPIIPAGLK	281	10	56	89	0.0370	10231

Table XVI
 IIIV A01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	QLGIPIAGLK	280	11	56	89		10232
POL	LTEEKIKK	213	8	56	88		10233
POL	VTLDVGDY	295	10	56	88	0.0001	10234
POL	ELKKIQQR	909	10	56	88		10235
POL	DFWEVQLGPH	275	11	56	88		10236
POL	SVTLVDGDA	294	11	56	88		10237
POL	VTLDVGDY	295	11	56	88		10238
POL	PAETQETAY	842	11	56	88		10239
POL	KTAVOMAVFI	925	11	56	88		10240
POL	TQETAYF	845	8	57	89		10241
POL	AIKKKDKTK	251	9	57	89	0.0017	10242
POL	ELNKRITQDF	268	9	57	89		10243
POL	VTLDVGDY	295	9	57	89		10244
POL	TYLDVGDY	296	9	57	89	0.0002	10245
POL	ITPDKKIIQK	404	9	57	89	0.0002	10246
POL	ETQETAYF	844	9	57	89		10247
POL	IILKTAVQMA	923	9	57	89	0.0003	10248
POL	KTAVQMAVF	925	9	57	89		10249
POL	FAIKKIDSTK	250	10	57	89	0.0004	10250
POL	SVTLVDGDA	294	10	57	89		10251
POL	TYLDVGDYF	296	10	57	89	0.0004	10252
POL	NTPLVKLWY	610	10	57	89	0.0002	10253
POL	AIKKKIDSTK	251	11	57	89		10254
POL	IILKTAVQMAV	923	11	57	89		10255
POL	MAVFIHFKR	930	11	57	89		10256
POL	GGIGYSAGER	941	11	57	89		10257
POL	NLKTGKYA	540	8	58	92		10258
POL	VLPQGWKGSF	337	11	58	92		10259
POL	KDSTKWRK	255	8	58	91		10260
POL	EVQLGPHI	278	8	58	91		10261
POL	TVLDVGDY	296	8	58	91		10262
POL	YALGIQA	693	8	58	91		10263
POL	GGNEQVDK	735	8	58	91		10264
POL	FIHFKRK	933	8	58	91		10265
POL	GGYSAGER	944	8	58	91		10266
POL	RVYRDSR	976	8	58	91		10267
POL	IGNEQVDK	734	9	58	91	0.0004	10268
POL	PAETGQETA	842	9	58	91	0.0004	10270
POL	VFIHFKRK	932	9	58	91	0.0004	10271
POL	IGYSAGER	943	9	58	91	0.0005	10272
POL	STKWRKLVDF	257	10	58	91		10273
POL	GIGNEQVDK	733	10	58	91		10274
POL	PAETGQETAY	842	10	58	91		10275
POL	AVFIHFKRK	931	10	58	91	0.6600	10276
POL	GIGYSAGER	942	10	58	91	0.0003	10277
POL	DSTKWRKLVDF	256	11	58	91		10278
POL	STKWRKLVDF	257	11	58	91		10279
POL	DSQYALGIQA	690	11	58	91		10280
POL	KGIGNEQVDK	732	11	58	91		10281
POL	VIPAEQETA	840	11	58	91		10281

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	QGWKGSQA	340	8	59	92		10282
POL	AVIVASGY	828	8	59	92		10283
POL	ETGQETAY	844	8	59	92		10284
POL	QAEILKTA	920	8	59	92		10285
POL	GGIGGYSA	941	8	59	92		10286
POL	GIWQLDCTH	811	9	59	92		10287
POL	VAVIVASGY	827	9	59	92		10288
POL	KGPAKLLWK	988	9	59	92	0.0004	10289
POL	QVWKGSPIAF	340	10	59	92	0.0021	10290
POL	EVNIVTDSQY	684	10	59	92	0.0004	10291
POL	PGIWQLDCTH	810	10	59	92		10292
POL	TAVQMAVEIII	926	10	59	92	0.0004	10293
POL	VQKLNWASQI	450	11	59	92		10294
POL	EVNIVTDSQYA	684	11	59	92		10295
POL	NFKRKGGIGGY	936	11	59	92		10296
POL	PAKLLWKGEIG	980	11	59	92		10297
POL	QLDCTHILEGK	814	10	60	95	0.0010	10298
POL	VFRELNR	265	8	60	94		10299
POL	VLDVGDAY	297	8	60	94		10300
POL	MAVEIINE	930	8	60	94		10301
POL	VDFRELNR	264	9	60	94		10302
POL	VLDVGDAYF	297	9	60	94		10303
POL	MGVELIIRDK	419	9	60	94	0.0640	10304
POL	KLNWASQIY	452	9	60	94	0.1200	10305
POL	AVQMAVEIII	927	9	60	94		10306
POL	QMAVEIINEF	929	9	60	94	0.0010	10307
POL	MAVEIINEF	930	9	60	94	0.0170	10308
POL	KLLWKGECA	992	9	60	94	0.0003	10309
POL	LVDFRELNR	263	10	60	94		10310
POL	WMGYELIIRDK	418	10	60	94	0.0005	10311
POL	QMAVEIINEF	929	10	60	94	0.6100	10312
POL	MAVEIINEF	930	10	60	94	0.0068	10313
POL	KLVDFRELNR	262	11	60	94		10314
POL	PDKKIQKEPIIF	406	11	60	94		10315
POL	AVQMAVEIIN	927	11	60	94		10316
POL	QMAVEIINEF	929	11	60	94		10317
POL	EALLDTGA	108	8	61	95		10318
POL	LDVGDAYF	298	8	61	95		10319
POL	LVGKLNWA	449	8	61	95		10320
POL	IVTDSQYA	687	8	61	95		10321
POL	TAVQMAVF	926	8	61	95		10322
POL	NIDQKLVGK	444	9	61	95		10323
POL	KLVGKLNWA	448	9	61	95	0.0003	10324
POL	NIVTDSQYA	686	9	61	95		10325
POL	LDCTHILEGK	815	9	61	95		10326
POL	TVNDIQKLVGK	442	11	61	95	0.0400	10327
POL	MIGGIGGF	133	8	62	97		10328
POL	VDFRELNR	264	8	62	97		10329
POL	WTVNDIQK	441	8	62	97	0.0003	10330
POL	DIQKLVGK	445	8	62	97		10331

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0J01	SEQ ID NO.
POL	NIVTDSQY	686	8	62	97		10332
POL	DCTHLEGK	816	8	62	97		10333
POL	AVFIHFK	931	8	62	97	0.0280	10334
POL	VFIHFKR	932	8	62	97		10335
POL	LLWKEGA	993	8	62	97		10336
POL	KMIGGIGF	132	9	62	97	0.0004	10337
POL	LVDFRELK	263	9	62	97	0.0110	10338
POL	AVFIHFKR	931	9	62	97	0.1700	10339
POL	MIGGIGFIK	133	10	62	97	0.0099	10340
POL	KLVDRELK	262	10	62	97	0.5100	10341
POL	KMIGGIGFIK	132	11	62	97	2.3000	10342
POL	NVLQGWK	336	8	63	100	0.0003	10343
POL	IGGIGFIK	134	9	63	98	0.0004	10344
POL	GGIGFIK	135	8	64	100		10345
POL	FLWMGYELI	416	9	64	100		10346
POL	FLWMGYELII	415	10	64	100		10347
REV	GTRQTKNR	37	9	01	50		10348
REV	TTRQARNR	37	9	01	50		10349
REV	GTRQTKNR	37	10	01	50		10350
REV	TTRQARNR	37	10	01	50		10351
REV	GTRQTKNR	37	11	01	50		10352
REV	TTRQARNR	37	11	01	50		10353
REV	GTETGVGR	103	8	06	19		10354
REV	OGTETGVGR	102	9	06	19		10355
REV	LLKTVKLIK	12	9	10	16		10356
REV	GDSDDELLK	6	9	11	17		10357
REV	PLQLPIER	76	9	11	17		10358
REV	SGDSDELLK	5	10	11	17		10359
REV	RGSDSDELLK	4	11	11	17		10360
REV	PVPLQLPIER	74	11	11	17		10361
REV	RARQRIK	50	8	12	19		10362
REV	DSDELLK	7	8	12	19		10363
REV	ILSTCLGR	63	8	12	19		10364
REV	RILSTCLGR	62	9	12	19		10365
REV	AVRIKILY	17	9	13	20		10366
REV	PSPEGTQQA	31	9	13	20		10367
REV	QLPPLERLI	78	9	13	20		10368
REV	PSPEGTQQA	31	10	13	20		10369
REV	PSPEGTQQA	31	11	13	20		10370
REV	PLQLPPLERLI	76	11	13	20		10371
REV	GTRQARKNR	36	11	14	22		10372
REV	RARQRII	36	8	15	24		10373
REV	GTRQARKNR	36	9	15	23		10374
REV	GTRQARKNR	36	10	15	23		10375
REV	QARKNR	40	9	16	25		10376
REV	QARKNR	40	11	16	25		10377
REV	QARKNR	40	8	17	27		10378
REV	IKILYQSNPY	20	11	18	28		10379
REV	KILYQSNPY	22	9	26	41		10380
REV	ILYQSNPY	23	8	27	42		10381

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HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.001$	SEQ ID NO.
REV	EGTROARR	35	8	27	42		10382
REV	EGTROARRNR	35	10	27	42		10383
REV	EGTROARRNR	35	11	27	42		10384
REV	GTRQARRNR	36	9	34	53		10385
REV	GTRQARRNR	36	10	34	53		10386
REV	GTRQARRNR	36	11	34	53		10387
REV	PVQLPLPLER	74	11	34	53		10388
REV	PLQLPLER	76	9	35	55		10389
REV	QARRNR	40	11	37	58		10390
REV	QARRNR	40	8	38	59		10391
REV	QARRNR	40	9	38	59		10392
TAT	PGGYPRK	104	8	01	50		10393
TAT	AGPGYPRR	102	9	01	50		10394
TAT	TGPGQPCII	102	9	01	50		10395
TAT	ETGPGQPCII	101	10	01	50		10396
TAT	KAGPGGYPRR	101	10	01	50		10397
TAT	AGPGGYPRK	102	10	01	50		10398
TAT	KAGPGGYPRR	101	11	01	50		10399
TAT	GGYPRKGGSC	105	11	01	50		10400
TAT	PGSQPRTA	17	8	10	16		10401
TAT	ACTNCCYCK	24	8	10	16		10402
TAT	TACTNCCYCK	23	9	10	16		10403
TAT	YCKKCCYII	29	8	11	17		10404
TAT	YCKKCCYII	29	8	11	17		10405
TAT	CFHCQVCF	34	8	11	17		10406
TAT	VDPRLPEWK	4	9	11	17		10407
TAT	ACNNCCYCK	24	9	11	17		10408
TAT	CCFLCQVCF	33	9	11	17	0.0005	10409
TAT	PVDPRLEPWK	3	10	11	17		10410
TAT	VDPRLPEWKII	4	10	11	17		10411
TAT	TACNNCCYCK	23	10	11	17		10412
TAT	PVDPRLEPWK	3	11	11	17		10413
TAT	RGDPTGPKES	84	11	11	17		10414
TAT	GDPTGPKESK	85	11	11	17		10415
TAT	ESKKKVIESK	93	9	12	19		10416
TAT	GDPTGPKESK	85	10	12	19		10417
TAT	PTGPKESKKK	88	10	12	19		10418
TAT	TGPKESKKK	89	9	13	20		10419
TAT	FLNKGGLGISY	41	10	14	22		10420
TAT	PVDNLEPWN	3	11	14	22		10421
TAT	CFLNKGGLGISY	40	11	14	22		10422
TAT	RGDPTGPK	84	8	16	25		10423
TAT	VDPNLEPWNII	4	10	16	25		10424
TAT	ACNNCCYCK	24	8	17	27		10425
TAT	TACNNCCYCK	23	9	17	27		10426
TAT	PTGPKESKK	88	9	18	28		10427
TAT	TGPKESKK	89	8	19	30		10428
TAT	PTGPKESK	88	8	20	31		10429
TAT	YGRKKRRQR	50	11	22	34		10430
TAT	PGSQPKTA	17	8	26	41		10431

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
TAT	YGRKKRQR	50	10	38	59		10432
TAT	ISYGRKKRQR	48	11	39	61		10433
TAT	YGRKKRQR	50	9	41	64		10434
TAT	GISYGRKKRR	47	10	45	70	0.0003	10435
TAT	LGISYGRKKRR	46	11	45	70		10436
TAT	ISYGRKKRR	48	9	46	72	0.0008	10437
TAT	GLGISYGRKKRR	45	11	54	86		10438
TAT	GLGISYGR	45	8	55	87		10439
TAT	GLGISYGRK	45	9	55	87	0.0340	10440
TAT	GLGISYGRKK	45	10	55	87		10441
TAT	KGLGISYGR	44	9	55	86	0.0006	10442
TAT	KGLGISYGRK	44	10	55	86	0.0100	10443
TAT	KGLGISYGRKK	44	11	55	86		10444
TAT	GISYGRKKR	47	9	57	89	0.0008	10445
TAT	LGISYGRKKR	46	10	57	89		10446
TAT	LGISYGRK	46	8	58	91		10447
TAT	GISYGRKK	47	8	58	91		10448
TAT	ISYGRKKR	48	8	58	91		10449
TAT	LGISYGRKK	46	9	58	91		10450
VIF	LIVWQVDR	8	8	10	16	0.0004	10451
VIF	RMINTWK	15	8	10	16		10452
VIF	LKPKKIK	158	8	10	16		10453
VIF	KGWFYRIIY	36	9	10	16		10454
VIF	ALIKPKIK	157	9	10	16		10455
VIF	VDRMINTWK	13	10	10	16		10456
VIF	GVSEWRLLR	87	10	10	16		10457
VIF	QVDRMRINTW	12	11	10	16		10458
VIF	RLVITYWGL	65	11	10	16		10459
VIF	QTGERDWILG	75	11	10	16		10460
VIF	GVSEWRLLR	87	11	10	16		10461
VIF	IDPLADQLIII	103	11	10	16		10462
VIF	LVEDRWKPKQ	178	11	10	16		10463
VIF	YSTQIDPDLA	99	10	11	17		10464
VIF	YSTQVDPDLA	99	10	11	17		10465
VIF	STEWRLRR	89	8	11	17		10466
VIF	TALIKPKK	156	8	11	17		10467
VIF	LVEDRWK	178	8	11	17		10468
VIF	VSIEWRLRR	88	9	11	17		10469
VIF	STEWRLRR	89	9	11	17		10470
VIF	STOVDPDLA	100	9	11	17		10471
VIF	SLQYLALKA	149	9	11	17		10472
VIF	LTALIKPKK	135	9	11	17		10473
VIF	KLVEDRWK	177	9	11	17		10474
VIF	VSIEWRLRR	88	10	11	17		10475
VIF	GLADQLIIMII	106	10	11	17		10476
VIF	IVSPCEYQA	133	10	11	17		10477
VIF	GSLOYLALKA	148	10	11	17		10478
VIF	ALTALIKPKK	154	10	11	17		10479
VIF	GLADQLIIMII	105	11	11	17		10480
VIF	GLADQLIIMH	106	11	11	17		10481

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^{\circ}0301$	SEQ ID NO.
VIF	VGSQYLALK	147	11	11	17		10482
VIF	LALTALPKPK	153	11	11	17		10483
VIF	WEYRIIYESR	34	11	12	19		10484
VIF	KGWFYRIIH	36	8	12	19		10485
VIF	WGLQTGER	72	8	12	19		10486
VIF	QTGERDWII	75	8	12	19		10487
VIF	SDSAIRKA	121	8	12	19		10488
VIF	SLOYLALA	149	8	12	19		10489
VIF	IVWQVDIRMK	9	9	12	19		10490
VIF	STQIDPOLA	100	9	12	19		10491
VIF	FSDSAIRKA	120	9	12	19		10492
VIF	FSESAIRNA	148	9	12	19		10493
VIF	GSLQYLALA	149	9	12	19		10494
VIF	SLOYLALAA	17	10	12	19		10495
VIF	KIRTWNSLVK	24	10	12	19		10496
VIF	LVKIIIMYVSK	73	10	12	19		10497
VIF	GLQTGERDWII	77	10	12	19		10498
VIF	TGERDWILGII	86	10	12	19		10499
VIF	IQVSIEWRLK	119	10	12	19		10500
VIF	CFSDSAIRKA	119	10	12	19		10501
VIF	CFESAJIUNA	147	10	12	19		10502
VIF	VGSQYLALA	148	10	12	19		10503
VIF	GSLQYLALAA	9	11	12	19		10504
VIF	IVWQVDRMKI	17	11	12	19		10505
VIF	KIRTWNSLVK	23	11	12	19		10506
VIF	SLVKIIIMYVS	24	11	12	19		10507
VIF	LVKIIIMYVSK	72	11	12	19		10508
VIF	WGLQTGERD	118	11	12	19		10509
VIF	DCFSESAIRKA	118	11	12	19		10510
VIF	DCFSESAIRNA	146	11	12	19		10511
VIF	KVGSQYLAL	147	11	12	19		10512
VIF	VGSQYLALA	38	10	13	21		10513
VIF	WEYRIIYESR	12	8	13	20		10514
VIF	QVDRMKIR	28	8	13	20		10515
VIF	IMYVSKKA	56	8	13	20		10516
VIF	HIPLGDAR	108	8	13	20		10517
VIF	ADQLIIMIH	119	8	13	20		10518
VIF	CFSDSAIR	120	8	13	20		10519
VIF	FSDSAIRK	149	8	13	20		10520
VIF	SLOYLALK	155	8	13	20		10521
VIF	LTAIIPK	107	9	13	20		10522
VIF	LADQLIIMH	108	9	13	20		10523
VIF	ADQLIIMHY	119	9	13	20		10524
VIF	CFSDSAIRK	120	9	13	20		10525
VIF	FSESAIRKA	148	9	13	20		10526
VIF	GSLQYLALK	154	9	13	20		10527
VIF	ALTALIKPK	174	9	13	20		10528
VIF	SVKKLTEDR	54	10	13	20		10529
VIF	EVHIPLGDAR	107	10	13	20		10530
VIF	LADQLIIMHY		10	13	20		10531

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
VIF	ADQLIIMIFY	108	10	13	20		10532
VIF	DCFSIAIRK	118	10	13	20		10533
VIF	CFSESARKA	119	10	13	20		10534
VIF	VGSLOYLALK	147	10	13	20		10535
VIF	LALTALIKPK	153	10	13	20		10536
VIF	PSVKRLTEIR	173	10	13	20		10537
VIF	LADQLIIMIFY	107	11	13	20		10538
VIF	QLIHLYFDCF	110	11	13	20		10539
VIF	FDCFSIAIRK	117	11	13	20		10540
VIF	YALTALIKPK	152	11	13	20		10541
VIF	QLIHLYF	110	8	14	22		10542
VIF	QLIIMIFY	110	8	14	22		10543
VIF	FSESARK	120	8	14	22		10544
VIF	IVSPICEY	133	8	14	22		10545
VIF	GVSIEWRLR	87	9	14	22		10546
VIF	ADQLIHLY	108	9	14	22		10547
VIF	CFSESARK	119	9	14	22		10548
VIF	VDRMRITWK	13	10	14	22		10549
VIF	LADQLIHLY	107	10	14	22		10550
VIF	ADQLIHLYF	108	10	14	22		10551
VIF	RCDYQAGIINK	137	10	14	22		10552
VIF	QVDRMRITW	12	11	14	22		10553
VIF	RRTWNSLVK	17	11	14	22		10554
VIF	LADQLIHLYF	107	11	14	22		10555
VIF	QLIIMIFYDCF	110	11	14	22		10556
VIF	RMRTWK	15	8	15	23		10557
VIF	RTWKSIVK	19	8	15	23		10558
VIF	VSIEWRLR	88	8	15	23		10559
VIF	ADQLIHLY	108	8	15	23		10560
VIF	IIMIFYDCF	113	8	15	23		10561
VIF	RTWKSIVKII	19	9	15	23		10562
VIF	QGVSIWRK	86	9	15	23		10563
VIF	LADQLIHLY	107	9	15	23		10564
VIF	AIRKAILGII	124	9	15	23		10565
VIF	CDYQAGIINK	138	9	15	23		10566
VIF	RRTWKSIVK	17	10	15	23		10567
VIF	RRTWNSLVK	17	10	15	23		10568
VIF	RTWKSIVKIII	19	10	15	23		10569
VIF	IIMIFYDCF	111	10	15	23		10570
VIF	SAIRKAILGII	123	11	15	23		10571
VIF	RRTWKSIVK	17	11	15	23		10572
VIF	LGOVSIWR	84	11	15	23		10573
VIF	VDRGLADQLIII	103	11	15	23		10574
VIF	ITTYWGLH	68	8	16	25		10575
VIF	GVSIEWRK	87	8	16	25		10576
VIF	ILYYEDCF	113	8	16	25		10577
VIF	RCDYQAGII	137	8	16	25		10578
VIF	LALTALIK	153	8	16	25		10579
VIF	VITTYWGLII	67	9	16	25		10580
VIF	YALTALIK	152	9	16	25		10581

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	KTKGIKGSII	188	9	16	25		10582
VIF	LVITYWGLII	66	10	16	25	0.0004	10583
VIF	LIILYYFDCF	111	10	16	25		10584
VIF	EDRWKPKQT	180	11	17	27		10585
VIF	KSLVKIIMY	22	9	18	28		10586
VIF	EDRWKPKQT	180	11	18	28		10587
VIF	RCEYQAGINK	137	10	19	30		10588
VIF	IIPPLGEAR	56	8	20	31		10589
VIF	EVIIPLGEAR	54	10	20	31		10590
VIF	ITGERDWH	75	8	21	33		10591
VIF	DLADQLIH	106	8	21	33		10592
VIF	PDLADQLIH	105	9	21	33		10593
VIF	VSPRCEYQA	134	9	21	33		10594
VIF	GLITGERDWH	73	10	21	33		10595
VIF	WGLITGERD	72	11	21	33		10596
VIF	VSPRCEYQAG	134	11	21	33		10597
VIF	LTEDRWKPKQ	178	11	21	33	0.0390	10598
VIF	GSITMNGII	194	8	22	34		10599
VIF	RGSITMNGII	193	9	22	34		10600
VIF	TTYWGLHTGE	69	11	22	34		10601
VIF	IILGIGVSIW	83	11	22	34		10602
VIF	SSEVIHPLGDA	52	11	23	36		10603
VIF	NSLVKIIIMY	22	9	24	38		10604
VIF	EVIIPLGDA	54	9	24	38		10605
VIF	QGVSIW	86	8	25	39		10606
VIF	EVIIPLGEA	54	9	25	39		10607
VIF	LOQGVSIW	84	10	25	39		10608
VIF	SSEVIHPLGEA	52	11	25	39		10609
VIF	IILGIGVSIW	83	11	25	39		10610
VIF	RCEYQAGII	137	8	26	41		10611
VIF	RTWNSLVKII	19	9	26	41		10612
VIF	RTWNSLVKIII	19	10	26	41		10613
VIF	RTWNSLVK	19	8	27	42		10614
VIF	IIGVSIW	86	8	27	42		10615
VIF	GLADQLIH	106	8	27	42		10616
VIF	LGHGVSIW	105	9	27	42		10617
VIF	YFDCFSESAR	84	10	27	42		10618
VIF	WGLITGER	116	11	27	42		10619
VIF	YFDCFSESA	72	8	28	44		10620
VIF	YFDCFSESA	116	9	28	44		10621
VIF	DCFSESAR	118	9	28	44		10622
VIF	FDCFSESAR	117	10	28	44		10623
VIF	FDCFSESA	117	8	29	45		10624
VIF	CFSESAR	119	8	29	45		10625
VIF	KLTEDRWK	177	9	29	45	0.0130	10626
VIF	VGSLQYLALT	147	11	30	47		10627
VIF	LTEDRWK	178	8	31	48	0.0803	10628
VIF	SLQYLALTA	149	9	31	48		10629
VIF	GSLQYLALTA	148	10	31	48		10630
VIF	IVWQVDRMRI	9	11	33	52		10631

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	QVDRMRIR	12	8	34	53		10632
VIF	EDRWKPKQ	180	9	39	61		10633
VIF	VMVWQVDR	7	11	41	64		10634
VIF	QVMVWQVDR	6	10	43	67		10635
VIF	MIVWQVDRM	8	10	43	67		10636
VIF	AGINKVGSQ	142	11	43	67	0.0062	10637
VIF	SLVKIIMY	23	8	44	69		10638
VIF	VMVWQVDR	7	9	44	69	0.0034	10639
VIF	MIVWQVDR	8	8	46	72		10640
VIF	IVWQVDRM	9	9	47	73		10641
VIF	KVGSQYLA	146	9	52	81		10642
VIF	VGSQYLA	147	8	58	91		10643
VPR	#LPGRRGR	85	8	01	50		10644
VPR	NIRGRVR	85	8	01	50		10645
VPR	#LPGRRGRG	85	11	01	50		10646
VPR	WALLELELK	18	10	09	15		10647
VPR	QLLVIFR	66	8	10	16		10648
VPR	ISRIGIIR	79	8	10	16		10649
VPR	RIGTRQR	81	8	10	16		10650
VPR	IGITRQR	82	8	10	16		10651
VPR	ALELEELK	19	9	10	16		10652
VPR	RIGTRQR	81	9	10	16		10653
VPR	ISRIGITRQR	79	10	10	16		10654
VPR	ISRIGITRQR	79	11	10	16		10655
VPR	WLIIGLQY	38	8	11	17		10656
VPR	IFRIGCRII	71	8	11	17		10657
VPR	ISRIGITR	79	8	11	17		10658
VPR	LIIFRIGCR	69	9	11	17		10659
VPR	LIIFRIGCR	68	10	11	17		10660
VPR	LIIFRIGCRH	69	10	11	17		10661
VPR	FVIFRIGCQH	69	10	11	17		10662
VPR	IFRIGCRIIS	71	10	11	17		10663
VPR	LIIFRIGCR	67	11	11	17		10664
VPR	LIIFRIGCRH	68	11	11	17		10665
VPR	LFVIFRIGCQH	68	11	11	17		10666
VPR	RIGCRIIS	74	8	12	19		10667
VPR	LGOIIVNTY	42	9	13	20		10668
VPR	LGOIIVNTY	42	9	13	20		10669
VPR	LGOIIVNTY	42	9	13	20		10670
VPR	IFPKIWLII	33	8	14	22		10671
VPR	KSEAVRHFPR	27	10	14	22		10672
VPR	AVRIIFRIWL	30	11	14	22		10673
VPR	KSEAVRHF	27	8	15	23		10674
VPR	ELKSEAVRIIF	25	10	15	23		10675
VPR	ELKSEAVR	25	8	16	25		10676
VPR	ETYGDTWA	48	8	16	25		10677
VPR	DTWAGVEA	52	8	16	25		10678
VPR	AGVEAIR	55	8	16	25		10679
VPR	LLELKSEA	22	9	16	25		10680
VPR	ELKSEAVRIH	25	9	16	25		10681
VPR	GDTWAGVEA	51	9	16	25		10682

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VPR	WAGVEAIR	54	9	16	25		10682
VPR	ELLELKNEA	21	10	16	25		10683
VPR	ELLELKSEA	21	10	16	25		10684
VPR	YGDWAGVEA	50	10	16	25		10685
VPR	LLEELKSEAVR	22	11	16	25		10686
VPR	DTWAGVEAIR	52	11	16	25		10687
VPR	ELKNEAVR	25	8	17	27		10688
VPR	LLELKNEA	22	9	17	27		10689
VPR	ELKNEAVRH	25	9	17	27		10690
VPR	LOQHYYET	42	9	17	27		10691
VPR	ELKNEAVRIIF	25	10	17	27		10692
VPR	LLEELKNEAVR	22	11	17	27		10693
VPR	EGVEAIR	55	8	18	28		10694
VPR	DTWEGVEAIR	52	11	18	28		10695
VPR	RAINGASR	93	8	19	30		10696
VPR	WLIGLGOH	38	8	20	31		10697
VPR	HGLQHHY	40	8	20	31		10698
VPR	WLIGLQHHY	38	10	20	31		10699
VPR	DTWEGVEA	52	8	23	36		10700
VPR	GDTWEGVEA	51	9	23	36		10701
VPR	YGDWEGVEA	50	10	23	36		10702
VPR	LFIHF RIGCCQH	68	11	29	45		10703
VPR	FIIHF RIGCCQH	69	10	30	47		10704
VPR	HFPRFWLI	33	8	31	49		10705
VPR	AVRIHPRPWL	30	11	31	48		10706
VPR	RIQLQLFIHF	62	11	33	53		10707
VPR	ILQLQLFIHF	63	10	34	55		10708
VPR	ILQLQLFIHF	63	11	35	55		10709
VPR	ILQLQLFIHF	62	10	36	56		10710
VPR	ILQLQLFIHF	63	9	37	58		10711
VPR	EDQGPQREPY	6	10	37	58	0.0130	10712
VPR	AIHILQQLLF	59	11	38	59		10713
VPR	QAPEDQGPQR	3	10	39	62		10714
VPR	IIRILQQLLF	60	10	41	64		10715
VPR	WTLELEELK	18	10	42	69		10716
VPR	QKQREPY	8	8	43	68		10717
VPR	QLLFIHF	66	8	44	69		10718
VPR	IIFRIGCCQH	71	8	44	69		10719
VPR	TELELEELK	19	9	44	69		10720
VPR	HFRIGCCQISR	71	10	44	69		10721
VPR	RIQLQLLF	62	8	45	70		10722
VPR	RIGCCQISR	74	8	47	73		10723
VPR	EAVRIHPR	29	8	59	92		10724
VPU	IDYRLGVGA	9	9	01	33		10725
VPU	VDYRLVIVA	9	9	01	33		10726
VPU	VDYRLGVGA	9	9	01	33		10727
VPU	KVDYRLVIVA	7	10	01	33		10728
VPU	KVDYRLGVGA	7	10	01	33		10729
VPU	RIDYRLGVGA	7	10	01	33		10730
VPU	VDYRLVIVAF	9	10	01	33		10731

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VPU	KVDYRIVIVAF	7	11	01	33		10732
VPU	LVQRKQDR	43	8	01	50		10733
VPU	GVEMGHIIA	91	8	01	50		10734
VPU	VTLSSSK	94	8	01	50		10735
VPU	LVQRKQDR	43	9	01	50		10736
VPU	LVTLLSSK	91	9	01	50		10737
VPU	RIKEIRDDSDY	64	11	01	50		10738
VPU	RIREIRDDSDY	64	11	01	50		10739
VPU	LAIVALVVA	13	9	09	15		10740
VPU	WTIVFIEYR	34	9	10	16		10741
VPU	TIVFIEYR	35	8	10	16		10742
VPU	IDRLIDKIR	54	9	10	16		10743
VPU	KLIDRIR	56	9	10	16		10744
VPU	KIDRLIDKIR	52	10	10	16		10745
VPU	VVWTVTFIEYR	31	11	10	16		10746
VPU	ESGIDQEELSA	75	11	10	16		10747
VPU	EGDQEELSA	77	9	11	17		10748
VPU	WTIVFIEY	34	8	12	19		10749
VPU	AIVALVVA	14	8	12	19		10750
VPU	IVFIEYRK	36	8	12	19		10751
VPU	IDRIRERA	59	8	12	19		10752
VPU	LIDRIRERA	58	9	12	19		10753
VPU	VVWTVTFIEY	31	10	12	19		10754
VPU	IVWTVTFIEY	30	11	12	19		10755
VPU	GDQEELSA	78	8	14	22		10756
VPU	LIDRIRER	58	8	14	22		10757
VPU	AIVWTVTF	29	9	14	22		10758
VPU	IVWTVTF	30	8	15	23		10759
VPU	KIDRLIDR	52	8	15	23		10760
VPU	ILRQKIDR	46	9	15	23		10761
VPU	KILRQKIDR	45	10	15	23	0.0039	10762

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*101	SEQ ID NO.
ENV	IGPGQTFY	361	8	01	25		10763
ENV	IGSQAFY	361	8	01	25		10764
ENV	GTAGNSSR	375	8	01	33		10765
ENV	NTSPRSR	375	8	01	33		10766
ENV	ADNLWVTYY	42	9	01	33		10767
ENV	GIGPGQTFY	360	9	01	33		10768
ENV	SIGSQAFY	360	9	01	33		10769
ENV	ADNLWVTYY	42	10	01	33		10770
ENV	EGKNEINDTY	217	10	01	33		10771
ENV	NTSPRSVAY	376	10	01	33		10772
ENV	TAGNSSRAAY	376	10	01	33		10773
ENV	GTAGNSSRAA	375	11	01	33		10774
ENV	NTSPRSRVA	375	11	01	33		10775
ENV	KLREIQFENK	405	11	01	25		10776
ENV	KNNTETNK	535	8	01	50		10777
ENV	INIITPI	584	8	01	50		10778
ENV	VISTRTHIR	584	8	01	50		10779
ENV	INIITHIR	585	8	01	50		10780
ENV	STRTHIREK	586	8	01	50		10781
ENV	SNNTSPKSR	374	9	01	50		10782
ENV	NANITPCIR	478	9	01	50		10783
ENV	INIITPIIR	584	9	01	50		10784
ENV	ISTRTHIREK	585	9	01	50		10785
ENV	NIITPIIREK	586	9	01	50		10786
ENV	STRTHIREKR	586	9	01	50		10787
ENV	VISTRTHIREK	584	10	01	50		10788
ENV	INIITHIREK	585	10	01	50		10789
ENV	ISTRTHIREKR	585	10	01	50		10790
ENV	NIITPIREKR	586	10	01	50		10791
ENV	IITEGNTLQCR	478	11	01	50		10792
ENV	NANITPCRIK	478	11	01	50		10793
ENV	GNSNGTETF	535	11	01	50		10794
ENV	INIITHIREK	584	11	01	50		10795
ENV	VISTRTHIREKR	584	11	01	50		10796
ENV	INIITHIREKR	585	11	01	50		10797
ENV	DSSNSTGNY	218	9	01	20		10798
ENV	STNGTETFR	537	9	01	17		10799
ENV	TNSSYTNDTY	458	10	01	17		10800
ENV	NDTENNTETFR	537	11	01	17		10801
ENV	NTETNKTETF	537	11	01	17		10802
ENV	NTGNTTETF	537	11	01	17		10803
ENV	NGSENGTETF	537	11	02	33		10804
ENV	GSENGTETFR	538	10	02	18		10805
ENV	NDITLTCR	477	9	03	20		10806
ENV	NDITLTCRIK	477	11	03	20		10807
ENV	RGWEALKY	895	8	06	19		10808
ENV	KGLRLGWEGGL	891	11	08	27		10809
ENV	LGWEGGLY	895	8	09	29		10810
ENV	RLGWEGGLY	894	9	09	29		10811
ENV	GLRLGWEGGLK	892	11	09	29		10812

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SFQ ID NO.
ENV	LGRRGWEALK	883	10	09	15		10813
ENV	LLGRRGWEAL	882	11	09	15		10814
ENV	RLGRGWEGLK	894	8	10	32		10815
ENV	GLRLGWEGLK	892	10	10	32		10816
ENV	ENLWVTYV	43	8	10	17		10817
ENV	ENLWVTYVY	43	9	10	17		10818
ENV	DIIGDIRQAH	372	10	10	16		10819
ENV	NNRKSIR	350	8	10	16		10820
ENV	PLGVAPTR	571	8	10	16		10821
ENV	DIITNLWLY	769	8	10	16		10822
ENV	DFILIAAR	870	8	10	16		10823
ENV	STITOACPK	243	9	10	16		10824
ENV	FDITNLWLY	768	9	10	16		10825
ENV	RDFILIAAR	869	9	10	16		10826
ENV	FAILKCNDDK	269	10	10	16		10827
ENV	MLQLTWGJK	651	10	10	16		10828
ENV	RVLAVERYLR	665	10	10	16		10829
ENV	WFDITNLWLY	767	10	10	16		10830
ENV	EGHIEEGGER	828	10	10	16		10831
ENV	GFALKCNDDK	268	11	10	16		10832
ENV	GDHIGIRQAH	371	11	10	16		10833
ENV	NVPWNSSWSN	693	11	10	16		10834
ENV	WMEWEIREIDN	723	11	10	16		10835
ENV	IAIAVAEFTDR	925	11	10	16		10836
ENV	RGWEALKY	886	8	11	18		10837
ENV	KLWVTYVY	44	8	11	17		10838
ENV	WNSSWSNR	696	8	11	17		10839
ENV	TITQACPK	244	8	11	17		10840
ENV	IGRGQTFY	358	8	11	17		10841
ENV	LAVERYLR	667	8	11	17		10842
ENV	SNWLWYIK	771	8	11	17		10843
ENV	NCLFSYII	859	8	11	17		10844
ENV	RIGRGQTFY	357	9	11	17		10845
ENV	ITTIISFNCR	431	9	11	17		10846
ENV	NITLPCRIK	482	9	11	17		10847
ENV	VLAVERYLR	666	9	11	17		10848
ENV	ISNLWLYIK	770	9	11	17		10849
ENV	NCLFSYII	858	9	11	17		10850
ENV	NCLFSYIIR	859	9	11	17		10851
ENV	EITTIISFNCR	430	10	11	17		10852
ENV	RNCLFSYIIR	858	10	11	17		10853
ENV	YATGDIIGDIR	368	11	11	17		10854
ENV	DLRNCLFSYII	856	11	11	17		10855
ENV	NCLFSYHRLR	859	11	11	17		10856
ENV	GNLWVTYVY	43	8	12	20		10857
ENV	GNLWVTYVY	43	9	12	20		10858
ENV	TGDIIGDIR	370	9	12	19		10859
ENV	EAQIILLK	646	8	12	19		10860
ENV	ILKCNDDK	271	8	12	19		10861
ENV	TTIISFNCR	432	8	12	19		10862

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*101	SEQ ID NO.
ENV	MTWMEWER	721	8	12	19		10863
ENV	GGERDRR	834	8	12	19		10864
ENV	AILKCNKK	270	9	12	19		10865
ENV	LAEEVVR	312	9	12	19	0.0002	10866
ENV	INMWQEVGK	493	9	12	19		10867
ENV	NMTWMEWER	720	9	12	19		10868
ENV	GIEEGGER	829	9	12	19		10869
ENV	EGGERDRR	833	9	12	19		10870
ENV	SLAEEVVR	311	10	12	19		10871
ENV	ATGIDGDIR	369	10	12	19		10872
ENV	INMWQEVGK	492	10	12	19		10873
ENV	ATAQQHLLK	644	10	12	19		10874
ENV	LLQYWSQELK	906	10	12	19		10875
ENV	AILHPRIR	946	10	12	19		10876
ENV	PTRIQGLER	951	10	12	19		10877
ENV	KTLFCASDA	60	11	12	19		10878
ENV	GSLAEEVVR	310	11	12	19		10879
ENV	QINMWQEVG	491	11	12	19		10880
ENV	KNEQLLELDK	750	11	12	19		10881
ENV	GIEEGGERDR	829	11	12	19		10882
ENV	NLLQYWSQEL	905	11	12	19		10883
ENV	RAILHPRIR	945	11	12	19		10884
ENV	SVEINCTR	340	8	13	20		10885
ENV	GDIGDIR	371	8	13	20		10886
ENV	KLTVWGK	653	8	13	20		10887
ENV	RAILHPR	945	8	13	20		10888
ENV	AILHPRR	946	8	13	20		10889
ENV	KAKRRVVQR	579	9	13	20	0.0002	10890
ENV	RAILHPRR	945	9	13	20		10891
ENV	ILHPRIR	947	9	13	20		10892
ENV	TNVSTVQCTH	286	10	13	20		10893
ENV	SGGDPFVMI	425	10	13	20		10894
ENV	LLKLTWGIK	651	10	13	20		10895
ENV	NTSVITQACP	241	11	13	20		10896
ENV	CTNVSTVQCT	285	11	13	20		10897
ENV	SSGDDLETTI	424	11	13	20		10898
ENV	SSGDDPEVMH	424	11	13	20		10899
ENV	PTKAKRRVVQ	576	11	13	20		10900
ENV	KAKRRVQRE	579	11	13	20		10901
ENV	ILLKLTWGI	650	11	13	20		10902
ENV	KNEQDLLALD	750	11	13	20		10903
ENV	TGEIGDIR	370	9	14	23		10904
ENV	AITQACP	244	8	14	22		10905
ENV	GDPEVMH	427	8	14	22		10906
ENV	QDLLALDK	753	8	14	22		10907
ENV	SAITQACP	243	9	14	22		10908
ENV	FAILKCNDR	269	9	14	22		10909
ENV	GGDPFVMI	426	9	14	22	0.0012	10910
ENV	TITLPCRIK	482	9	14	22		10911
ENV	TSATQACP	242	10	14	22		10912

Table XVII
IIIY A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
ENV	TSVITQACP	242	10	14	22		10913
ENV	GFAILKCNDK	268	10	14	22		10914
ENV	IFAVLSIVNR	793	10	14	22		10915
ENV	NTSAITQACP	241	11	14	22		10916
ENV	AGFAILKCNDK	267	11	14	22		10917
ENV	IFAVLSIVNR	792	11	14	22		10918
ENV	KIEPLGVAPTK	568	11	15	24		10919
ENV	FDPIPIIY	255	8	15	23		10920
ENV	PAGYAILK	266	8	15	23		10921
ENV	NMWQEVGK	494	8	15	23		10922
ENV	TNWLWYIK	771	8	15	23		10923
ENV	ITNLWYIK	770	9	15	23		10924
ENV	SGDLEITII	425	10	15	23		10925
ENV	IFRPGGDMR	545	10	15	23		10926
ENV	NMWQEVGKA	494	11	15	23		10927
ENV	EIERIGGIDMR	544	11	15	23		10928
ENV	DDLRLNLCFSY	855	11	15	23		10929
ENV	FNCTGPK	279	8	16	25		10930
ENV	RNLCLFSY	858	8	16	25		10931
ENV	ITKWLWYIK	770	9	16	25		10932
ENV	SPNCRGIEFFY	437	10	16	25		10933
ENV	DLRLNLCFSY	856	10	16	25		10934
ENV	ISFNCRGIEFFY	434	11	16	25		10935
ENV	WNASWSNK	696	8	17	27		10936
ENV	KAYDTEVII	72	8	17	27		10937
ENV	VITQACP	244	8	17	27		10938
ENV	RVQREKR	587	8	17	27	0.0001	10939
ENV	SVITQACP	243	9	17	27		10940
ENV	VAPTKAKRR	574	9	17	27	0.0002	10941
ENV	DAKAYDTEVII	70	10	17	27		10942
ENV	GVAPTKAKRR	573	10	17	27		10943
ENV	VFAVLSIVNR	793	10	17	27		10944
ENV	SDAKAYDTEV	69	11	17	27		10945
ENV	DTEVINWAT	75	11	17	27		10946
ENV	NCTRPNNTR	344	11	17	27		10947
ENV	LGVAPTKAKR	572	11	17	27		10948
ENV	IVFAVLSIVNR	792	11	17	27		10949
ENV	WNSSWSNK	696	8	18	29		10950
ENV	ENVTFNFMW	100	11	18	29		10951
ENV	VLAVERYLK	666	9	18	28		10952
ENV	RVLAVERYLK	665	10	18	28		10953
ENV	NCRGEFFY	439	8	19	30		10954
ENV	GVAPTKAK	573	8	19	30		10955
ENV	VAPTKAKR	574	8	19	30		10956
ENV	FNCRGEFFY	438	9	19	30		10957
ENV	LGVAPTKAK	572	9	19	30		10958
ENV	GVAPTKAKR	573	9	19	30		10959
ENV	PLGVAPTKAK	571	10	19	30		10960
ENV	LGVAPTKAKR	572	10	19	30		10961
ENV	SSNITGLLLTR	516	11	19	30		10962

Table XVII
 HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	PLQVAPTKAK	571	11	19	30		10963
ENV	AILKCNCK	270	8	20	31		10964
ENV	ETRPGGGDM	544	11	20	31		10965
ENV	LIESQNQKEK	740	11	20	31		10966
ENV	GDLEITTH	427	8	21	33		10967
ENV	GGLEITTH	426	9	21	33		10968
ENV	TAIAVAEGTDR	925	11	21	33		10969
ENV	RIVELLGR	878	8	22	34		10970
ENV	IVELLGR	879	8	22	34	0.0100	10971
ENV	RIVELLGR	878	9	22	34		10972
ENV	NCTRPNNTR	344	10	22	34		10973
ENV	CTRPNNTRK	345	10	22	34		10974
ENV	TTLFCASDA	60	11	22	34		10975
ENV	INCTRPNNTR	343	11	22	34		10976
ENV	TVQCTIGIR	290	9	23	36	0.0008	10977
ENV	STVQCTIGIR	289	10	23	36		10978
ENV	VSTVQCTIGIR	288	11	23	36		10979
ENV	TRPQGGIMR	545	10	24	38		10980
ENV	ALAWDDL	851	8	25	39		10981
ENV	LALAWDDL	850	9	25	39		10982
ENV	KNVSTVQCTI	286	10	25	39		10983
ENV	IVQQQNLLR	634	10	25	39	0.0190	10984
ENV	FLALAWDLR	849	10	25	39		10985
ENV	GIVQQQNLLR	633	11	25	39		10986
ENV	GFLALAWDL	848	11	25	39		10987
ENV	ITLPCRIK	483	8	26	41		10988
ENV	PLGVAPTK	571	8	26	41		10989
ENV	LAVERYLK	667	8	26	41		10990
ENV	KNNMVEQMH	110	9	26	41		10991
ENV	IVQQQNLLR	634	10	26	41		10992
ENV	GIVQQQNLLR	633	11	26	41		10993
ENV	IIGDIRQAI	377	9	27	44		10994
ENV	ESQNQKEK	743	8	27	42		10995
ENV	IGDIRQAI	378	8	28	44		10996
ENV	NNMVEQMII	111	8	28	44		10997
ENV	TVQCTIGIK	290	9	28	44	0.0460	10998
ENV	CTRPNNTR	345	9	28	44		10999
ENV	VSFEPPIHY	253	10	28	44		11000
ENV	STVQCTIGIK	289	10	28	44		11001
ENV	ASITLTQAR	619	10	28	44		11002
ENV	KVSFEPPIHY	252	11	28	44		11003
ENV	YCAPAGFAILK	263	11	28	44		11004
ENV	VSTVQCTIGIK	288	11	28	44		11005
ENV	AASITLTQAR	618	11	28	44		11006
ENV	VSFEPPII	253	9	29	45		11007
ENV	KVSFEPPII	252	10	29	45		11008
ENV	CAPAGFAILK	264	10	29	45		11009
ENV	RSELYKYKV	558	11	29	45		11010
ENV	AVLSIVNR	795	8	31	48		11011
ENV	AVAEQTD	928	8	31	48		11012

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	VTENFMNWK	102	9	31	48		11013
ENV	SPEMPLITY	254	9	31	48		11014
ENV	FAVLSIVNR	794	9	31	48		11015
ENV	SLCLFSYIIR	859	9	31	48		11016
ENV	IAVAEGTDR	927	9	31	48	0.0003	11017
ENV	NYTENFMNW	101	10	31	48		11018
ENV	AVLSIVNRVR	795	10	31	48		11019
ENV	RSCLFSYIIR	858	10	31	48		11020
ENV	AIAVAEGTDR	926	10	31	48		11021
ENV	FAVLSIVNRVR	794	11	31	48		11022
ENV	DDLRSCLFSY	855	11	31	48		11023
ENV	SLCLFSYIIRLR	859	11	31	48		11024
ENV	ELYKYKVK	560	9	32	51		11025
ENV	RYVEREKR	587	8	32	50		11026
ENV	ITLTVOAR	621	8	32	50		11027
ENV	SLCLFSYII	859	8	32	50		11028
ENV	SNLTVOAR	620	9	32	50		11029
ENV	RSCLFSYII	858	9	32	50		11030
ENV	DLRSCLFSYII	856	11	32	50		11031
ENV	SPEMPLII	254	8	33	52		11032
ENV	RVLAVERY	665	8	33	52	0.0003	11033
ENV	QARVLAVR	663	9	33	52		11034
ENV	QARVLAVRY	663	10	33	52		11035
ENV	QLQARVLAVE	661	11	33	52		11036
ENV	IMVGGGLIGLR	781	11	34	54	0.0110	11037
ENV	LLQLTVWGII	651	10	34	53		11038
ENV	ILLQLTVWGI	650	11	34	53		11039
ENV	LSIVNRVRQGY	797	11	34	53		11040
ENV	NLWVTVYY	44	8	35	56		11041
ENV	NCGGIEFF	439	8	35	55		11042
ENV	RSCLFSY	858	8	35	55		11043
ENV	EVINRWATH	77	9	35	55		11044
ENV	FNCGGIEFF	438	9	35	55		11045
ENV	NITGLLLTR	519	9	35	55	0.0001	11046
ENV	SFNCGGIEFF	437	10	35	55		11047
ENV	SNITGLLLTR	517	10	35	55	0.0014	11048
ENV	DLRSCLFSY	856	10	35	55		11049
ENV	IISFNCGGIEFF	434	11	35	55		11050
ENV	GGGDMRDNW	549	10	36	56		11051
ENV	MIVGGGLIGLR	782	10	36	56		11052
ENV	SIVNRVRQGY	798	10	36	56	0.0008	11053
ENV	PGGDMRDN	548	11	36	56		11054
ENV	ITGLLLTR	520	8	37	58		11055
ENV	DMRDNRSEL	552	11	37	58		11056
ENV	PAGFAILK	266	8	38	59		11057
ENV	LSIVNRVR	797	8	38	59		11058
ENV	VLSIVNRVR	796	9	38	59		11059
ENV	IVNRVRQGY	799	9	38	59		11060
ENV	ISLWDQSLK	121	10	38	59	0.0540	11061
ENV	DIISLWDQSLK	120	11	38	59		11062

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	GDMRDNR	551	8	39	61		11063
ENV	GGDMRDNR	550	9	39	61		11064
ENV	RDNWRSELY	554	9	40	63	0.0001	11065
ENV	RDNWRSELYK	554	10	40	63	0.0028	11066
ENV	TLFCASDAKA	64	11	40	63		11067
ENV	RDNWRSELYK	554	11	40	63		11068
ENV	TVYYGVPVWK	48	10	41	64	7.8000	11069
ENV	TVYYGVPVW	47	11	41	64	4.1000	11070
ENV	CASDAKAY	67	8	42	66		11071
ENV	LCLFSYIIR	860	8	42	66		11072
ENV	FCASDAKAY	66	9	42	66		11073
ENV	IVGGLIGLR	783	9	42	66		11074
ENV	CLFSYIIRL	861	9	42	66		11075
ENV	LFCASDAKAY	65	10	42	66	0.0002	11076
ENV	LCLFSYIIRL	860	10	42	66		11077
ENV	VGHIGLR	784	8	43	67		11078
ENV	QLTVWGJK	653	8	44	69		11079
ENV	LFSYIIRL	862	8	44	69		11080
ENV	RIRQGLER	959	8	44	69		11081
ENV	VNRVRQGY	800	8	45	71		11082
ENV	SLWDOSLK	123	8	47	75		11083
ENV	WDQSLKPCVK	122	9	47	73		11084
ENV	QSLKPCVK	125	10	47	73	0.0090	11085
ENV	TVWGKQLQA	127	8	48	75		11086
ENV	DNWRSELY	555	11	48	75		11087
ENV	GIKQLQAR	658	8	49	77		11088
ENV	DNWRSELYK	555	9	49	77	0.0014	11089
ENV	WGKQLQAR	657	9	49	77	0.0001	11090
ENV	DNWRSELYK	555	10	49	77	0.0001	11091
ENV	DNWRSELYK	555	11	49	77		11092
ENV	LGWGCSCG	679	9	50	78	0.0023	11093
ENV	TLFCASDAK	61	10	50	78	0.2200	11094
ENV	LLGIWGCSCG	678	10	50	78	0.0120	11095
ENV	NLLRAIEAQH	640	11	50	78		11096
ENV	QLLGIWGCSCG	677	11	50	78		11097
ENV	VSTVQCTH	288	8	51	80		11098
ENV	RAIEAQH	643	8	51	80		11099
ENV	NVSTVQCTH	287	9	51	80		11100
ENV	LLRAIEAQH	641	10	51	80		11101
ENV	GIWGCSCG	680	8	52	81		11102
ENV	TLFCASDAK	64	9	52	81		11103
ENV	RSELYKY	558	8	54	84	0.5300	11104
ENV	LFCASDAK	65	8	57	89		11105
GAG	AAAMMQK	405	8	01	25		11106
GAG	SATIMMQR	405	8	01	25		11107
GAG	KDKDKELY	535	8	01	25		11108
GAG	ETIDKELY	537	8	01	25		11109
GAG	NSATIMMQR	404	9	01	33		11110
GAG	TAMPESFR	508	9	01	33		11111
							11112

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	NGKQANFLGK	461	10	01	25		11113
GAG	NGRQANFLGK	461	10	01	25		11114
GAG	PTAPPESFR	507	10	01	33		11115
GAG	NGKQANFLGK	461	11	01	25		11116
GAG	NGRQANFLGK	461	11	01	25		11117
GAG	PAADKDEK	123	8	01	50		11118
GAG	ASAQDLK	392	8	01	50		11119
GAG	ATAQDLK	392	8	01	50		11120
GAG	AADKGVSNY	130	10	01	50		11121
GAG	SAQDLKGGY	393	10	01	50		11122
GAG	TAQDLKGGY	393	10	01	50		11123
GAG	GTRPGNYVQK	480	10	01	50		11124
GAG	GTRPGNYVQR	480	10	01	50		11125
GAG	ITSLPKQEQK	526	10	01	50		11126
GAG	PAADKDEKIS	123	11	01	50		11127
GAG	GANSIIPGDIY	276	11	01	50		11128
GAG	PNQPIPVGDIY	276	11	01	50		11129
GAG	ASAQDLKGG	392	11	01	50		11130
GAG	ATAQDLKGG	392	11	01	50		11131
GAG	ETSLPKQEQK	525	11	01	50		11132
GAG	YTAVFMQR	405	8	02	50		11133
GAG	TAPIAESFR	508	9	02	67		11134
GAG	PTAPPESFR	507	10	02	67		11135
GAG	EGRQANFLGK	462	10	02	100		11136
GAG	AADKGVSN	129	11	02	18		11137
GAG	EADKGVSNY	129	10	04	36		11138
GAG	AAIMMQK	400	8	04	19		11139
GAG	AAIMMQSNF	406	11	06	15		11140
GAG	KTVKCFNCGK	421	10	08	16		11141
GAG	GARASILR	2	8	10	16		11142
GAG	PGNFIQSR	483	8	10	16		11143
GAG	MGARASILR	1	9	10	16		11144
GAG	KIWPSSKGR	472	9	10	16		11145
GAG	TGNSSQVSN	139	11	10	16		11146
GAG	NFLGKIWPSSK	468	11	10	16		11147
GAG	PVATPGQMR	243	8	10	16		11148
GAG	MMQKSNFK	409	8	10	16		11149
GAG	MMQGNFK	409	8	10	16		11150
GAG	KLDKWEKIR	12	9	10	16	0.0001	11151
GAG	GGKKKYKLLK	24	9	10	16		11152
GAG	RDTEALDK	97	9	10	16		11153
GAG	IMMQKSNFK	408	9	10	16		11154
GAG	LGIWPFSSK	470	9	10	16		11155
GAG	PGKKKYKLLK	23	10	10	16		11156
GAG	GGKKKYKLLH	24	10	10	16		11157
GAG	AGPVAPQMR	241	10	10	16		11158
GAG	FLGKIWPSSK	469	10	10	16		11159
GAG	KLDKWEKIRL	12	11	10	16		11160
GAG	PGKKKYKLLK	23	11	10	16		11161
GAG	LGIWPFSSKGR	470	11	10	16		11162

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	ATIMQGRGNF	406	11	11	28		11163
GAG	PSQKQEMDK	528	10	11	18		11164
GAG	PIPVGDIV	279	8	11	17		11165
GAG	TIKCFNCGK	422	9	11	17		11166
GAG	TVKCFNCGK	422	9	11	17		11167
GAG	GNSQVSONY	140	10	12	23		11168
GAG	TIMMQRGNFR	407	10	12	21		11169
GAG	QTGSEELR	71	8	12	19		11170
GAG	FNGCKEGIIAR	426	11	12	19		11171
GAG	PGKKKKYK	23	8	12	19		11172
GAG	TYCYVIOK	86	8	12	19		11173
GAG	DTKEALEK	98	8	12	19		11174
GAG	MLNIVGGH	208	8	12	19		11175
GAG	PTSILDIR	103	8	12	19		11176
GAG	GSEELRSLY	73	9	12	19		11177
GAG	ATLYCVIIQK	85	9	12	19		11178
GAG	KDTKEALEK	97	9	12	19		11179
GAG	MMNIVGGH	207	9	12	19		11180
GAG	TGSEELRSLY	72	10	12	19		11181
GAG	VATLYCVIIQK	84	10	12	19		11182
GAG	NMMLNIVGGH	206	10	12	19		11183
GAG	YSP'TSILDIR	301	10	12	19		11184
GAG	RAIQASQEVK	329	10	12	19		11185
GAG	RLRPGKKKY	20	11	12	19		11186
GAG	TVATLYCVIIQ	83	11	12	19		11187
GAG	LNMLNIVGG	205	11	12	19		11188
GAG	SNPPVGEIY	273	11	12	19		11189
GAG	TSILDIRQGP	304	11	12	19		11190
GAG	PGNFQNR	483	8	13	21		11191
GAG	IARNCRAPR	434	9	13	21		11192
GAG	KIWPNSKGR	472	9	13	21		11193
GAG	NCGKEGIIAR	427	10	13	21		11194
GAG	IARNCRAPRK	434	10	13	21		11195
GAG	IARNCRAPRK	434	11	13	21		11196
GAG	NELGKIWPNSK	468	11	13	21		11197
GAG	KGR'GNFLQN	478	11	13	21		11198
GAG	RIEVKDTK	93	8	13	20		11199
GAG	IVKCFNCGK	422	9	13	20		11200
GAG	CGKEGIIAR	428	9	13	20		11201
GAG	EGHIANCR	431	9	13	20		11202
GAG	LGIKIWPNSK	470	9	13	20		11203
GAG	KLKIIIVWASR	31	10	13	20		11204
GAG	HIARNCRAPR	433	10	13	20		11205
GAG	FLGIKIWPNSK	469	10	13	20		11206
GAG	EVKDTKEALD	95	11	13	20		11207
GAG	AAEWDRVIVP	230	11	13	20		11208
GAG	HIARNCRAPRK	433	11	13	20		11209
GAG	LGIKIWPNSKG	470	11	13	20		11210
GAG	NSSQVSONY	144	9	14	31		11211
GAG	NCGKEGIIAR	427	10	14	22		11212

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*1101	SEQ ID NO.
GAG	FNCCKEGHIAK	426	11	14	22		11213
GAG	IAKNCRAPRK	434	11	14	22		11214
GAG	QNAQGMVIL	157	9	14	22		11215
GAG	RGFRNQRK	412	9	14	22		11216
GAG	CKEGHIAK	428	9	14	22		11217
GAG	EGHIAKNCR	431	9	14	22		11218
GAG	FNVTATLYCV	81	11	14	22		11219
GAG	TVATLYCVLIQ	83	11	14	22		11220
GAG	IVQNAQGMV	155	11	14	22		11221
GAG	SSQVSQNY	145	8	15	31		11222
GAG	RSLYNTVATL	78	11	15	24		11223
GAG	FNVTATLY	81	8	15	23		11224
GAG	TYLCVIQR	86	8	15	23		11225
GAG	AAEWDVII	230	8	15	23		11226
GAG	WDRVILPVI	233	8	15	23		11227
GAG	RGFRNQR	412	8	15	23		11228
GAG	LFNTVATLY	80	9	15	23		11229
GAG	ATLYCVIQR	85	9	15	23		11230
GAG	EAAEWDRVII	229	9	15	23	0.7100	11231
GAG	TAIPESFR	496	9	15	23		11232
GAG	SGKLDLAWEK	9	10	15	23		11233
GAG	SLFNTVATLY	79	10	15	23		11234
GAG	VATLYCVIQR	84	10	15	23		11235
GAG	KIEEQNKSK	105	10	15	23		11236
GAG	RAEQATQDYK	329	10	15	23		11237
GAG	PTAPPEESFR	495	10	15	23		11238
GAG	LSGKLDLAWE	8	11	15	23		11239
GAG	PGLETSEGR	50	11	15	23		11240
GAG	KIEEQNKSKK	105	11	15	23		11241
GAG	MMQRGNFRN	409	11	15	23		11242
GAG	IAKNCRAPRK	434	10	16	25		11243
GAG	LDAWEKIR	13	8	16	25		11244
GAG	NAQGMVII	158	8	16	25		11245
GAG	PVSILDIK	303	8	16	25		11246
GAG	GNFRNQRK	413	8	16	25		11247
GAG	KLDWEKIR	12	9	16	25		11248
GAG	GGKKKYRLK	24	9	16	25		11249
GAG	LDAWEKIRL	13	10	16	25		11250
GAG	PGKKKYRLK	23	10	16	25		11251
GAG	GGKKKYRLKII	24	10	16	25		11252
GAG	GLLETSEGR	51	10	16	25		11253
GAG	YSPVSILDIK	301	10	16	25		11254
GAG	GGKLDLAWEKI	10	11	16	25		11255
GAG	KLDWEKIRL	12	11	16	25		11256
GAG	PGKKKYRLK	23	11	16	25		11257
GAG	VSILDIKQPK	304	11	16	25		11258
GAG	IAKNCRAPRK	433	11	16	25		11259
GAG	PIPPQMR	243	8	17	27		11260
GAG	GGKLDLAWEK	10	9	17	27		11261
GAG	DAWEKIRL	14	9	17	27		11262

Table XVII
 HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	Np. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
GAG	LLETSEGR	52	9	17	27		11263
GAG	RLKILVWASR	31	10	17	27		11264
GAG	LDKIEEQNK	103	10	17	27		11265
GAG	AGPIPPQMR	241	10	17	27		11266
GAG	ALDKIEEQNK	102	11	17	27		11267
GAG	LSPTLNWV	168	11	17	27		11268
GAG	IAGPIPPQMR	240	11	17	27		11269
GAG	PIPIPPQMR	243	11	17	27		11270
GAG	IAKNCRAPR	434	9	18	29	0.0003	11271
GAG	LDKWEKIR	13	8	18	28		11272
GAG	PVGDIYKR	281	8	18	28		11273
GAG	PDCKTILR	352	8	18	28		11274
GAG	LDKWEKILR	13	10	18	28		11275
GAG	SILDIKQIPK	305	10	18	28		11276
GAG	ANPDCKTILR	350	10	18	28		11277
GAG	IIAKNCRAPR	433	10	18	28		11278
GAG	IAGPIPPQMR	240	11	18	28		11279
GAG	NNPIPVGEIY	273	11	18	28		11280
GAG	NANPDCKTILR	349	11	18	28		11281
GAG	LARNCRAPRK	434	11	19	30		11282
GAG	PIAPQMR	243	8	19	30		11283
GAG	LDIKQIPK	307	8	19	30		11284
GAG	ILDIKQIPK	306	9	19	30		11285
GAG	AGPIPPQMR	241	10	19	30		11286
GAG	IAPQMR	244	10	19	30		11287
GAG	RLIPGGKKKY	20	11	19	30		11288
GAG	PIAPQMR	243	11	19	30		11289
GAG	DIKQIPKEPR	308	11	19	30		11290
GAG	LARNCRAPRK	434	9	20	32		11291
GAG	PGGKKKYR	23	8	20	31		11292
GAG	IMMQRNFR	408	9	20	31		11293
GAG	KNCRAPRK	436	9	20	31		11294
GAG	IIVWASRELER	35	10	20	31	0.0066	11295
GAG	IIANNCRAPR	433	10	20	31		11296
GAG	IIANNCRAPR	34	11	20	31		11297
GAG	EGIIARNCR	431	9	21	33		11298
GAG	KIWPISIIGR	472	9	22	35	0.0005	11301
GAG	GGPSIIGR	378	8	22	34		11302
GAG	KNCRAPRK	436	8	22	34		11303
GAG	VGGPSIIGR	377	9	22	34		11304
GAG	SLYNTVATLY	79	10	22	34		11305
GAG	GVGGPSIIGR	376	10	22	34		11306
GAG	QGVGGPSHKA	375	11	22	34		11307
GAG	LGIWPSHKG	470	11	22	34		11308
GAG	NFLKIWPISHK	468	11	23	37		11309
GAG	YNTVATLY	81	8	23	36		11310
GAG	KIEEQNK	105	8	23	36		11311
GAG	QGVGGPSH	375	8	23	36		11312

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	GVGGPSIIK	376	8	23	36		1313
GAG	MMQRGNFR	409	8	23	36		1314
GAG	QGVGGPSIIK	375	9	23	36		1315
GAG	LGKIWIPIIK	470	9	23	36		1316
GAG	ACQGVGGPSH	373	10	23	36		1317
GAG	FLGKIWIPIIK	469	10	23	36		1318
GAG	YNTVATLYCV	81	11	23	36	0.0013	1319
GAG	TACQGVGGPS	372	11	23	36		1320
GAG	ACQGVGGPSII	373	11	23	36		1321
GAG	NCGKEGILAR	427	10	24	38		1322
GAG	FNCGKEGILR	426	11	24	38		1323
GAG	CGKEGILAR	428	9	24	38		1324
GAG	YSPVSLDIR	301	10	24	38		1325
GAG	NFLGKIWIPII	468	10	25	40		1326
GAG	PVSILDIR	303	8	25	39		1327
GAG	LGKIWIPII	470	8	25	39		1328
GAG	KDTKEALDK	97	9	25	39		1329
GAG	FLGKIWIPII	469	9	25	39		1330
GAG	VSILDIRQGP	304	11	25	39		1331
GAG	ANFLGKIWIPII	467	11	25	39		1332
GAG	LVWASRELER	35	10	26	41		1333
GAG	ILVWASRELE	34	11	26	41		1334
GAG	MVLIQAISPR	163	9	27	42	0.0670	1335
GAG	VDRFKTLR	321	9	27	42	0.0010	1336
GAG	QMVLIQAISPR	162	10	27	42		1337
GAG	YVDRFKTLR	320	10	27	42		1338
GAG	RAEQATQEVK	329	10	27	42		1339
GAG	ANPDKTILK	350	10	27	42	0.0002	1340
GAG	NANPDKTILK	349	11	27	42		1341
GAG	KGRIGNFLQS	478	11	28	44		1342
GAG	PDKTILK	352	8	28	44		1343
GAG	VDRFYKTLR	321	9	28	44		1344
GAG	PERIYVDRFY	316	10	28	44		1345
GAG	YVDRFYKTLR	320	10	28	44		1346
GAG	PERIYVDRFY	316	11	28	44	0.0166	1347
GAG	GARASVLSGG	2	11	29	46		1348
GAG	ASVLSGGK	5	8	29	45		1349
GAG	NLQGMVVI	158	8	29	45		1350
GAG	WVKVIEK	176	8	29	45		1351
GAG	WDRLIPIVI	233	8	29	45		1352
GAG	ROYVDRFY	318	8	29	45		1353
GAG	RASVLSGGK	4	9	29	45		1354
GAG	QNLQGMVVI	157	9	29	45	0.0400	1355
GAG	RDYVDRFYK	318	9	29	45		1356
GAG	NAWKVIEK	174	10	29	45		1357
GAG	IVQNLQGMV	155	11	29	45		1358
GAG	LNAWKVIEE	173	11	29	45		1359
GAG	AAEWDRLIPIV	230	11	29	45		1360
GAG	PQNFQSR	483	8	30	48		1361
GAG	NAWKVVEEK	174	10	30	47	0.0402	1362

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	KIRLPQGGKK	18	11	30	47		11363
GAG	LNAWVKVVEE	173	11	30	47		11364
GAG	WVKVVEEK	176	8	31	48	0.0001	11365
GAG	RDYVDIRFEK	318	9	33	52		11366
GAG	RNCRAPRKK	436	9	33	52		11367
GAG	PRDYVDREFF	316	11	33	52		11368
GAG	RNCRAIRK	436	8	34	53		11369
GAG	RLRPGGKKK	20	9	34	53		11370
GAG	RLRPGGKKKY	20	10	34	53		11371
GAG	PIPVGEIYKR	279	10	34	53	0.0001	11372
GAG	PIPVGEIY	279	8	35	55		11373
GAG	PIPVGEIYK	279	9	35	55	0.0012	11374
GAG	DTKEALDK	98	8	36	56	0.0001	11375
GAG	QGVGGIGIIL	375	8	36	56		11376
GAG	QGVGGIGIHK	375	9	36	56	0.0001	11377
GAG	ACQVYGGIGIIL	373	10	36	56		11378
GAG	ISPTLNAAW	168	11	36	56		11379
GAG	TACQVGGIGI	372	11	36	56	0.0001	11380
GAG	ACQVYGGIGIHK	373	11	36	56		11381
GAG	QGVGGIGIKA	375	11	36	56		11382
GAG	GVGGIGIHK	376	8	37	58	0.0018	11383
GAG	GVGGIGIHKAR	378	8	37	58		11384
GAG	VGGIGIHKAR	377	9	37	58		11385
GAG	AAEWDRLLI	230	10	37	58	0.0001	11386
GAG	AAEWDRLLI	229	8	39	61		11387
GAG	PGVEYKR	281	9	39	61		11388
GAG	TVATLYCVII	83	8	40	63	0.0001	11389
GAG	NTVATLYCVII	82	9	40	63		11390
GAG	SILDIRQGP	305	10	40	63	0.7100	11391
GAG	DIRQGPKEPFR	308	11	41	64		11392
GAG	VATLYCVII	84	8	42	66		11393
GAG	LDIRQGP	307	8	42	66		11394
GAG	LDIRQGP	306	9	42	66	0.0048	11395
GAG	NTMLNTVGGII	206	10	42	66		11396
GAG	LNTMLNTVGG	205	11	42	66		11397
GAG	TMLNTVGGII	207	9	43	66		11398
GAG	KGCWKCGK	444	8	44	67		11399
GAG	KIRLRPGGK	18	9	44	69		11400
GAG	KIRLRPGGKK	18	10	44	69		11401
GAG	KGCWKCGKEG	444	11	44	69	0.0010	11402
GAG	PGQMPREPR	246	8	45	69		11403
GAG	CGKEGIQMK	449	9	45	70		11404
GAG	KCGKEGIQMK	448	10	45	70		11405
GAG	MLNTVGGII	208	8	47	73		11406
GAG	WASRELER	37	8	48	75		11407
GAG	GCWKCGKEGII	445	10	48	75		11408
GAG	RLRPGGKK	20	8	49	77		11409
GAG	QMKDCTER	455	8	49	77		11410
GAG	EGHQMKDCTE	452	11	49	77		11411
							11412

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*101	SEQ ID NO.
GAG	RAPRKKGCK	439	10	51	80		11413
GAG	CTERQANFLG	459	11	52	83		11414
GAG	NCRAPRK	437	8	53	84		11415
GAG	TINEEAIEWD	225	11	53	84		11416
GAG	INEFAIEWDR	226	10	55	86		11417
GAG	FNC'GKEGII	426	8	57	90		11418
GAG	WILGLNK	289	8	57	89		11419
GAG	CFNCKEGII	425	9	57	89		11420
GAG	IILGLNKIVR	290	10	57	89	0.0006	11421
GAG	KCFNCKEGII	424	10	57	89		11422
GAG	WILGLNKIVR	289	11	57	89		11423
GAG	IILGLNKIVRMY	291	11	57	89		11424
GAG	ILGLNKIVR	291	9	58	91	0.0001	11425
GAG	LGLNKIVRMY	292	10	58	91	0.0002	11426
GAG	LLVQANPDC	345	11	58	91		11427
GAG	LGLNKIVR	292	8	59	92		11428
GAG	LVQANPDC	346	10	59	92	0.0110	11429
GAG	LNKIVRMY	294	8	60	94		11430
GAG	GLNKIVRMY	293	9	60	94	0.0002	11431
GAG	QAAQMQLK	216	8	61	95		11432
GAG	QANPDK	348	8	61	95		11433
GAG	GIIQAAMQM	213	11	61	95		11434
GAG	RTLNAWVK	171	8	63	98	0.0560	11435
GAG	QGPKEPR	311	8	63	98		11436
GAG	PRDYVDR	316	8	63	98		11437
GAG	QGPKEPRDY	311	10	63	98	0.0002	11438
NEF	AADGVGAVSR	42	10	09	15		11439
NEF	ANEGENSLII	249	11	09	15		11440
NEF	VGWPAIRER	11	9	10	17		11441
NEF	FDSRLAFII	310	8	10	16		11442
NEF	FDSRLAFIII	310	9	10	16		11443
NEF	DSRLAFIII	311	8	10	16		11444
NEF	AVSQDLQK	48	8	10	16		11445
NEF	PLRPMTFK	102	8	10	16		11446
NEF	GAVSQDLQK	47	9	10	16		11447
NEF	GLEGLYSK	125	9	10	16		11448
NEF	MARELIPEY	321	9	10	16		11449
NEF	VGAVSQDLQK	46	10	10	16		11450
NEF	QVPLRPMTFK	100	10	10	16		11451
NEF	GAFDLSFFLK	110	10	10	16		11452
NEF	GGLEGLYSK	124	10	10	16		11453
NEF	CFKLVPVDR	226	10	10	16		11454
NEF	HMARELIPEY	320	10	10	16		11455
NEF	MARELIPEY	321	10	10	16		11456
NEF	GVGAVSQDLQ	45	11	10	16		11457
NEF	KGAFDLSFFLK	109	11	10	16		11458
NEF	XGGLGLYSK	122	11	10	16		11459
NEF	WCFKLVPVDF	225	11	10	16		11460
NEF	NNSLLIPICQH	254	11	10	16		11461
NEF	HMARELIPEY	320	11	10	16		11462

Table XVII
HIV ALL Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
NEF	MARELIPEYY	321	11	10	16		11463
NEF	ANEENNCLL	249	11	11	18		11464
NEF	AVSRDEK	48	8	11	17		11465
NEF	VSRDEKII	49	8	11	17		11466
NEF	KLPVDPK	228	8	11	17		11467
NEF	GAVSRDEK	47	9	11	17	0.0009	11468
NEF	AVSRDEKII	48	9	11	17		11469
NEF	VGAVSRDEK	46	10	11	17		11470
NEF	GAVSRDEKII	47	10	11	17		11471
NEF	QNYTPGQVR	205	10	11	17		11472
NEF	NSLLIPIQII	255	10	11	17		11473
NEF	GVGAVSRDLE	45	11	11	17		11474
NEF	VGAVSRDEK	46	11	11	17		11475
NEF	EGENNCLLII	251	9	12	19		11476
NEF	YTPGQVR	207	8	12	19		11477
NEF	DILDWVYII	185	9	12	19		11478
NEF	QDILDWVYII	184	10	12	19		11479
NEF	EGENNSLLII	251	9	13	21		11480
NEF	VDSIIFLKEK	112	10	13	20		11481
NEF	AVDLSIIFLKEK	111	11	13	20		11482
NEF	VDLSIIFLK	112	8	14	22		11483
NEF	DGLIYSKK	172	8	14	22		11484
NEF	ELIPIFYK	324	8	14	22	1.1000	11485
NEF	AVDLSIIFLK	111	9	14	22		11486
NEF	LDGLIYSKK	171	9	14	22		11487
NEF	DGLIYSKKR	172	9	14	22		11488
NEF	SLLIPIQII	256	9	14	22		11489
NEF	GLDGLIYSKK	125	10	14	22		11490
NEF	LDGLIYSKKR	171	10	14	22		11491
NEF	GLDGLIYSKK	124	11	14	22		11492
NEF	GLDGLIYSKKR	125	11	14	22		11493
NEF	NNCLLIIPMSQ	254	11	14	22		11494
NEF	CLLIIPMSQII	256	9	15	23		11495
NEF	NCLLIIPMSQII	255	10	15	23		11496
NEF	QNYTPGQIRY	205	11	15	23		11497
NEF	LDGLIYSK	171	8	16	25		11498
NEF	GLDGLIYSK	125	9	16	25		11499
NEF	GGLDGLIYSK	124	10	16	25		11500
NEF	KGGLDGLIYSK	122	11	16	25		11501
NEF	RFPLTFQWCF	216	11	17	27		11502
NEF	FFPDWQNY	199	8	17	27		11503
NEF	LLIIPMSQII	257	8	17	27		11504
NEF	GFFPDWQNY	198	9	17	27		11505
NEF	YTPGQIRY	207	9	17	27		11506
NEF	FDSFLKEK	112	10	17	27		11507
NEF	QKFFPDWQNY	196	10	17	27		11508
NEF	AFDLSFELKEK	111	11	17	27		11509
NEF	FDSFLK	112	8	18	28		11510
NEF	LLIPIQII	257	8	18	28		11511
NEF	AFDLSFELK	111	9	18	28		11512

Table XVII
 HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
NEF	QNYTPGIR	205	10	18	28		11513
NEF	GGLEGLY	124	8	19	30		11514
NEF	KGGLEGLY	122	9	19	30		11515
NEF	DILDWVY	185	8	20	31		11516
NEF	YTPGTGR	207	8	20	31		11517
NEF	QDILDWVY	184	9	20	31		11518
NEF	QNYTPGTR	205	10	20	31		11519
NEF	GOLDGLY	124	8	21	33		11520
NEF	WVYITQY	191	8	21	33		11521
NEF	YTPGTGR	207	8	21	33		11522
NEF	KGGLDGLY	122	9	21	33		11523
NEF	DLWVYITQY	188	10	21	33		11524
NEF	LDLWVYITQY	187	11	21	33		11525
NEF	LSFLKEK	114	8	22	34		11526
NEF	ELIHFEYK	324	8	22	34		11527
NEF	DLSPFLKEK	113	9	22	34		11528
NEF	EILDWVYH	185	9	22	34		11529
NEF	GLYSKRR	173	8	23	36		11530
NEF	LSHFLKEK	114	8	27	42		11531
NEF	DLSHFLKEK	113	9	27	42		11532
NEF	EILDWVY	185	8	33	52		11533
NEF	ILDLWVYH	186	8	34	53		11534
NEF	YFPDWQNY	199	8	36	56		11535
NEF	QGYFPOWQNY	196	10	36	56	0.0017	11536
NEF	LTGWCCK	221	8	39	61		11537
NEF	PLTFGWCFK	219	9	39	61		11538
NEF	QVPLRPMTY	100	9	46	72		11539
NEF	QVPLRPMTYK	100	10	46	72	0.6300	11540
NEF	PVRQVPLR	95	9	48	75		11541
NEF	GFPVRQVPLR	93	11	48	75		11542
NEF	PLRPMYK	102	8	49	77		11543
POL	STNSPTR	32	8	01	33	0.0003	11544
POL	RANSPSR	35	8	01	33		11545
POL	NSNSPTR	31	9	01	33		11546
POL	ITSRELOVR	36	9	01	33		11547
POL	QTRANSISR	33	10	01	33		11548
POL	QTRANSPTR	35	10	01	33		11549
POL	NSPTSRELOVR	34	11	01	33		11550
POL	RANSPTR	37	8	01	50		11551
POL	PSSRELOVR	39	9	01	50		11552
POL	PSRANSPTR	24	10	01	50		11553
POL	NSPSSRELOVR	37	11	01	50		11554
POL	NSPTRELOV	39	11	01	50		11555
POL	NNSLEAGAD	55	11	05	25		11556
POL	NLAPPGEAR	5	10	10	16		11557
POL	ILIEICGI	149	8	10	16		11558
POL	LIEICGIK	150	8	10	16		11559
POL	YAKMRTAI	546	8	10	16		11560
POL	RSALTNDVK	550	9	10	16		11561
POL	ETWETWTD	588	10	10	16		11562

Table XVII
HIV All Motif Peptides with Binding Information

Protein	Sequence	Position	Nn. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	ETWTWTE	588	10	10	16		11563
POL	VSLDTTNQK	659	10	10	16		11564
POL	ENLAFQGEAR	4	11	10	16		11565
POL	TGKYAKMRTA	543	11	10	16		11566
POL	VVSLDTTNQ	638	11	10	16		11567
POL	QTRKELQKQIK	961	11	10	16		11568
POL	QTRANSPTRR	21	10	11	18		11569
POL	TNNETGIR	324	9	11	17		11570
POL	TNNETPGIRY	324	10	11	17		11571
POL	LDGIDKAQEDII	754	11	11	17		11572
POL	IGGFIKVK	137	8	11	17		11573
POL	RIGPENPY	238	8	11	17		11574
POL	TAIITNDVK	551	8	11	17		11575
POL	QLTEVVQK	559	8	11	17		11576
POL	IDKAQEDII	757	8	11	17		11577
POL	VVPRRKVK	1012	8	11	17		11578
POL	KIKDYGK	1019	8	11	17		11579
POL	GIGGFIKVK	136	9	11	17		11580
POL	SLDTTNQK	660	9	11	17		11581
POL	GIDKAQEDII	756	9	11	17		11582
POL	SNFTSTTVK	871	9	11	17		11583
POL	KVVPKKVK	1011	9	11	17		11584
POL	GGGIGGFIKVK	135	10	11	17		11585
POL	ISRIGPENPY	236	10	11	17		11586
POL	STNNETGIR	323	10	11	17		11587
POL	ESWTVNDIQK	439	10	11	17		11588
POL	ETTNQKTELH	663	10	11	17		11589
POL	DGIDKAQEDII	755	10	11	17		11590
POL	GSNFTSTTVK	870	10	11	17		11591
POL	GIOQEGIPY	886	10	11	17		11592
POL	SDIQTKELQK	958	10	11	17		11593
POL	FNPQITLWQR	85	11	11	17		11594
POL	IGGIGGFIKVK	134	11	11	17		11595
POL	KISRIGPENPY	235	11	11	17		11596
POL	PSTNNETPGIR	322	11	11	17		11597
POL	STNNETGIRY	323	11	11	17		11598
POL	VVSLTETTNQ	658	11	11	17		11599
POL	NGSNFTSTTV	869	11	11	17		11600
POL	AGIQEGIPY	885	11	11	17		11601
POL	IDIASDIQTK	953	11	11	17		11602
POL	VDIATDIQTK	953	11	11	17		11603
POL	ASDIQTKELQK	957	11	11	17		11604
POL	NSEIKVVPK	1007	11	11	17		11605
POL	QTRANSPTSR	21	10	12	19		11606
POL	IIKIQNER	969	8	12	19		11607
POL	QIYPGIKVK	458	9	12	19		11608
POL	QDQWYTYIY	526	9	12	19		11609
POL	IIKIQFRVY	969	10	12	19		11610
POL	ASQIYPGIKVK	456	11	12	19		11611
POL	IIKIQFRVY	969	11	12	19		11612

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	AFPOGEAR	7	8	12	19		11613
POL	TNQTLEII	665	8	12	19		11614
POL	KTELOAIY	668	8	12	19		11615
POL	LAFPOGEAR	6	9	12	19		11616
POL	EINLPQKWK	122	9	12	19		11617
POL	TTNQKTEII	664	9	12	19		11618
POL	QIKIONFR	968	9	12	19		11619
POL	VIQDNSEIK	1003	9	12	19		11620
POL	NSEIKVVPR	1007	9	12	19		11621
POL	VLEEINLPQK	119	10	12	19		11622
POL	VVIQDNSEIK	1002	10	12	19		11623
POL	DNSEIKVVPR	1006	10	12	19		11624
POL	NSEIKVVPRR	1007	10	12	19		11625
POL	TVLEEINLPQK	118	11	12	19		11626
POL	EINLPQKWKPK	122	11	12	19		11627
POL	QGQDQWYTI	524	11	12	19		11628
POL	RMRGAIITNDV	548	11	12	19		11629
POL	TNQTLEQAIY	665	11	12	19		11630
POL	QIKIONFRVY	968	11	12	19		11631
POL	AVVIQDNSEIK	1000	11	12	19		11632
POL	QDNSEIKVVPR	1005	11	12	19		11633
POL	DNSEIKVVPRR	1006	11	12	19		11634
POL	ELOKQIK	964	8	13	21		11635
POL	KTGYARMR	542	9	13	21		11636
POL	NLKTGKYAIRM	540	11	13	21		11637
POL	EDINLPQK	121	8	13	20		11638
POL	TGKYARMR	543	8	13	20		11639
POL	YARMGAH	546	8	13	20		11640
POL	QVREQAEII	916	8	13	20		11641
POL	DINLPQKWK	122	9	13	20		11642
POL	VLEDINLPQK	119	10	13	20		11643
POL	EDINLPQKWK	121	10	13	20		11644
POL	RAKIELREII	388	10	13	20		11645
POL	TVQHVLPQK	429	10	13	20		11646
POL	AGRWPVKTHI	857	10	13	20	5.6000	11647
POL	IQVREQAEH	914	10	13	20		11648
POL	QVREQAEIILK	916	10	13	20		11649
POL	TLWQRPVTV	91	11	13	20		11650
POL	LVTKIGGQKL	97	11	13	20		11651
POL	TVLEDINLPQK	118	11	13	20		11652
POL	DINLPQKWKPK	122	11	13	20		11653
POL	KIELREIILK	390	11	13	20		11654
POL	WTVQHVLPQK	428	11	13	20	0.0510	11655
POL	TGKYARMRGA	543	11	13	20		11656
POL	LAGRWPVKTI	856	11	13	20		11657
POL	IIGVREQAEII	913	11	13	20		11658
POL	EIKVVPKAK	1009	11	13	20		11659
POL	EFSEQTR	16	8	14	22		11660
POL	QIYPGIKVR	458	9	14	22		11661
POL	ASQIYPGIKVR	456	11	14	22		11662

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SIQ ID NO.
POL	IATESIVWGK	567	11	14	22		11663
POL	ILIEICGK	149	8	14	22		11664
POL	LIEICGKK	150	8	14	22		11665
POL	QNPDIVY	363	8	14	22		11666
POL	NFTSTIVK	872	8	14	22		11667
POL	IASDIQTK	956	8	14	22		11668
POL	DSKIDPLWK	981	8	14	22		11669
POL	QILIEICGK	148	9	14	22		11670
POL	ILIEICGKK	149	9	14	22		11671
POL	IASDIQTK	955	9	14	22		11672
POL	RDSRDPLWK	980	9	14	22		11673
POL	QILIEICGKK	148	10	14	22		11674
POL	QNPDIVYQY	363	10	14	22		11675
POL	RTKIELRQII	388	10	14	22		11676
POL	PGIKVRQLCK	461	10	14	22		11677
POL	DIASDIQTK	954	10	14	22		11678
POL	RDPLVKGIPAK	983	10	14	22		11679
POL	FSPQYTLWQR	85	11	14	22		11680
POL	YDQILIEICGK	146	11	14	22		11681
POL	KTPKFKLHOK	577	11	14	22		11682
POL	GIIDKAQEEIER	756	11	14	22		11683
POL	QTRANSPTK	21	9	15	24	0.0120	11684
POL	LVEICTEMEK	221	10	15	24		11685
POL	ELRQIILLR	393	8	15	23		11686
POL	QGQDQWTY	524	8	15	23		11687
POL	KTELQAHII	668	8	15	23		11688
POL	EIKVVPKRR	1009	9	15	23		11689
POL	LGHQAQPR	695	10	15	23		11690
POL	VDKLVAGIR	740	10	15	23		11691
POL	IDKAQEEIER	757	10	15	23		11692
POL	ALVIECTEMEK	220	11	15	23		11693
POL	KIEELRQIILLR	390	11	15	23		11694
POL	TNOKTELQAHII	665	11	15	23		11695
POL	ALGHQAQPR	694	11	15	23		11696
POL	LVNQIEQLIK	709	11	15	23		11697
POL	QVDKLVAGIR	739	11	15	23		11698
POL	VDKLVAGIRK	740	11	15	23		11699
POL	IDKAQEEIER	757	11	15	23		11700
POL	KAQEEIER	759	8	16	25		11701
POL	KAQEEIER	759	9	16	25		11702
POL	NLAFOQGEAR	5	10	16	25		11703
POL	KAQEEIER	759	10	16	25		11704
POL	AFQQGEAR	7	8	16	25		11705
POL	RANSPTRR	26	8	16	25		11706
POL	SAITNDVK	551	8	16	25		11707
POL	IIQAQPR	697	8	16	25		11708
POL	KLVAGIR	742	8	16	25		11709
POL	LVSAGIRK	743	8	16	25		11710
POL	EIKVVPRR	1009	8	16	25	0.0054	11711
POL	LAFQQGEAR	6	9	16	25		11712

Table XVII
HIV All Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	Sl:Q ID NO.
POL	GHQAQPIR	696	9	16	25		11713
POL	KLVSAGIRK	742	9	16	25	0.0770	11714
POL	ENLAFQGEA	4	11	16	25		11715
POL	RANSPTR	26	8	17	27		11716
POL	KIEELRQH	390	8	17	27		11717
POL	ELREHLK	393	8	17	27		11718
POL	WGKTPFK	575	8	17	27		11719
POL	TIKIGGQLK	99	9	17	27	0.0330	11720
POL	TVQPIQLPEK	429	10	17	27	0.2100	11721
POL	VIWGTTPFK	573	10	17	27		11722
POL	TLWQRPLVTI	91	11	17	27		11723
POL	WTVPQLPEK	428	11	17	27		11724
POL	VIWGTTPFK	572	11	17	27		11725
POL	YFSVPLDKDFR	304	11	18	27		11726
POL	NLKTGKYAKM	540	11	18	29		11727
POL	PIIVIVQY	365	8	18	28		11728
POL	SVPLDKDFR	306	9	18	28		11729
POL	FSVPLDKDFR	305	10	18	28		11730
POL	SVPLDKDFR	306	10	18	28		11731
POL	AGIKVKQLCK	461	10	18	28		11732
POL	VNQHQLIK	710	10	18	28		11733
POL	FSVPLDKDFR	305	11	18	28		11734
POL	SVPLDKDFR	306	11	18	28		11735
POL	YAGIKVKQLCK	460	11	18	28		11736
POL	LVSQHEQLIK	709	11	18	28		11737
POL	VNQHQLIK	710	11	18	28		11738
POL	PLDKDFR	308	8	19	30		11739
POL	PLDKDFRKY	308	9	19	30		11740
POL	KTGKYAKMR	542	9	19	30		11741
POL	LDKDFRKY	309	8	19	30		11742
POL	KIEELREI	390	8	19	30		11743
POL	TGKYAKMR	543	8	19	30		11744
POL	GAITNDVK	531	8	19	30		11745
POL	LTDTINQK	661	8	19	30		11746
POL	PLWKGPAK	985	8	19	30		11747
POL	GKVKQLCK	462	9	19	30		11748
POL	RGAITNDVK	550	9	19	30		11749
POL	KVRQLCKLLR	464	10	19	30		11750
POL	ATESIWIWGK	568	10	19	30		11751
POL	VSQHEQLIK	710	10	19	30	0.0370	11752
POL	MAGDDCVASR	1028	10	19	30		11753
POL	VSQHEQLIK	710	11	19	30		11754
POL	QMAGDDCVAS	1027	11	19	30		11755
POL	QIYAGIKVK	458	9	20	30		11756
POL	KVYLAWVPFH	722	10	20	32	0.0036	11757
POL	KACWAGIK	879	10	20	32	0.0740	11758
POL	ASQIYAGIKVK	456	11	20	32		11759
POL	KVYLAWVPFH	722	11	20	32		11760
POL	KFKLPIQK	580	8	20	31	2.3000	11761
POL							11762

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	GDDCVASR	1030	8	20	31		11763
POL	AGDDCVASR	1029	9	20	31		11764
POL	VSLETNNQK	659	10	20	31		11765
POL	LLKLAGRWPV	853	11	20	31		11766
POL	YFSVPLDK	304	8	21	33		11767
POL	ACWWAGIK	881	8	21	33		11768
POL	SLTETNNQK	660	9	21	33		11769
POL	AACWWAGIK	880	9	21	33	0.0470	11770
POL	DAYFSVPLDK	302	10	21	33		11771
POL	DLKQIRTK	381	10	21	33		11772
POL	QLCKLLRGTK	467	10	21	33		11773
POL	IFAIKKKDSK	249	11	21	33		11774
POL	GDAYFSVPLD	301	11	21	33		11775
POL	SDLKQIRTK	380	11	21	33		11776
POL	SDNLPPIVAK	776	11	21	33		11777
POL	AGIKQEFQIPY	885	11	21	33		11778
POL	EIGQIRTK	383	8	22	34		11779
POL	RTKIEELR	388	8	22	34		11780
POL	YLAWVPAII	724	8	22	34		11781
POL	YLAWVPAIIK	724	9	22	34	0.0570	11782
POL	NFQITLWQR	86	10	22	34		11783
POL	MTKILEPFRK	353	10	22	34	0.0380	11784
POL	AGRWPVKVHI	857	10	22	34		11785
POL	GIKQEFQIPY	886	10	22	34	0.0002	11786
POL	SMTKILEPFRK	352	11	22	34		11787
POL	KTPKFRLPQK	577	11	22	34		11788
POL	LAGRWPVKVI	856	11	22	34		11789
POL	KVYLSWVPAII	722	10	23	37		11790
POL	KVYLSWVPAII	722	11	23	37		11791
POL	KILEPFRK	355	8	23	36		11792
POL	KVILVAVII	823	8	23	36		11793
POL	SFTQITLWQR	86	10	23	36		11794
POL	DFNLPPIVAK	777	10	23	36		11795
POL	IGKVILVAVII	821	10	23	36		11796
POL	LLKWGFTTID	398	11	23	36		11797
POL	LLRWGFTTID	398	11	23	36		11798
POL	IDHATDIQTK	953	11	23	36		11799
POL	NTRIFAIRK	246	8	24	38		11800
POL	GDDCVAGR	1030	8	24	38		11801
POL	NTRIFAIRK	245	9	24	38		11802
POL	NTRIFAIRK	246	9	24	38		11803
POL	LCKLLRGTK	468	9	24	38	0.0001	11804
POL	AGDDCVAGR	1029	9	24	38		11805
POL	NTRIFAIRK	245	10	24	38		11806
POL	NTRIFAIRKK	246	10	24	38		11807
POL	MAGDDCVAGR	1028	10	24	38		11808
POL	NTRIFAIRKK	245	11	24	38		11809
POL	QGGQWYTYQI	524	11	24	38		11810
POL	KLGRAGYVTD	643	11	24	38		11811
POL							11812

Table XVII
 HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
POL	TAYFLKLAG	849	11	24	38		11813
POL	QMAGDDCVAG	1027	11	24	38		11814
POL	QGQWTYQIV	526	9	25	40	0.0001	11815
POL	PIFAIKKK	248	8	25	39		11816
POL	QGQGWY	524	8	25	39		11817
POL	FLKLKGR	852	8	25	39		11818
POL	YFLKLGR	851	9	25	39		11819
POL	QLCKLRGAK	467	10	25	39		11820
POL	LGKAGYVDR	644	10	25	39		11821
POL	IDKAEIEIK	757	10	25	39		11822
POL	PSKDLAEIQK	513	11	25	39		11823
POL	GIDKAEIEIK	756	11	25	39		11824
POL	IDKAEIEIEKY	757	11	25	39		11825
POL	SDFNLPVAVK	776	11	25	39		11826
POL	RAKIEELR	388	8	26	41		11827
POL	KFRLPIQK	580	8	26	41		11828
POL	NLPPIVAK	774	8	26	41		11829
POL	LC'LLRGAK	468	9	26	41		11830
POL	FNLPIVAK	778	9	26	41		11831
POL	SNFTSAAVK	871	9	26	41		11832
POL	DFNLPVAVK	777	10	26	41		11833
POL	GSNFTSAAVK	870	10	26	41		11834
POL	TGQETAYFL	845	11	26	41		11835
POL	NGSNFTSAAV	869	11	26	41		11836
POL	KAQEEIEIK	759	8	27	43	0.3400	11837
POL	ASQIYAGIK	456	9	27	43		11838
POL	KAQEEIEIKY	759	9	27	43		11839
POL	KAQEEIEIKYII	759	10	27	43		11840
POL	INLPKWK	123	8	27	42		11841
POL	EICTEMEK	223	8	27	42		11842
POL	EIQHIRAK	383	8	27	42		11843
POL	LYSSGIRK	743	8	27	42		11844
POL	NLPVAVK	779	8	27	42		11845
POL	ETAYFLK	848	8	27	42	0.0430	11846
POL	KLVSSGIRK	742	9	27	42		11847
POL	FNLPPVAVK	778	9	27	42		11848
POL	INLPKWKPK	123	10	27	42		11849
POL	DLEIQHIRAK	381	10	27	42		11850
POL	WASQIYAGIK	455	10	27	42		11851
POL	KVKQLCKLLR	464	10	27	42		11852
POL	EICTEMEKECK	223	11	27	42		11853
POL	SULEIQHIRAK	380	11	27	42		11854
POL	VCKLVSSGIRK	740	11	27	42		11855
POL	ASQIYPIGK	456	9	28	44		11856
POL	KDLIAEIQK	515	9	28	44		11857
POL	NLKTGYAK	540	9	28	44		11858
POL	DLIAEIQK	516	8	28	44		11859
POL	IVGAETFY	626	8	28	44		11860
POL	NFTSAAVK	872	8	28	44		11861
POL	CTEMEKECK	225	9	28	44	0.0001	11862

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	GIVKQLCK	462	9	28	44		11863
POL	IVGAETFY	625	9	28	44		11864
POL	QIKKEKVV	716	9	28	44		11865
POL	ICTEMEKEGK	224	10	28	44		11866
POL	WASQYFGK	455	10	28	44		11867
POL	KNLKTGKYAK	539	10	28	44		11868
POL	NLKTGKYAR	540	9	29	46		11869
POL	KLVSSGIR	742	8	29	45	0.0001	11870
POL	KNLKTGKYAR	539	10	29	45		11871
POL	VIWGTPKFR	573	10	29	45		11872
POL	VDKLVSSGIR	740	10	29	45		11873
POL	IVWGTTPKFR	572	11	29	45		11874
POL	QVDKLVSSGIR	739	11	29	45		11875
POL	WGKTPKFR	575	8	30	47		11876
POL	LTETTNOK	661	8	30	47		11877
POL	ANRETKLCK	638	9	30	47	0.0001	11878
POL	ANRETKLCK	637	10	30	47	0.0016	11879
POL	IEQLIKKEK	711	10	30	47	0.0003	11880
POL	GAANRETKLG	636	11	30	47		11881
POL	QHIEQLIKKEK	712	11	30	47		11882
POL	ILKLAGRWPF	853	11	30	47		11883
POL	KILVAVII	823	8	31	48		11884
POL	ETAYFILK	848	8	31	48		11885
POL	YFILKLGR	851	9	31	48		11886
POL	EGRILVAVII	821	10	31	48		11887
POL	PSINNETGIR	322	11	31	48		11888
POL	TQQTAYFILK	845	11	31	48		11889
POL	TAYFILKLGR	849	11	31	48		11890
POL	INNETGIR	374	9	32	51		11891
POL	INNETGIRY	374	10	32	51		11892
POL	FILKLGR	852	8	32	50		11893
POL	SINNETGIR	323	10	32	50		11894
POL	SINNETGIRY	323	11	32	50		11895
POL	SSMTKILEPFR	351	11	32	50		11896
POL	QTKELQKQITK	961	11	32	50	0.0100	11897
POL	EMEKEGKISK	229	10	33	52	0.0001	11898
POL	DKQLTEAVQ	556	11	33	52	0.0240	11899
POL	DIATDIQTK	954	10	34	53	0.0130	11900
POL	ELQKQITK	964	8	35	56		11901
POL	LIKKEKVV	717	8	35	55		11902
POL	DSRDPWK	981	8	35	55		11903
POL	ETKLKAGY	641	9	35	55		11904
POL	IIATDIQTK	955	9	35	55	0.0980	11905
POL	QITKIQNFR	968	9	35	55	0.0045	11906
POL	RDSRDPWK	980	9	35	55		11907
POL	TDIQTKELOK	958	10	35	55	0.0001	11908
POL	RDPWKGPAP	983	10	35	55		11909
POL	ATDIQTKELQK	957	11	35	55	0.1800	11910
POL	QITKIQNFRVY	968	11	35	55		11911
POL	ITKIQNFR	969	8	36	57		11912

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	ITKIQNFRVY	969	10	36	57	0.0012	11913
POL	ITKIQNFRVY	969	11	36	57		11914
POL	IATIDIQTK	956	8	36	56		11915
POL	PIWKGPAK	985	8	36	56		11916
POL	NLPKGWKPK	124	9	36	56		11917
POL	AIQSSMTK	347	9	36	56	0.9600	11918
POL	PAIQSSMTK	346	10	36	56	0.0830	11919
POL	VFAIKKDKSTK	249	11	36	56		11920
POL	NTVFAIK	246	8	37	58	0.0003	11921
POL	PVFAIKK	248	8	37	58	0.0001	11922
POL	QLTEAVQK	559	8	37	58		11923
POL	QIEQLIK	712	8	37	58		11924
POL	IEQLIKK	713	8	37	58		11925
POL	YLSWVPAI	724	8	37	58		11926
POL	LSWVPAIK	725	8	37	58	0.0002	11927
POL	YNTVFAIK	245	9	37	58	0.0040	11928
POL	NTVFAIKK	246	9	37	58	0.1600	11929
POL	QIEQLIKK	712	9	37	58		11930
POL	YLSWVPAIK	724	9	37	58		11931
POL	VIQNSDIK	1003	9	37	58	0.0068	11932
POL	YNTVFAIKK	245	10	37	58		11933
POL	NTVFAIKK	246	10	37	58	0.0046	11934
POL	VVIQNSDIK	1002	10	37	58	0.0210	11935
POL	YNTVFAIKK	245	11	37	58		11936
POL	AVVIQNSDIK	1000	11	37	58	0.0150	11937
POL	IFQSSMTK	348	8	38	59	0.0073	11938
POL	ILKEPVHGVY	498	11	38	59		11939
POL	LDGIDKAEI	754	11	39	62		11940
POL	AGYVTDGR	647	9	39	61		11941
POL	YVTDGRQK	649	9	39	61	0.0010	11942
POL	KAGYVTDGR	646	10	39	61		11943
POL	LGIIQAQPK	695	10	39	61	0.0001	11944
POL	DGIDKAEI	755	10	39	61		11945
POL	PVIGVYDPS	505	11	39	61		11946
POL	AGYVTDGRQ	647	11	39	61		11947
POL	ALGIIQAQPK	694	11	39	61		11948
POL	DIKVVPRKAK	1009	11	39	61		11949
POL	VTDGRQK	650	8	40	63	0.0065	11950
POL	IIQAQPK	697	8	40	63		11951
POL	GIIQAQPK	696	9	40	63	0.0400	11952
POL	GIDKAEI	756	9	40	63		11953
POL	NSDIKVVPR	1007	9	40	63		11954
POL	ILKEPVHGVY	498	10	40	63		11955
POL	NSDIKVVPR	1006	10	40	63		11956
POL	NSDIKVVPR	1007	10	40	63	0.0001	11957
POL	EILKEPVHGVY	497	11	40	63		11958
POL	WTYQIQEFP	529	11	40	63	0.0540	11959
POL	QIYQIEFKNLK	532	11	40	63	0.2900	11960
POL	QNSDIKVVPR	1005	11	40	63		11961
POL	NSDIKVVPR	1006	11	40	63		11962

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	NSDIKVVPRK	1007	11	40	63		11963
POL	ESIVWGTTPK	570	11	41	65		11964
POL	QYQEPFK	532	8	41	64	0.0013	11965
POL	IDKAQEEII	757	8	41	64		11966
POL	KAKIRDY	1017	8	41	64		11967
POL	KAKIRDYCK	1017	10	41	64	0.0018	11968
POL	KISKIGPENPY	235	11	41	64		11969
POL	KAGYVTR	236	8	42	66		11970
POL	ISKIGPENPY	352	10	42	66		11971
POL	SMTKILEPR	571	10	42	66	0.0004	11972
POL	SIVWGTTPK	367	11	42	66		11973
POL	IVYQYMDLLY	1012	11	42	66		11974
POL	VVPRKAKIIR	508	8	43	67		11975
POL	GVYDPSK	791	8	43	67		11976
POL	SCDKCQLK	353	9	43	67	0.0160	11977
POL	MTKILIFPR	507	9	43	67	0.0001	11978
POL	IIGVYDPSK	790	9	43	67	0.0001	11979
POL	ASCDKCOLK	439	10	43	67	0.0140	11980
POL	DSWTVDNIQK	631	10	43	67	0.0002	11981
POL	TFYVDGAANR	789	10	43	67	0.0008	11982
POL	VASCDKCOLK	438	11	43	67	0.0004	11983
POL	KDSWTVDNIQ	630	11	43	67		11984
POL	ETFYVDGAAN	788	11	43	67		11985
POL	IVASCDKCOLK	1008	8	44	69	0.1000	11986
POL	SDIKVVPR	1008	9	44	69		11987
POL	SDIKVVPRR	634	10	44	69	0.0001	11988
POL	VDGAANRET	914	10	44	69		11989
POL	IGQVRDQAEII	916	10	44	69		11990
POL	OVRDQAEIILK	1008	10	44	69	0.0093	11991
POL	ENREILKEPVII	494	11	44	69	0.0001	11992
POL	YVDGAANRET	633	11	44	69		11993
POL	IIGQVRDQAEII	913	11	44	69		11994
POL	VAKETVASCDC	784	11	45	71		11995
POL	GAANRET	636	8	45	70		11996
POL	EIVASCDK	787	8	45	70		11997
POL	DGAANRET	635	9	45	70		11998
POL	PFKNLKTGKY	537	10	45	70	0.0002	11999
POL	PLVKLWYQLE	613	11	45	70		12000
POL	EILKEPVII	497	8	46	72		12001
POL	KLWYQLEK	616	8	46	72		12002
POL	RDQAEIILK	918	8	46	72		12003
POL	PFKNLKTGK	537	9	46	72		12004
POL	DIQTKELQK	959	9	46	72		12005
POL	LVKLWYQLEK	614	10	46	72	0.0006	12006
POL	KVKQWPLTEE	207	11	46	72	0.0820	12007
POL	VIWGTTPK	573	8	48	75	0.0330	12008
POL	OVRDQAEII	916	8	48	75		12009
POL	DIKVVPRR	1009	8	48	75		12010
POL	IVIWGTTPK	572	9	48	75	0.3700	12011
POL							12012

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	DIKVVIRRK	1009	9	48	75	0.0001	12013
POL	KVFLDGIDK	750	10	48	75	0.7800	12014
POL	KCQLKGEAMII	794	10	48	75		12015
POL	VVESMNKELK	902	10	48	75		12016
POL	GVVESMNKEL	901	11	48	75		12017
POL	VVESMNKELK	902	11	48	75		12018
POL	GVVESMNK	901	8	49	77		12019
POL	QGVVESMNK	900	9	49	77		12020
POL	KLKPMDDGPK	197	10	49	77	0.0760	12021
POL	QSQGVVESMIN	898	11	49	77		12022
POL	ESIVWGK	570	8	50	79		12023
POL	YVDCANR	633	8	50	78	0.0001	12024
POL	LAQRWPK	856	8	50	78		12025
POL	KIIRDYK	1019	8	50	78		12026
POL	KLAGRWPK	855	9	50	78	0.0690	12027
POL	QNRVYYRDS	973	11	50	78		12028
POL	GMDGPKVK	201	8	51	80	0.0004	12029
POL	KIGPENPY	238	8	51	80		12030
POL	NNETPGIR	325	8	51	80		12031
POL	FTTPDKII	403	8	51	80		12032
POL	PGMDGPKVK	200	9	51	80	0.0001	12033
POL	NNETPGIRY	325	9	51	80		12034
POL	GFTTPDKII	402	9	51	80		12035
POL	VFLDGDK	751	9	51	80	0.0320	12036
POL	VIIQYMDDL	368	10	51	80	0.0090	12037
POL	WGFTTPDKII	401	10	51	80		12038
POL	FTTPDKIIQK	403	10	51	80	0.0150	12039
POL	NNETPGIRYQY	325	11	51	80		12040
POL	GFTTPDKIIQ	402	11	51	80		12041
POL	PAGLKKKK	286	8	52	81		12042
POL	SDLEIGQII	380	8	52	81		12043
POL	DLIGQIIR	381	8	52	81		12044
POL	WGFTTPDK	401	8	52	81		12045
POL	GFTTPDKK	402	8	52	81		12046
POL	KIQNFRVY	971	8	52	81		12047
POL	VVPRRKAK	1012	8	52	81	0.0001	12048
POL	ETPGIRYQY	327	9	52	81		12049
POL	GSDLEIGQII	379	9	52	81		12050
POL	SDLEIGQIIR	380	9	52	81	0.0001	12051
POL	WGFTTPDKK	401	9	52	81	0.0039	12052
POL	KIQNFRVY	971	9	52	81	0.1400	12053
POL	KVPRRKAK	1011	9	52	81	0.0039	12054
POL	VGSDLEIGQII	378	10	52	81		12055
POL	GSDLEIGQIIR	379	10	52	81		12056
POL	KIQNFRVYR	971	10	52	81	0.2100	12057
POL	NFRVYYRDSR	974	10	52	81		12058
POL	IGGIGGFIKVR	134	11	52	81		12059
POL	VGFTVYNIQR	164	11	52	81		12060
POL	YVGSDEIGQII	377	11	52	81		12061
POL	VGSDLEIGQIIR	378	11	52	81		12062

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	GIPHPAGLKK	282	11	53	84		12063
POL	IGGFIKVR	137	8	53	83		12064
POL	GFIKVRQY	139	8	53	83		12065
POL	PIETVPVK	190	8	53	83		12066
POL	ETVPVKLK	192	8	53	83	0.0001	12067
POL	ELEAENR	489	8	53	83		12068
POL	QLKGEAMH	796	8	53	83		12069
POL	ESMNKELK	904	8	53	83		12070
POL	SMNKELK	905	8	53	83		12071
POL	GIGGFIKVR	136	9	53	83	0.0005	12072
POL	GQFIKVRQY	138	9	53	83	0.0001	12073
POL	ESMNKELK	904	9	53	83		12074
POL	GIGGFIKVR	135	10	53	83	0.0002	12075
POL	IGGFIKVRQY	137	10	53	83	0.0002	12076
POL	ISPIETVPVK	188	10	53	83	0.0310	12077
POL	PIETVPVKLK	190	10	53	83	0.0001	12078
POL	EAELEAENR	487	10	53	83		12079
POL	LVAVIIVASGY	826	10	53	83		12080
POL	GIGGFIKVRQY	136	11	53	83		12081
POL	ISPIETVPVK	187	11	53	83		12082
POL	ILVAVIIVASGY	825	11	53	83		12083
POL	FVNTPLPVK	608	9	54	86	0.0660	12084
POL	GIPHPAGLKK	282	10	54	86	0.1700	12085
POL	LGIPHPAGLKK	281	11	54	86		12086
POL	QNERVYVR	973	8	54	84		12087
POL	PTPVNIGR	166	9	54	84	0.0001	12088
POL	LAENREILK	492	9	54	84	0.0003	12089
POL	ELAENREILK	491	10	54	84	0.0003	12090
POL	EFVNTPLPVK	607	10	54	84		12091
POL	PLTEEKIK	212	8	55	86		12092
POL	LFLDGIHK	752	8	55	86		12093
POL	GIPHPAGLK	282	9	56	89	0.0650	12094
POL	LGIPHPAGLK	281	10	56	89	0.0150	12095
POL	QLGIPHPAGLK	280	11	56	89		12096
POL	VTVLDVGDAY	295	10	56	88	0.0004	12097
POL	ELKKIGQVR	909	10	56	88		12098
POL	DFWEVQLGPII	275	11	56	88		12099
POL	SVTVLDVGDAY	294	11	56	88		12100
POL	KTAVQMAVFI	925	11	56	88		12101
POL	VNTPLPVK	609	8	57	89		12102
POL	AIKKKDKTK	251	9	57	89	0.0006	12103
POL	TVLDVGDAY	296	9	57	89	0.0056	12104
POL	TPDKKIIQK	404	9	57	89	0.0042	12105
POL	FAIKKDKSTK	250	10	57	89	0.0002	12106
POL	NTPPLVKLWY	610	10	57	89	0.0002	12107
POL	AIKKKDKTKW	251	11	57	89		12108
POL	VNTPLVKLW	609	11	57	89		12109
POL	MAVFIINFKR	930	11	57	89		12110
POL	GGIGYSAGER	941	11	57	89		12111
POL	KDSTKWRK	255	8	58	91		12112

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	EVQLGPIH	278	8	58	91		12113
POL	GGNEQVDK	735	8	58	91		12114
POL	FIHFKRK	933	8	58	91		12115
POL	GGYSAGER	944	8	58	91		12116
POL	RYYRDSR	976	8	58	91		12117
POL	IGGNEQVDK	734	9	58	91	0.0001	12118
POL	VFIHFKRK	932	9	58	91	0.0003	12119
POL	IGGYSAGER	943	9	58	91	0.0001	12120
POL	GICGNEQVDK	733	10	58	91	0.0001	12121
POL	PAETGOETAY	842	10	58	91	0.8500	12122
POL	AVFIHFKRK	931	10	58	91	0.0001	12123
POL	GIGGYSAGER	942	10	58	91		12124
POL	STKWRKLVDF	257	11	58	91		12125
POL	KGIGNEQVDK	732	11	58	91		12126
POL	AVIVASGY	828	8	59	92		12127
POL	ETGQETAY	844	8	59	92		12128
POL	GIWQLDCTH	811	9	59	92		12129
POL	VAVIVASGY	827	9	59	92	0.0001	12130
POL	KGPAKLLWK	988	9	59	92	0.0007	12131
POL	EVNIVTDSQY	684	10	59	92		12132
POL	PGIWQLDCTH	810	10	59	92		12133
POL	TAVQMAVFIH	926	10	59	92	0.0110	12134
POL	VGKLNWASQI	450	11	59	92		12135
POL	NFKRKGGIGGY	936	11	59	92		12136
POL	QLDCTIILEGK	814	10	60	95	0.0003	12137
POL	DFRELNR	265	8	60	94		12138
POL	VLDVGDAY	297	8	60	94		12139
POL	KNLKTGKY	539	8	60	94		12140
POL	VDFRELNR	264	9	60	94		12141
POL	MGYELIIPDK	419	9	60	94	0.0960	12142
POL	KLNWASQIY	452	9	60	94	0.0006	12143
POL	AVQMAVFIH	927	9	60	94		12144
POL	MAVFIHFK	930	9	60	94	0.3000	12145
POL	LYDFRELNR	263	10	60	94		12146
POL	WMGYELIIPDK	418	10	60	94	0.0001	12147
POL	QMAVFIHFK	929	10	60	94	0.6400	12148
POL	MAVFIHFKR	930	10	60	94	0.0003	12149
POL	KLVDRELNR	262	11	60	94		12150
POL	QMAVFIHFK	929	11	60	94		12151
POL	LNWASQIY	453	8	61	95		12152
POL	NDIQKLVGK	444	9	61	95		12153
POL	LDCTHLEGG	815	9	61	95		12154
POL	VNDIQKLVGK	443	10	61	95		12155
POL	TVNDIQKLVGK	442	11	61	95		12156
POL	VDFRELNR	264	8	62	97	0.1700	12157
POL	WTVNDIQK	441	8	62	97		12158
POL	DIQKLVGK	445	8	62	97	0.0001	12159
POL	NIVTDSQY	686	8	62	97		12160
POL	DCTHLEGG	816	8	62	97		12161
POL	AVFIHFK	931	8	62	97	0.0380	12162

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SIQ ID NO.
POL	VHIIFKR	932	8	62	97		12163
POL	LVDFRELNK	263	9	62	97	0.0300	12164
POL	VNIYDSQY	685	9	62	97		12165
POL	AVIHIIFKR	931	9	62	97	1.0000	12166
POL	MIGIGGFIK	133	10	62	97	0.0550	12167
POL	KLVDRELNK	262	10	62	97	0.0900	12168
POL	KMIGIGGFIK	132	11	62	97	0.7000	12169
POL	NVLPQGWK	336	8	63	100	0.0012	12170
POL	IGGIGGFIK	134	9	63	98	0.0037	12171
POL	YNVLPQGWK	335	9	63	98	0.0001	12172
POL	GGIGGFIK	135	8	64	100		12173
POL	FLWMGYELII	416	9	64	100		12174
POL	PFLWMGYELII	415	10	64	100		12175
REV	GTRQTRKNR	37	9	01	50		12176
REV	TTRQARRNR	37	9	01	50		12177
REV	GTRQTRKNR	37	10	01	50		12178
REV	TTRQARRNR	37	10	01	50		12179
REV	GTRQTRKNR	37	11	01	50		12180
REV	TTRQARRNR	37	11	01	50		12181
REV	GTETGVGR	103	8	06	19		12182
REV	QGTETGVGR	102	9	06	19		12183
REV	LLKTVRLIK	12	9	10	16		12184
REV	GDSDELLK	6	9	11	17		12185
REV	PLQLPIIER	76	9	11	17		12186
REV	SGDSDELLK	5	10	11	17		12187
REV	RSQDSDELLK	4	11	11	17		12188
REV	PVPLPIIER	74	11	11	17		12189
REV	RAIQRIK	50	8	12	19		12190
REV	DSDELLK	7	8	12	19		12191
REV	ILSTCLGR	63	8	12	19		12192
REV	RIISTCLGR	62	9	12	19		12193
REV	SNPPIISPECTR	27	11	12	19		12194
REV	AVRIKILY	17	9	13	20		12195
REV	QLPPIELII	78	9	13	20		12196
REV	PSPEGTQAR	31	10	13	20		12197
REV	RNRIRWRER	43	10	13	20		12198
REV	PSPEGTQAR	31	11	13	20		12199
REV	PLQLPIELRII	76	11	13	20		12200
REV	GTRQARKNR	36	11	14	22		12201
REV	RAIQRII	50	8	15	24		12202
REV	GTRQARKNR	36	9	15	23		12203
REV	GTRQARKNR	36	10	15	23		12204
REV	QARKNRNR	40	9	16	25		12205
REV	QARKNRNR	40	11	16	25		12206
REV	QARKNR	40	8	17	27		12207
REV	IKILYQSNPY	20	11	18	28		12208
REV	KNRRRWRA	43	10	19	30		12209
REV	KNRRRWRA	43	8	21	33		12210
REV	RNRIRWRER	43	10	23	36		12211
REV	KILYQSNPY	22	9	26	41		12212

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HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*1001	SEQ ID NO.
REV	ILYQSNPY	23	8	27	42		12213
REV	EGTRQARR	35	8	27	42		12214
REV	EGTRQARRNR	35	10	27	42		12215
REV	EGTRQARRNR	35	11	27	42		12216
REV	GTRQARRNR	36	9	34	53		12217
REV	GTRQARRNRNR	36	10	34	53		12218
REV	GTRQARRNRNR	36	11	34	53		12219
REV	PVPLQLPPLER	74	11	34	53		12220
REV	PLQLPPLER	76	9	35	55		12221
REV	QARRNRNRNR	40	11	37	58		12222
REV	QARRNRNR	40	8	38	59		12223
REV	QARRNRNRNR	40	9	38	59		12224
REV	RNRNRNRNR	43	8	40	63		12225
TAT	PGGYPRRK	104	8	01	50		12226
TAT	AGPGGYPRR	102	9	01	50		12227
TAT	TGPGSQPCII	102	9	01	50		12228
TAT	ETGPGSQPCII	101	10	01	50		12229
TAT	KAGPGGYPRR	101	10	01	50		12230
TAT	AGPGGYPRRK	102	10	01	50		12231
TAT	KAGPGGYPRR	101	11	01	50		12232
TAT	GGYPRRKQSC	105	11	01	50		12233
TAT	ACTNCCYCK	24	8	16	16		12234
TAT	TACTNCCYCK	23	9	10	16		12235
TAT	CNCCYCKK	25	8	11	17		12236
TAT	YCKKCCFII	29	8	11	17		12237
TAT	YCKKCCYII	29	8	11	17		12238
TAT	VDPRLEPWK	4	9	11	17		12239
TAT	ACNNCCYCKK	24	9	11	17		12240
TAT	VDPRLEPWK	3	10	11	17		12241
TAT	VDPRLEPWKII	4	10	11	17		12242
TAT	TACNNCCYCKK	23	10	11	17		12243
TAT	VDPRLEPWK	3	11	11	17		12244
TAT	RGDPTGPKES	84	11	11	17		12245
TAT	GDIPTGPKESK	85	11	11	17		12246
TAT	ESKKKVESK	93	9	12	19		12247
TAT	GDIPTGPKESK	85	10	12	19		12248
TAT	PTGPKESKKK	88	10	12	19		12249
TAT	TGPKESKKK	89	9	13	20		12250
TAT	LNKGLGISY	42	9	14	22		12251
TAT	FLNKGLGISY	41	10	14	22		12252
TAT	PVDNPLEPWN	3	11	14	22		12253
TAT	CFLNKGLGISY	40	11	14	22		12254
TAT	LNKGLGISYOR	42	11	14	22		12255
TAT	WNHFGSQPK	14	9	15	23		12256
TAT	RGDPTGPK	84	8	16	25		12257
TAT	VDNPLEPWNII	4	10	16	25		12258
TAT	PNLEPWNH	9	8	17	27		12259
TAT	ACNNCCYCK	24	8	17	27		12260
TAT	TACNNCCYCK	23	9	17	27		12261
TAT	PTGPKESKK	88	9	18	28		12262

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
TAT	TGPKESKK	89	8	19	30		12263
TAT	PTGPKESK	88	8	20	31		12264
TAT	YGRKKRRQRR	50	11	22	34		12265
TAT	YGRKKRRQRR	50	10	38	59		12266
TAT	ISYGRKKRRQRR	48	11	39	61		12267
TAT	YGRKKRRQRR	50	9	41	64		12268
TAT	GISYGRKKRR	47	10	45	70	0.0001	12269
TAT	LGISYGRKKRR	46	11	45	70		12270
TAT	ISYGRKKRR	48	9	46	72	0.0005	12271
TAT	GLGISYGRKKRR	45	11	54	86		12272
TAT	GLGISYGR	45	8	55	87		12273
TAT	GLGISYGRK	45	9	55	87	0.0006	12274
TAT	GLGISYGRKK	45	10	55	87		12275
TAT	KGLGISYGR	44	9	55	86	0.0180	12276
TAT	KGLGISYGRK	44	10	55	86	0.0007	12277
TAT	KGLGISYGRKK	44	11	55	86		12278
TAT	GISYGRKKR	47	9	57	89	0.0005	12279
TAT	LGISYGRKKR	46	10	57	89		12280
TAT	LGISYGRK	46	8	58	91		12281
TAT	GISYGRKK	47	8	58	91		12282
TAT	ISYGRKKR	48	8	58	91		12283
TAT	LGISYGRKK	46	9	58	91	0.0005	12284
VIF	LIVWQVDR	8	8	10	16		12285
VIF	RMKINTWK	15	8	10	16		12286
VIF	LKPKKIK	158	8	10	16		12287
VIF	KGWFRYRIIY	36	9	10	16		12288
VIF	ALIKPKKIK	157	9	10	16		12289
VIF	VDRMRINTWK	13	10	10	16		12290
VIF	GVSEIWRLLR	87	10	10	16		12291
VIF	QVDRMRINTW	12	11	10	16		12292
VIF	RLVITYWGL	65	11	10	16		12293
VIF	QTGERDWILG	75	11	10	16		12294
VIF	GVSEIWRLLR	87	11	10	16		12295
VIF	IDPDLADQLII	103	11	10	16		12296
VIF	LVEDRWNKIQ	178	11	10	16		12297
VIF	SEIWRLLR	89	8	11	17		12298
VIF	TALIKPKK	156	8	11	17		12299
VIF	LVEDRWNK	178	8	11	17		12300
VIF	VSIEWRLLR	88	9	11	17		12301
VIF	SEIWRLLR	89	9	11	17		12302
VIF	LTALIKPKK	155	9	11	17		12303
VIF	KLVEDRWNK	177	9	11	17		12304
VIF	VSIEWRLLR	88	10	11	17		12305
VIF	GLADQLIIMH	106	10	11	17		12306
VIF	ALTALIKPKK	154	10	11	17		12307
VIF	WNPQKTRGH	183	10	11	17		12308
VIF	PGLADQLIIMH	105	11	11	17		12309
VIF	GLADQLIIMH	106	11	11	17		12310
VIF	LALTALIKPKK	153	11	11	17		12311
VIF	WNPQKTRGH	183	11	11	17		12312

Table XVII
 HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VIF	WYRIHIESR	38	11	12	19		12313
VIF	KGWYRIHII	36	8	12	19		12314
VIF	WGLQTGR	72	8	12	19		12315
VIF	QTGERDWII	75	8	12	19		12316
VIF	IVWQVDRMK	9	9	12	19		12317
VIF	KIRTWNSLVK	17	10	12	19		12318
VIF	LVKIHIMYVSK	24	10	12	19		12319
VIF	GLQTGERDWII	73	10	12	19		12320
VIF	TGERDWILGH	77	10	12	19		12321
VIF	IIGVSEWRLR	86	10	12	19		12322
VIF	IVWQVDRMKI	9	11	12	19		12323
VIF	KIRTWNSLVK	17	11	12	19		12324
VIF	SLVKIHIMYVS	23	11	12	19		12325
VIF	LVKIHIMYVSK	24	11	12	19		12326
VIF	WGLQTGERD	72	11	12	19		12327
VIF	WYRIHIESR	38	10	13	21		12328
VIF	QVDRNKIR	12	8	13	20		12329
VIF	IIPLGDAR	56	8	13	20		12330
VIF	ADQLIHIMII	108	8	13	20		12331
VIF	CFSDSAIR	119	8	13	20		12332
VIF	FSDSAIRK	120	8	13	20		12333
VIF	SLOYLALK	149	8	13	20		12334
VIF	LTALIKPK	155	8	13	20		12335
VIF	LADQLIHIMII	107	9	13	20		12336
VIF	ADQLIHIMY	108	9	13	20		12337
VIF	CFSDSAIRK	119	9	13	20		12338
VIF	GSLQYLALK	148	9	13	20		12339
VIF	AL'TALIKPK	154	9	13	20		12340
VIF	SVKKLIEDR	174	9	13	20		12341
VIF	EVIIHPLGDAR	54	10	13	20		12342
VIF	LADQLIHIMY	107	10	13	20		12343
VIF	DCFESAIRK	118	10	13	20		12344
VIF	VGSLOYLALK	147	10	13	20		12345
VIF	LALTALIKPK	153	10	13	20		12346
VIF	PSVKKLIEDR	173	10	13	20		12347
VIF	FDCFESAIRK	117	11	13	20		12348
VIF	YALTALIKPK	152	11	13	20		12349
VIF	FESAIRK	120	8	14	22		12350
VIF	IVSPRCY	133	8	14	22		12351
VIF	GVSEWRLR	87	9	14	22		12352
VIF	ADQLIHILY	108	9	14	22		12353
VIF	CFESAIRK	119	9	14	22		12354
VIF	VDRMRRTWK	13	10	14	22		12355
VIF	LADQLIHILY	107	10	14	22		12356
VIF	RCDYQAGHNK	137	10	14	22		12357
VIF	QVDRMRRTWK	12	11	14	22		12358
VIF	RIRTWNSLVK	17	11	14	22		12359
VIF	RMRTWK	15	8	15	23		12360
VIF	RTWKSIVK	19	8	15	23		12361
VIF	VSIEWRLR	88	8	15	23		12362

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VIF	ADQLIILY	108	8	15	23		12363
VIF	RTWKSLSVKII	19	9	15	23		12364
VIF	QQVSIEWRK	86	9	15	23		12365
VIF	LADQLIILY	107	9	15	23		12366
VIF	AIRKAILGII	124	9	15	23		12367
VIF	CDYQAGINK	138	9	15	23		12368
VIF	RIRTWKSLSVK	17	10	15	23		12369
VIF	RIRTWNSLVK	17	10	15	23		12370
VIF	RTWKSLSVKIIII	19	10	15	23		12371
VIF	SAIRKAILGII	123	10	15	23		12372
VIF	RIRTWKSLSVK	17	11	15	23		12373
VIF	LQGVSVIEWR	84	11	15	23		12374
VIF	VDRGLADQLIHH	103	11	15	23		12375
VIF	ITTYWGLII	68	8	16	25		12376
VIF	GYSIEWRK	87	8	16	25		12377
VIF	NCIDYQAGII	137	8	16	25		12378
VIF	LALTALIK	153	8	16	25		12379
VIF	VITTYWGLII	67	9	16	25		12380
VIF	YLALTALIK	152	9	16	25		12381
VIF	KTKGIIRGSH	188	9	16	25		12382
VIF	LVITTYWGLII	66	10	16	25		12383
VIF	WINKPQTKGII	183	10	16	25		12384
VIF	WINKPQTKGII	183	11	16	25		12385
VIF	EDRWNKIPQKT	180	11	17	27		12386
VIF	WINKPQTK	183	8	18	28		12387
VIF	KSLVKIIIMY	22	9	18	28		12388
VIF	EDRWNKIPQKT	180	11	18	28		12389
VIF	RCEYQAGIINK	137	10	19	30		12390
VIF	HIPLGEAR	56	8	20	31		12391
VIF	WINKPQKTR	183	8	20	31		12392
VIF	EVIIPLGEAR	54	10	20	31		12393
VIF	ITGERDWII	75	8	21	33		12394
VIF	DLADQLII	106	8	21	33		12395
VIF	PDADQLII	105	9	21	33		12396
VIF	GLITGERDWII	73	10	21	33		12397
VIF	WGLITGERD	72	11	21	33		12398
VIF	VSPRCEYQAG	134	11	21	33		12399
VIF	LTEDRWNKPKQ	178	11	21	33		12400
VIF	GSIIIMNGII	194	8	22	34		12401
VIF	RGSIITMNGII	193	9	22	34		12402
VIF	TTYWGLITGE	69	11	22	34		12403
VIF	IILGIGVSVIEW	83	11	22	34		12404
VIF	NSLVKIIIMY	22	9	24	38		12405
VIF	WNSLVKIIIM	21	10	24	38		12406
VIF	QQVSIEWR	86	8	25	39		12407
VIF	LQGVSVIEWR	84	10	25	39		12408
VIF	HLGGVSVIEW	83	11	25	39		12409
VIF	RCEYQAGII	137	8	26	41		12410
VIF	RTWNSLVKII	19	9	26	41		12411
VIF	RTWNSLVKIIH	19	10	26	41		12412

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	Site ID NO.
VIF	RTWSLVK	19	8	27	42		12413
VIF	IGVSIEWR	86	8	27	42		12414
VIF	GLADQLII	106	8	27	42		12415
VIF	PGADQLIHI	105	9	27	42		12416
VIF	LGHGVSEWR	84	10	27	42		12417
VIF	YDFCFESAIR	116	11	27	42		12418
VIF	WGLHTGIER	72	8	28	44		12419
VIF	DCFSFAIR	118	9	28	44		12420
VIF	FDCFSFAIR	117	10	28	44		12421
VIF	WNSLVKIII	21	8	29	45		12422
VIF	CFSESAR	119	8	29	45		12423
VIF	KLTEDRWNK	177	9	29	45	0.2700	12424
VIF	LTEDRWNK	178	8	31	48	0.0045	12425
VIF	IVWQVDRMRI	9	11	33	52		12426
VIF	QVDRMRIR	12	8	34	53		12427
VIF	EDRWNKIQK	180	9	39	61		12428
VIF	VMIVWQVDR	7	11	41	64		12429
VIF	QVMIVWQVDR	6	10	43	67		12430
VIF	VMIVWQVDRM	8	10	43	67	0.0001	12431
VIF	AGIINKVGSLSQ	142	11	43	67		12432
VIF	SLVKIIIMY	23	8	44	69		12433
VIF	VMIVWQVDR	7	9	44	69		12434
VIF	MIWQVDR	8	8	46	72	0.0220	12435
VIF	IVWQVDRMR	9	9	47	73	0.0007	12436
VIF	IINKVGSLSQY	144	9	47	73		12437
VPR	ALPGRGR	85	8	01	50		12438
VPR	NIRGRVR	85	8	01	50		12439
VPR	WALLEELK	18	10	09	15		12440
VPR	QLLFVIIR	66	8	10	16		12441
VPR	ISHIIR	79	8	10	16		12442
VPR	RIGTRQR	81	8	10	16		12443
VPR	IGTRQR	82	8	10	16		12444
VPR	ALELEELK	19	9	10	16		12445
VPR	RIGTRQR	81	9	10	16		12446
VPR	ISRIGTRQR	79	10	10	16		12447
VPR	ISRIGTRQRR	79	11	10	16		12448
VPR	WLIGLGQY	38	8	11	17		12449
VPR	IFRIGCRH	71	8	11	17		12450
VPR	ISRIGTR	79	8	11	17		12451
VPR	FLIFRIGCR	69	9	11	17		12452
VPR	FLIFRIGCRH	68	10	11	17		12453
VPR	FVIFRIGCQH	69	10	11	17		12454
VPR	HFRIGCRISR	71	10	11	17		12455
VPR	LLFIFRIGCR	67	11	11	17		12456
VPR	LFIFRIGCRH	68	11	11	17		12457
VPR	LFVIFRIGCQH	68	11	11	17		12458
VPR	RIGCRISR	74	8	12	19		12459
VPR	LOQHYNTY	42	9	13	20		12460
VPR	LOQYIYET	42	9	13	20		12461
VPR							12462

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VPR	IFPRWLII	33	8	14	22		12463
VPR	KSEAVRIIPR	27	10	14	22		12464
VPR	AVRIIPRIWL	30	11	14	22		12465
VPR	ELKSEAVR	25	8	16	25		12466
VPR	AGVEAIR	55	8	16	25		12467
VPR	ELKSEAVRII	25	9	16	25		12468
VPR	WAGVEAIR	54	9	16	25		12469
VPR	LLELKSEAVR	22	11	16	25		12470
VPR	DTWAGVEAIR	52	11	16	25		12471
VPR	ELKNEAVR	25	8	17	27		12472
VPR	ELKNEAVRII	25	9	17	27		12473
VPR	LQHIYETY	42	9	17	27		12474
VPR	LLEELKNEAVR	22	11	17	27		12475
VPR	EGVEAIR	55	8	18	28		12476
VPR	DTWEGVEAIR	52	11	18	28		12477
VPR	RARGASR	93	8	19	30		12478
VPR	KNEAVRIIPR	27	10	19	30		12479
VPR	WLHGLQHI	38	8	20	31		12480
VPR	HLGLQHII	40	8	20	31		12481
VPR	WLHGLQHII	38	10	20	31		12482
VPR	LFIIRIGCQII	68	11	29	45		12483
VPR	FIIRIGCQII	69	10	30	47		12484
VPR	IFPRPWLI	33	8	31	49		12485
VPR	AVRIIPRI'WL	30	11	31	48		12486
VPR	ILQQLFIIR	63	10	35	55		12487
VPR	RIQQLFIH	63	11	36	56		12488
VPR	ILQQLFIH	63	9	37	58		12489
VPR	EDQGQREPY	6	10	37	58		12490
VPR	QAFEDQGPQR	3	10	39	62		12491
VPR	WTLELLELK	18	10	42	69		12492
VPR	QQQREPY	8	8	43	68		12493
VPR	QLFIIR	66	8	44	69		12494
VPR	IFRIGCQII	71	8	44	69		12495
VPR	TELELELK	19	9	44	69		12496
VPR	IFRIGCQISR	71	10	44	69		12497
VPR	RIGCQISR	74	8	47	73		12498
VPR	EAVRIIPR	29	8	59	92		12499
VPR	LVQRKQDR	43	8	01	50		12500
VPR	VTLLSSK	94	8	01	50		12501
VPR	LVQRKQDR	43	9	01	50		12502
VPR	LVTLSSK	91	9	01	50		12503
VPR	RIKERDSDY	64	11	01	50		12504
VPR	RIKERDSDY	64	11	01	50		12505
VPR	WTIVFIEYR	34	9	10	16		12506
VPR	TIVFIEYR	35	8	10	16		12507
VPR	IDRLDIR	34	9	10	16		12508
VPR	RLDIRIR	36	9	10	16		12509
VPR	KIDRLDIR	52	10	10	16		12510
VPR	VWTVFIEYR	31	11	12	19		12511
VPR	WTIVFIEY	34	8	12	19		12512

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VPV	IVFIEYRK	36	8	12	19		12513
VPV	VVWTVVPIEY	31	10	12	19		12514
VPV	IVVWTVVPIEY	30	11	12	19		12515
VPV	LIDRIKER	58	8	14	22		12516
VPV	KIDRLIDR	52	8	15	23		12517
VPV	ILRQRKIDR	46	9	15	23		12518
VPV	KILRQRKIDR	45	10	15	23	0.0001	12519

Table XVIII
HIV Δ24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ ²⁴⁰¹	SEQ ID NO.
ENV	IIMQLTVW	650	8	10	16		12520
ENV	WFDITNWL	767	8	10	16		12521
ENV	WFDITNWL	767	9	10	16		12522
ENV	IYCTPAGFAI	262	10	10	16		12523
ENV	IWNNTWME	717	10	10	16		12524
ENV	WFDITNWL	767	11	10	16		12525
ENV	SYIHLRDLII	864	11	10	16		12526
ENV	IYCTPAGF	262	8	11	17		12527
ENV	FYATGDIIGDI	367	11	11	17		12528
ENV	FYATGDII	367	8	12	19		12529
ENV	WMEWEREI	723	8	12	19		12530
ENV	GWEALKYL	896	8	12	19		12531
ENV	GWEGLKYL	896	8	12	19		12532
ENV	TWMEWEREI	722	9	12	19		12533
ENV	SYIHLRDLII	864	10	12	19		12534
ENV	NMTWMEWER	720	11	12	19		12535
ENV	YWQELKNSA	909	11	12	19		12536
ENV	LYKYKVEI	561	9	13	20		12537
ENV	SYIHLRDFI	864	9	13	20		12538
ENV	SYIHLRDFI	864	10	13	20		12539
ENV	YMIISFNCGGE	432	11	13	20		12540
ENV	LFSYIHLRDFI	862	11	13	20		12541
ENV	LFSYIHLRDLI	862	11	13	20		12542
ENV	SYIHLRDLI	864	9	14	22		12543
ENV	KYWNLLQY	901	10	14	22		12544
ENV	WWNLLQYW	903	8	15	23		12545
ENV	YWNNLLQYW	902	9	15	23		12546
ENV	KWASLWNWF	760	11	15	23		12547
ENV	SFNCRGIEF	437	8	16	25		12548
ENV	KWLWYKIF	772	9	16	25		12549
ENV	KWLWYKIFI	772	10	16	25		12550
ENV	RYLRDQQL	671	9	17	27	0.2300	12551
ENV	RYLRDQQLGI	671	11	17	27		12552
ENV	RYLRDQQL	671	11	17	27		12553
ENV	SYIHLRDF	864	8	18	28		12554
ENV	AYDTEVIINW	73	10	18	28		12555
ENV	LFSYIHLRDF	862	10	18	28		12556
ENV	KWLWYKIF	772	8	19	30		12557
ENV	AWDDLRLS	853	8	20	31	0.0004	12558
ENV	NMVEQMIEDI	112	10	20	31		12559
ENV	AWDDLRLSL	853	10	20	31		12560
ENV	NMVEQMIEDII	112	11	20	31		12561
ENV	AWDDLRLSL	853	11	20	31		12562
ENV	FYCNLSGL	445	8	21	33		12563
ENV	FYCNLSGL	444	9	21	33		12564
ENV	FYCNLSGL	445	9	21	33		12565
ENV	EFFYCNLSGL	443	10	21	33		12566
ENV	EFFYCNLSGL	444	10	21	33		12567
ENV	EFFYCNLSGL	443	11	21	33		12568
ENV	EFFYCNLSGL	443	11	21	33		12569

Table XVIII
HIV Δ24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SFQ ID NO.
ENV	VWKEATITL	55	9	22	34	0.03100	12570
ENV	VWKEATITLF	55	10	22	34	0.27100	12571
ENV	LFSYIHLRLDL	862	10	22	34		12572
ENV	SYIKLRDL	864	8	23	36		12573
ENV	NWLWYIKI	772	8	25	39		12574
ENV	NWLWYIKIF	772	9	25	39		12575
ENV	KYKVVYKIEIL	563	10	25	39		12576
ENV	NWLWYIKIFI	772	10	25	39		12577
ENV	GFLALAWDDL	848	10	25	39		12578
ENV	RYLKDQQLGI	671	11	25	39		12579
ENV	KWASLWNW	760	8	26	41		12580
ENV	KWASLWNWF	760	9	26	41		12581
ENV	IICAPAGF	262	8	27	42		12582
ENV	IICAPAGFAI	262	10	27	42		12583
ENV	IICAPAGFAIL	262	11	27	42		12584
ENV	QMIIIDISL	116	9	29	45		12585
ENV	LYKYKVVKI	561	9	29	45	0.02100	12586
ENV	RYLKDQQL	671	9	29	45	0.7600	12587
ENV	QMIIIDISLW	116	10	29	45		12588
ENV	GYSPISFQTL	806	10	29	45		12589
ENV	RYLKDQQL	671	8	30	47		12590
ENV	IFIMVGGI	779	10	33	52		12591
ENV	IMIVGGI	781	10	34	54		12592
ENV	IMIVGGI	781	8	35	56		12593
ENV	SFNCGGEFF	437	9	35	55		12594
ENV	SFNCGGEF	437	8	36	56		12595
ENV	DMRDNRSEL	552	10	37	58		12596
ENV	TMGAASITL	615	9	39	61		12597
ENV	IFIMVGGI	779	9	41	64		12598
ENV	WYIKIFIMI	775	9	43	67		12599
ENV	LWYIKIFIMI	774	10	43	67		12600
ENV	IWGCCKLI	681	8	48	75		12601
ENV	IWGCCKLI	681	9	48	75		12602
ENV	LWYIKIF	774	8	49	77		12603
ENV	VYVGVPVW	49	8	55	86	0.0270	12604
GAG	LYPLASLKS	544	10	59	17		12605
GAG	LYPLASLKSIF	544	11	59	17		12606
GAG	KYKLIIVW	29	9	10	16		12607
GAG	GWMTSNPII	269	9	10	16		12608
GAG	IMMQSNF	408	8	11	17		12609
GAG	LYCVIIOKI	87	8	13	20		12610
GAG	MYSPSILDI	300	10	13	20		12611
GAG	MYSPSILDI	299	11	13	20		12612
GAG	MYSPSIL	299	8	14	22		12613
GAG	MYSPSIL	300	8	14	22		12614
GAG	MYSPSIL	299	9	14	22		12615
GAG	RFVNPGL	45	8	16	25		12616
GAG	LFNTVATL	80	8	16	25		12617
GAG	WMTSNPII	270	8	16	25		12618
GAG	NWMTDTLL	339	8	16	25		12619

Table XVIII
HIV Δ24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
GAG	KYRLKILVW	29	9	16	25		12620
GAG	REAVNPGLL	45	9	16	25	0.0100	12621
GAG	LYCVIQR	87	8	18	28		12622
GAG	GWMTNNPPI	269	9	18	28	0.0140	12623
GAG	RFALNPGL	45	8	20	31		12624
GAG	WM'TNNPPI	270	8	20	31		12625
GAG	RFALNPGLL	45	9	20	31		12626
GAG	LYNTVATL	80	8	22	34		12627
GAG	AWVKVIEKA	175	11	24	38		12628
GAG	AMQMLKETI	218	9	26	41		12629
GAG	IMMQRGNF	408	8	27	42		12630
GAG	DYVDRFFKTL	319	10	27	42		12631
GAG	CFNCGKEGHI	425	10	27	42		12632
GAG	CFNCGKEGII	425	10	27	42		12633
GAG	DYVDRFYKTL	319	10	28	44	0.0010	12634
GAG	AWVKVVEKA	175	11	28	44		12635
GAG	NYIVIQNL	152	8	31	48		12636
GAG	AMQMLKDTI	218	9	33	52		12637
GAG	PFRDYVDRFF	316	10	35	55		12638
GAG	NWMTETLL	339	8	36	56		12639
GAG	RMYSVPSILDI	299	11	38	59		12640
GAG	RMYSVPSI	299	8	40	63		12641
GAG	RMYSVPSIL	299	9	40	63		12642
GAG	MYSVPSILDI	300	10	40	63		12643
GAG	MYSVPSIL	300	8	42	66		12644
GAG	QMRPROSDI	248	10	44	69		12645
GAG	VWASRELERF	36	10	45	70		12646
GAG	AFSPFVPMF	184	10	50	78	0.0078	12647
GAG	IYKRWIIL	285	8	54	84		12648
GAG	IYKRWIILGL	285	10	54	84	0.0140	12649
GAG	RWILGLNKI	288	10	56	88		12650
GAG	PFRDYVDRF	316	9	63	98		12651
NEF	PMTYKGAF	105	8	12	19		12652
NEF	TYKGAFDL	107	8	12	19		12653
NEF	PMTYKGAFDL	105	10	12	19		12654
NEF	VYIITQGF	192	8	13	20		12655
NEF	LWVYIITQGF	190	9	13	20		12656
NEF	LWVYIITQGF	190	10	13	20		12657
NEF	NYITGTRF	206	10	13	20		12658
NEF	VYIITQGF	192	11	13	20		12659
NEF	RFPLTFGWCF	216	10	17	27		12660
NEF	IYSKKRQEI	175	9	18	29		12661
NEF	IYSKKRQEI	175	10	18	29		12662
NEF	AFDLSFL	111	8	18	28		12663
NEF	DWQNYTQPG	203	11	18	28		12664
NEF	REPLTFGW	216	8	20	32		12665
NEF	NYITGPGI	206	8	20	31		12666
NEF	KWSKSSIVGW	4	10	20	31		12667
NEF	RYPLTFGWCF	216	10	21	33		12668
NEF	VYIITQGF	192	8	21	33		12669

Table XVIII
 HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
NIF	LWVYITQGYF	190	10	21	33		12670
NIF	VYIITQGYFD	192	11	21	33		12671
NIF	SFPLKIKGGI	115	10	22	34		12672
NIF	FFLKEKGGI	116	9	26	41		12673
NIF	RYPLTFGW	216	8	27	43		12674
NIF	IIFLKEKGGI	116	9	29	45		12675
NIF	TFGWCFKL	222	8	40	63		12676
NIF	GFPVRIQVPL	93	10	48	75		12677
POL	AFQGEAREF	7	10	10	16		12678
POL	NMLTQLGCTL	175	10	10	16		12679
POL	TWETWWTDY	589	10	10	16		12680
POL	TWWTDYWQA	592	11	10	16		12681
POL	CWAGIQQEF	882	10	11	17		12682
POL	IWKIKPKF	574	8	11	17		12683
POL	WYQLETEPI	618	9	11	17		12684
POL	WWAGIQQEF	883	9	11	17		12685
POL	IYIGIKVKQL	459	10	11	17		12686
POL	LWYQLETEPI	617	10	11	17		12687
POL	WWAGIQQEF	883	11	11	17		12688
POL	QYIQIHEI	145	9	12	19		12689
POL	KWTIQPIVL	427	9	12	19		12690
POL	LWQRPLVTIK	92	11	12	19		12691
POL	TWWTYWQA	592	11	12	19		12692
POL	SFSFQITLW	84	10	13	20		12693
POL	SFSFQITL	84	9	14	22		12694
POL	WYQLIKDPI	618	9	14	22		12695
POL	YYRDSRDL	978	9	14	22		12696
POL	WWTYWQAT	593	10	14	22		12697
POL	LWYQLEKDI	617	10	14	22		12698
POL	VYRDSRDL	977	10	14	22		12699
POL	YYRDSRDLW	978	10	14	22		12700
POL	LWQRPLVTIK	92	11	14	22		12701
POL	PFKQNPDI	359	11	14	22		12702
POL	WWTYWQAT	593	11	14	22		12703
POL	GYSAGERIVDI	945	11	14	22		12704
POL	VYRDSRDL	977	11	14	22		12705
POL	FFREDLAF	1	8	15	23		12706
POL	IYIGIKVRQL	459	10	15	23		12707
POL	PFKQNPDI	359	9	16	25		12708
POL	RWKPKMIGGI	128	10	17	27		12709
POL	IWKITPKFKL	574	10	17	27		12710
POL	YFSVPLDKDF	304	10	18	29		12711
POL	LWKGPAKLL	986	9	18	28		12712
POL	NMLTQIGCTL	175	10	18	28		12713
POL	IYAGIKVKQL	459	10	18	28		12714
POL	LWKGPAKLLW	986	10	18	28		12715
POL	AYFSVPLDKDF	303	11	18	28		12716
POL	AMASDFNLPI	773	11	18	28		12717
POL	LWKGPAKL	986	8	19	30		12718
POL	DYWQATWIPE	596	11	19	30		12719

Table XVIII
HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
POL	DYWQATWI	596	8	20	31		12720
POL	KFKLPQKETW	580	11	20	31		12721
POL	CWVAGIKQEF	882	10	21	33		12722
POL	LWQPLVTI	92	9	21	33	0.0190	12723
POL	WWAGIKQEF	883	9	21	33	0.0120	12724
POL	WWAGIKQFEG	883	11	21	33		12725
POL	NFQITLW	86	8	22	34		12726
POL	AWVPAIKGI	726	9	22	34		12727
POL	SFQITLW	86	8	23	36		12728
POL	WWTEYWOAT	593	10	23	36		12729
POL	WWTEYWOAT	593	11	23	36		12730
POL	PYNTPIFAL	244	9	24	38		12731
POL	YFLKLAGRW	851	10	25	39		12732
POL	AYFLKLAGR	850	11	25	39		12733
POL	KFRLPIQKETW	580	11	26	41		12734
POL	QYDQILIEI	145	9	27	42		12735
POL	NWASQIYAGI	454	10	27	42		12736
POL	KWTQPIQL	427	9	28	44		12737
POL	NWASQIYPGI	454	10	29	45		12738
POL	IWCKTPKFLR	574	10	30	47		12739
POL	WYQLIKKPI	618	9	31	48	0.0001	12740
POL	VYYDPSKDLI	509	10	31	48	0.0150	12741
POL	LWYQLEKEPI	617	10	31	48		12742
POL	YFLKLAGRW	851	10	31	48		12743
POL	AYFLKLAGR	850	11	31	48		12744
POL	EMEKEGKISKI	229	11	32	50		12745
POL	EYWOATWIPE	596	11	33	52		12746
POL	YYRDSRDI	978	9	34	53		12747
POL	VYYRDSRDI	977	10	34	53		12748
POL	YYRDSRDIW	978	10	34	53		12749
POL	VYYRDSRDI	977	11	34	53		12750
POL	YYDISKDLI	510	9	35	55		12751
POL	IWKGPAKLL	986	9	35	55		12752
POL	IWKGPAKLLW	986	10	35	55		12753
POL	IWKGPAKL	986	8	36	56		12754
POL	EYWOATWI	596	8	37	58	0.0310	12755
POL	PYNTPIVFAI	244	9	37	58		12756
POL	SWVPAIKGI	726	9	37	58		12757
POL	KYTAFTISI	315	10	37	58		12758
POL	IFQSSMTKI	348	9	38	59	0.0029	12759
POL	IFQSSMTKIL	348	10	38	59	0.0002	12760
POL	VYYDPSKDL	509	9	39	61	0.0004	12761
POL	IYQEPKLN	533	9	40	63	0.0520	12762
POL	GYSAGERIIDI	945	11	40	63		12763
POL	FFRENLAFL	1	8	41	64		12764
POL	GYSAGERII	945	9	41	64		12765
POL	GFIKVRQYDQI	139	11	41	64		12766
POL	NWRAMASDF	770	11	41	64		12767
POL	EMEKEGKI	229	8	42	66		12768
POL	DFRKYTAF	312	8	42	66		12769

Table XVIII
HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
POL	TYIQVEFF	530	9	42	66	0.3000	12770
POL	KWKPKMIGGI	128	10	42	66		12771
POL	DFRKYTAFTI	312	10	42	66		12772
POL	QWYIQYQEP	528	11	42	66		12773
POL	YYDISKIDL	510	8	43	67		12774
POL	SMTKILEPF	352	9	43	67	0.0110	12775
POL	NWRAMASDF	770	9	43	67	0.0016	12776
POL	AMASDFNL	773	8	45	70		12777
POL	IWGTIKTF	574	8	48	75		12778
POL	EWIEFVNTPL	605	10	50	78		12779
POL	GMIDGPKVKQ	201	10	51	80		12780
POL	TWIPEWEF	601	8	52	81		12781
POL	YWOATWIPE	597	10	52	81	0.0660	12782
POL	SMNKELKKI	905	9	53	83		12783
POL	EFVNTPL	607	8	54	84		12784
POL	GYIEAEVI	834	8	54	84		12785
POL	SWTVNDIQKL	440	10	54	84		12786
POL	EFVNTPLVKL	607	11	54	84		12787
POL	QWPLTHEKI	210	9	56	88		12788
POL	DFWVQLGI	275	9	56	88		12789
POL	FWEVQLGI	276	8	57	89		12790
POL	GYSAGERI	945	8	57	89		12791
POL	LYVGSLEI	376	9	58	91		12792
POL	KWIKLVDF	259	8	59	92		12793
POL	GWKGSPI	341	8	59	92		12794
POL	GWKGSPIAF	341	9	59	92	0.0095	12795
POL	IWQLDCTIIL	812	9	59	92		12796
POL	LWKGEAVVI	994	10	59	92		12797
POL	KWIKLVDFRE	259	11	59	92		12798
POL	NFKRKGGI	936	8	60	94		12799
POL	GYELIIPDKW	420	9	60	94	0.0001	12800
POL	QMAVFIINF	929	9	60	94	0.0190	12801
POL	WMGYELIIPDK	418	11	60	94		12802
POL	IYQYMDL	369	8	61	95		12803
POL	YMDLTVGSD	372	11	61	95		12804
POL	KMIGGIGGF	132	9	62	97	0.0011	12805
POL	KMIGGIGGF	132	10	62	97	0.0001	12806
POL	QYNVLPQGW	334	9	63	98	0.0036	12807
POL	RYQYNVLPQG	332	11	63	98		12808
POL	PELWMGYEL	415	9	64	100		12809
REV	RWRERQRQI	48	9	11	17		12810
REV	RWRARQRQI	48	9	35	55		12811
TAT	CYCKKCCF	28	8	11	17		12812
TAT	CFHCQVCF	34	8	11	17		12813
TAT	CFLNKGGLI	40	9	14	22		12814
VIF	RWQVLIVW	4	8	10	16		12815
VIF	RYSTOVDPGL	98	10	10	16		12816
VIF	CFSDSARKAI	119	11	16	16		12817
VIF	QYLALKAL	151	8	11	17		12818
							12819

Table XVIII
HIV Δ24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SIQ ID NO.
VIF	QYLALAAL	151	8	12	19		12820
VIF	RMKRTWNSL	15	10	12	19		12821
VIF	YWGLQTGERD	71	11	12	19		12822
VIF	CFSESARKAI	119	11	12	19		12823
VIF	CFSESARKAI	119	11	12	19		12824
VIF	VWQVDRMKI	10	9	13	20		12825
VIF	IMITYHDCF	113	8	15	23		12826
VIF	RMRTWKS	15	10	15	23		12827
VIF	RMRTWNSL	15	10	15	23		12828
VIF	DWILGQVSI	81	10	18	28		12829
VIF	YFDCFSESAL	115	11	20	31		12830
VIF	DWILGIGVSI	81	10	21	33		12831
VIF	YWGLHTGERD	71	11	22	34		12832
VIF	QYLALTAI	151	9	28	44		12833
VIF	YFDCFSESAL	116	10	44	44		12834
VIF	QYLALTAI	151	8	33	52		12835
VIF	RWQVMIVW	4	8	43	67		12836
VIF	VWQVDRMRI	10	9	48	75		12837
VPR	IIFRIWLIISL	33	10	10	16		12838
VPR	IIFRICRISRI	71	11	11	17		12839
VPR	PWLIIGLQIII	37	10	12	19		12840
VPR	QYIYETYGDT	44	11	14	22		12841
VPR	TWEGVEAIIRI	53	11	14	22		12842
VPR	TWAGVEAIIRI	53	11	15	23		12843
VPR	TWAGVEAI	53	8	16	25		12844
VPR	TWAGVEAI	53	9	16	25		12845
VPR	IYNTYGDITW	46	9	18	28		12846
VPR	TWEGVEAI	53	9	19	30		12847
VPR	TWEGVEAI	53	8	20	31		12848
VPR	IIFRPWLIGL	33	10	24	38		12849
VPR	PYNEWTLLEL	14	9	30	47	0.1400	12850
VPR	PYNEWTLLEL	14	10	30	47		12851
VPR	IYETYGDTW	46	9	31	48	0.0580	12852
VPR	EWTLLELEL	17	10	40	63		12853
VPR	IIFRICQIISRI	71	11	44	69		12854
VPU	NYELAVGAL	5	9	01	25		12855
VPU	NYELAVGALI	5	10	01	25		12856
VPU	DYKLGVGAL	10	9	02	29		12857
VPU	DYKLGVGALI	10	10	02	29		12858
VPU	DYRLGVGAL	10	9	03	43		12859
VPU	DYRLGVGALI	10	10	03	43		12860
VPU	EMGIHAPW	89	8	17	17		12861
VPU	VFIEYRKI	37	8	12	19		12862
VPU	EYRKILRQRKI	41	11	13	21		12863

Table XIXa
IIIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
ENV	VSTQLLNG	61	95	KPVVSTQLLNGSLA	299	29	45	12864
ENV	VVSTQLLN	60	94	IKPVVSTQLLNQSL	298	29	45	12865
ENV	LTVWGKQL	59	92	LLQLTVWGKQLQAR	651	26	41	12866
ENV	LLSGVQQQ	58	91	ARQLLSGVQQQSNL	627	22	34	12867
ENV	WATHACVPT	56	88	HNWVWATHACVPTDPN	79	44	69	12868
ENV	LGAAGTMG	55	86	LQFLGAAGTMGAAS	605	36	56	12869
ENV	VRQYSPLS	55	86	VNRVRQYSPLSFQT	800	36	57	12870
ENV	LLNGSLAE	54	84	STQLLNGSLAEVEV	303	16	25	12871
ENV	VKLTPLCVT	53	83	KPCVKLTPLCVTFLNC	130	29	45	12872
ENV	LRAIEAQH	51	80	NNLLRAIEAQHLLQ	639	18	28	12873
ENV	VSTVQCTHG	51	80	CKNVSTVQCTHGKRP	285	14	22	12874
ENV	LGIWGSCK	50	78	QQLLGIWGSCKLIC	676	46	72	12875
ENV	LWDQSLKPC	50	78	ILSLWDQSLKPCVKL	121	35	55	12876
ENV	LGFLGAAGS	49	77	AVFLGLGAAGSTMG	602	19	30	12877
ENV	VWATHACVP	49	77	VHNVWATHACVPTDP	78	34	53	12878
ENV	WGKQLQAR	49	77	LTVWGKQLQARVLA	654	39	61	12879
ENV	WYIKIFIM	43	67	TNWLWYIKIFIMVG	771	11	17	12880
ENV	FCASDAKAY	42	66	TTLFCASDAKAYDTE	61	18	28	12881
ENV	IVGGLIGLR	42	66	FIMIVGGLIGLRIF	780	22	34	12882
ENV	IFIMVGGL	41	64	YIKIFIMVGGLGL	776	30	47	12883
ENV	VYGVVPWK	41	64	WYTVYGVVPWKKEAT	46	22	34	12884
ENV	IKQLQARVL	40	63	VWGKQLQARVLA	656	31	49	12885
ENV	IKIFIMVG	39	61	LWYIKIFIMVGGLI	774	31	48	12886
ENV	MGAASITLT	39	61	GSTMGAASITLTVOA	613	28	44	12887
ENV	YIKIFIMV	39	61	WLWYIKIFIMVGGL	773	38	59	12888
ENV	ITGLLLTRD	37	58	SSNITGLLLTRDGGK	516	06	9	12889
ENV	IFHYCAPA	36	56	FEPIHYCAPAGFA	255	21	33	12890
ENV	MIWGGLGL	36	56	IFIMIVGGLGLRIV	779	22	34	12891
ENV	VQARQLLSQ	36	56	TLTVQARQLLSQVQ	622	35	55	12892
ENV	FEPIHYC	35	55	KVSFEPIHYCAPA	252	17	27	12893
ENV	LRSLCLFSY	35	55	WDDLRLSLCLFSYIHL	854	28	44	12894
ENV	MVKNNMVEQ	35	55	NENMWKNNMVEQMIIE	105	11	17	12895
ENV	VIRNVWATHA	35	55	DTEVINVWATHIACVP	75	17	27	12896
ENV	WKNNMVEQM	35	55	FNMWKNNMVEQMHEH	106	20	31	12897
ENV	YTGVPVWKE	35	55	VTYGVVPVWKEATT	47	22	34	12898
ENV	LLQLTVWGI	34	53	VVKLEPQVAPTKAK	648	34	53	12899
ENV	IEPLGVAPT	33	52	QQHLLQLTVWGKQL	566	12	19	12900
ENV	IKPVVSTQL	33	52	THQIKPVVSTQLLN	295	32	50	12901
ENV	LQARVLAVE	33	52	IKQLQARVLAVERYL	659	32	50	12902
ENV	WDDLRLSL	33	52	ALAWDDLRLSLCLFSY	851	18	28	12903
ENV	INIHPTIRE	01	50	SRPINIHPTIREKRA	581	01	2	12904
ENV	INIHPTIRE	01	50	RPIINIHPTIREKRA	582	01	2	12905
ENV	ITQACPKVS	32	50	TSVITQACPKVSFEP	242	08	13	12906
ENV	IVQQSNLL	32	50	LSGIVQQSNLLRAI	631	26	41	12907
ENV	LGNNTNST	01	50	NKTLGNNTNSTLGN	151	01	2	12908
ENV	VISTRHRE	01	50	ARPVISTRHREKRA	580	01	2	12909
ENV	WRWGTFLG	01	50	QNLWRWGTFLGMLM	12	01	2	12910
ENV	WRWGTMLG	01	50	QILWRWGTMLGMLM	12	03	5	12911
ENV	FAVLISNR	31	48	RIVFAVLISNVRVQ	791	14	22	12912
ENV	LLNGSLAE	31	48	TQLLNGSLAEVEV	304	14	22	12913

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	LTPLCVTLN	29	45	CVKLTPLCVTLNCTD	132	11	17	12914
ENV	LYKYKVKI	29	45	RSELYKYKVKVIEPL	558	23	36	12915
ENV	VPWNSWSN	29	45	TNPVWNSWSNKSLS	691	03	5	12916
ENV	YRLNCTS	28	44	YKEYRLNCTSALT	232	01	8	12917
ENV	IHYCAPAG	27	42	PIPIHYCAPAGFALL	258	26	41	12918
ENV	LKDQQLGI	27	42	ERYLKDQQLGIWGC	670	25	39	12919
ENV	YKYKVKIE	27	42	SELYKYKVKVIEPLG	559	24	38	12920
ENV	IRPVVSTQL	26	41	THIRPVVSTQLLIN	295	26	41	12921
ENV	LDKWASLWN	26	41	LLALDKWASLWNWFD	755	08	13	12922
ENV	LHIVFVLS	26	41	LIGLRIVFAVLSVN	787	10	16	12923
ENV	LNGSLABEE	25	39	QLLNGSLAEEVVI	305	13	20	12924
ENV	YKYVKIEPL	25	39	LYKYKVKVIEPLGVA	561	23	36	12925
ENV	LKGLRLGWE	11	37	RSLKGLRLGWEGLK	885	04	7	12926
ENV	FSYHRLRDL	23	36	LCLFSYHRLRDLILI	860	08	13	12927
ENV	INCTRPNN	23	36	SVEINCTRPNNTRK	340	05	8	12928
ENV	VYKIEPLGV	23	36	KYKVVYKIEPLGVAPT	563	23	36	12929
ENV	WKEATTLF	23	36	VPWVKEATTLFCAAS	53	22	34	12930
ENV	IGLRIVFAV	22	34	GGLIGLRIVFAVLSI	785	12	19	12931
ENV	FFYCNISGL	21	33	GOEFFYCNISGLFNS	441	07	11	12932
ENV	FGLGALFLG	01	33	RAAFGLGALFLGFLG	594	01	2	12933
ENV	FYCNISGLF	21	33	GEFFYCNISGLFNST	442	07	11	12934
ENV	LIGLRIVFA	21	33	VGGLIGLRIVFAVLS	784	17	27	12935
ENV	VGLGAVFLG	01	33	KRAVGLGAVFLGFLG	593	06	9	12936
ENV	ICITAVPWN	20	31	KRAVGLGMLFLGVLS	594	01	2	12937
ENV	ICITAVPWN	20	31	GKLICTTAVPWNSSW	686	09	14	12938
ENV	LOVAPTRAK	19	30	GKLICTTAVPWNSSW	686	08	13	12939
ENV	LICTTAVPW	19	30	IEPLGVAPTAKRRV	569	15	23	12940
ENV	LRDQQLGI	19	30	SGKLICTTAVPWNSS	685	09	14	12941
ENV	VFLGFLGAA	19	30	ERYLRDQQLGIWGC	670	17	27	12942
ENV	FSYHRLRDF	18	28	LQAVFLGFLGAGST	600	09	14	12943
ENV	IPHYCTPA	18	28	LCLFSYHRLRDFILI	860	08	13	12944
ENV	IVFAVLSIV	18	28	FEPIPIHYCTPAGFA	255	10	16	12945
ENV	VFAVLSIVN	18	28	GLRIVFAVLSIVNRV	789	16	25	12946
ENV	VPWNASWSN	18	28	LRIVFAVLSIVNRV	790	16	25	12947
ENV	IGLRIVFAV	17	27	TTAVPWNASWSNKSLS	691	06	9	12948
ENV	IRQAHCNIS	17	27	GGLIGLRIVFAVLSI	785	11	17	12949
ENV	VAPTKAKRR	17	27	IGDIRQAHCNISRAK	378	02	3	12950
ENV	FNGTQPCKN	16	25	PLGVAPTAKRRVYVQ	571	10	16	12951
ENV	IGRGOTFYA	01	25	DKXFNGTQPCKNVST	276	05	8	12952
ENV	IGSQQAFYV	01	25	SVRIGPGQTFYATGD	355	03	5	12953
ENV	IRYLNLYNQ	01	25	RYSIGSGQAFYVTDK	358	01	2	12954
ENV	LLQYWSQEL	01	25	QTAIRYNLYNQTEN	400	01	2	12955
ENV	LRLNCLFSY	16	25	VGGLIGLRIVFAVLS	784	12	19	12956
ENV	LVSGFLALAW	16	25	WWNLQYWSQELKNS	903	09	14	12957
ENV	VSGFLALAW	16	25	WDDLRLNCLFSYHRL	854	11	17	12958
ENV	FDPIPIHYC	15	23	SIRLVSGFLALAWDDL	842	09	14	12959
ENV	LINCNTSAI	15	23	IRLVSGFLALAWDDL	843	09	14	12960
ENV		15	23	KYTEDPIPIHYCTPA	252	03	5	12961
ENV		15	23	GLRIIFAVLSIVNRV	789	13	20	12962
ENV		15	23	EYRLINCNSTSAITQA	234	04	9	12963

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	LLNATAIV	15	23	AVSLNATAIAVAEG	918	10	16	12964
ENV	LRUIFAVLS	15	23	LIGLRIFA VLSYN	787	11	17	12965
ENV	VITQACPKV	15	23	NTSVITQACPKVSFE	241	08	13	12966
ENV	YWVWNLQYW	15	23	VLYWVWNLQYWQOE	899	07	11	12967
ENV	FAILKCNCK	14	22	PAGFAILKCNCKFN	266	09	14	12968
ENV	IFAVLSVN	14	22	LRIIFAVLSVNRVR	790	13	20	12969
ENV	INCNTSAIT	14	22	YRLNCNTSAITOAC	235	14	22	12970
ENV	LNATAIIVA	14	22	YSLNATAIAVAEGT	919	10	16	12971
ENV	WNSSWSNKS	14	22	NVPWNSSWSNKSDE	693	03	5	12972
ENV	WNASWSNKS	13	21	NVPWNASWSNKSVED	693	02	3	12973
ENV	ICTTTVPWN	13	20	GKLICTTTVPWNASW	686	06	9	12974
ENV	LLKLTWVGI	13	20	QQHLLKLTWGIKQL	648	13	20	12975
ENV	LYKYKVEI	13	20	RSELYKYKVVVEIKPL	538	05	8	12976
ENV	MELFLOAA	13	20	LGAMFLGFLGAAGST	600	07	11	12977
ENV	MHSFNCQGE	13	20	EIVMHSFNCQGEFF	430	13	20	12978
ENV	YWQELKNS	13	20	LQYVWSQELKNSAVS	906	10	16	12979
ENV	ICAVFLGFL	12	19	AVYICAVFLGFLGAA	595	09	14	12980
ENV	LIAARTVEL	12	19	DFILIAARTVELLGI	870	04	6	12981
ENV	LICTTTVPW	12	19	SGKLICTTTVPWNAS	685	06	9	12982
ENV	LLNGSLAEG	12	19	TQLLNGSLAEGEII	304	03	5	12983
ENV	YWGQELKNS	12	19	LWYVWGQELKNSAIS	906	02	3	12984
ENV	IAARTVELL	11	17	FILIAARTVELLGHIS	871	03	5	12985
ENV	LFLGFLGAA	11	17	IQALFLGFLGAAGST	600	08	9	12986
ENV	LKNSAVSL	11	17	SQELKNSAVSLLNAT	911	08	13	12987
ENV	VGIGAVFLO	11	17	KRAVGIGAVFLGFLG	593	09	17	12988
ENV	VSLNATAI	11	17	NSAVSLNATAIAVA	916	09	14	12989
ENV	YATGDIQD	11	17	QTYATGDIQDIRQ	365	04	6	12990
ENV	IAIAVAEOT	10	16	LDHIAIAVAEOTDRI	922	02	3	12991
ENV	IHYCTAGF	10	16	PIPIHYCTAGFAIL	258	08	13	12992
ENV	ILGLVICS	10	16	GTILILGLVICSASN	19	03	5	12993
ENV	INNNMTWME	10	16	VDEINNNMTWMEWER	714	01	2	12994
ENV	LGLVICS	10	16	TLILGLVICSASN	20	04	6	12995
ENV	LRFILAA	10	16	YIIRLRFILAAARTV	865	06	9	12996
ENV	LTPLCVTL	10	16	CVKLTPLCVTLDCN	132	03	5	12997
ENV	MLQLTVWGI	10	16	QQHMLQLTVWGIKQL	648	08	13	12998
ENV	VBINGTRPN	10	16	NESVBINGTRPNNT	338	02	3	12999
ENV	VRQLLSQIV	10	16	TVQVRQLLSQIVQQQ	624	08	13	13000
ENV	LILQLVIIC	09	15	WGTLILQLVIICSAS	18	07	11	13001
GAG	VGHQAAMQ	60	94	LNTVGGHQAAMQMLK	209	47	73	13002
GAG	LLVQNAPD	59	92	TETLLVQNAPDCKT	342	26	41	13003
GAG	VQANPDK	59	92	TLLVQANPDKTIL	344	44	69	13004
GAG	LGLNKIVRM	58	91	WILGLNKIVRMYSF	289	55	86	13005
GAG	LSEGAIPD	58	91	FSALSEGAIPDQNT	193	29	45	13006
GAG	WILOLNKI	57	89	YKRWILGLNKIVRM	286	54	84	13007
GAG	LEEMMTACQ	56	88	QATLEEMMTACQVGV	364	27	42	13008
GAG	YKRWILGL	55	86	GEIYKRWILGLNKI	283	37	58	13009
GAG	YKRWILGL	54	84	VGEIYKRWILGLNK	282	37	58	13010
GAG	VSONYPIVQ	48	83	SSQVSONYPIVQNLQ	145	09	19	13011
GAG	WEKIRLRQ	50	78	LDKWEKIRLRPGKK	13	16	25	13012
GAG	IAGTSTLQ	46	72	GSDIAGTSTLQEQI	254	45	70	13013

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
GAG	WASRELERF	46	72	HLVWASRELERFALN	34	17	27	13014
GAG	IPMFSALE	45	70	PEVPMFSALESEAT	187	44	69	13015
GAG	MFSALEGA	45	70	VPMFSALESEATQ	189	43	67	13016
GAG	VPMFSALEGA	45	70	SPEVPMFSALEGA	186	40	63	13017
GAG	MYSPVSLD	41	64	IVRMYSVSLDIRQ	297	23	36	13018
GAG	IVRMYSVPS	40	63	LNKIVRMYSVPSILD	294	39	61	13019
GAG	VRMYSVPSI	40	63	NKIVRMYSVPSILDI	295	38	59	13020
GAG	YSPVSLDI	40	63	VRMYSVPSILDIRQ	298	23	36	13021
GAG	MTETLLVQN	38	59	KNWMTETLLVQNANP	338	34	53	13022
GAG	MTETLLVQ	37	58	VKNWMTETLLVQNAN	337	34	53	13023
GAG	ISPKTLNAW	36	56	HQASPKTLNAWVKV	334	14	22	13024
GAG	VKNWMTETL	36	56	TQEVKNWMTETLLVQ	334	14	22	13025
GAG	IKCFNCGKE	34	53	QKRIKCFNCGKEGHL	418	05	8	13026
GAG	IPVGEIKR	34	53	NPPVGEIKRWIL	277	32	51	13027
GAG	YTAVFMRQR	02	50	KGTATAVFMRQRQNP	399	02	3	13028
GAG	VATLYCVHQ	30	47	YNTVATLYCVHQRIE	81	07	11	13029
GAG	WDLRLPVHA	29	45	AAEWDRLIPVHAQHI	230	22	34	13030
GAG	FLQSRPEPT	28	44	PGNFLOSRPEPTAPP	483	27	43	13031
GAG	FKTLRAEQA	27	42	DRFKTLRAEQAQTE	322	16	25	13032
GAG	MVHQASPR	27	42	QQQMVIHQASPRTLN	160	26	41	13033
GAG	VHQASPR	27	42	QQMVIHQASPRTLNA	161	27	42	13034
GAG	YKTLRAEQA	27	42	DRFYKTLRAEQAQSE	322	12	19	13035
GAG	VSILDIRQ	25	39	YSVSVSILDIRQPKF	301	24	38	13036
GAG	LAEMSQVT	23	37	ARVLAEMSQVTNSA	384	08	13	13037
GAG	LOKIWFSHK	23	36	ANFLGKIWFSHKGRP	467	22	34	13038
GAG	VKCFNCGKE	23	36	RKTVCNCFNCGKEGHI	420	07	11	13039
GAG	YNTVATLYC	23	36	RSLYNTVATLYCVIIQ	78	11	17	13040
GAG	LHPVHAGPI	22	34	LRSLYNTVATLYCVII	233	13	23	13041
GAG	MTDTLLVQN	22	34	KNWMTDTLLVQNANP	338	16	20	13042
GAG	WMTDTLLVQ	22	34	VKNWMTDTLLVQNAN	337	16	25	13043
GAG	ISVKDTKEA	21	33	HQRIEVDKDTKEALDK	91	07	25	13044
GAG	LQQQMVRQA	21	31	VQNLOGQMVRQAISP	136	15	11	13045
GAG	MTNNPPIP	20	31	IGWMTNNPPIPVGEI	268	16	23	13046
GAG	WMTNNPPIP	20	31	QIGWMTNNPPIPVGE	267	16	25	13047
GAG	LAQQMREP	19	30	AGPIAQQMREPRGS	241	16	23	13048
GAG	VHAGPIAPG	19	30	LHPVHAGPIAPGQMR	236	14	30	13049
GAG	LGPQATLEE	18	28	LRALGPQATLEEMMT	358	09	22	13050
GAG	VHAGPIPG	18	28	VHPVHAGPIPGQMR	236	16	14	13051
GAG	IPPGQMR	17	27	AGPIPPGQMRPRGS	241	10	16	13052
GAG	LSPRTLNAW	17	27	HQALSRLNAWVKV	165	10	25	13053
GAG	YRLKHLVWA	17	27	KKKYRLKHLVWASRE	27	13	20	13054
GAG	LCPAATLEE	16	25	LKALCPAATLEEMMT	338	16	23	13055
GAG	LKALOPAT	16	25	KTILKALOPATLEE	355	16	25	13056
GAG	LKDKPEPLA	01	23	QEQLKDKPEPLASLR	532	01	2	13057
GAG	LSGGKLDW	16	25	ASVLSGGKLDWKEI	5	14	22	13058
GAG	MTSNPPIP	16	25	IGWMTSNPPIPVGEI	268	06	9	13059
GAG	VKNWMTDTL	16	25	TQDVKNWMTDTLLVQ	334	11	17	13060
GAG	VSILDIKQ	16	25	YSPVVSILDIKQPKF	301	16	23	13061
GAG	WMTSNPPIP	16	25	QIGWMTSNPPIPVGE	267	06	10	13062
GAG								13063

Table XIXa
IIIY DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
GAG	FNTVATLYC	13	23	KSLENTVATLYCVIIQ	78	07	11	13064
GAG	IPMFTALSE	13	23	PEVIPMFTALSEQAT	187	13	20	13065
GAG	LASLSLFG	13	23	LYPLASLSLFGNDP	544	06	11	13066
GAG	LERFAVNPQ	13	23	SRELERFAVNPGLLE	39	14	22	13067
GAG	LFNTVATLY	13	23	LSLENTVATLYCVII	77	07	11	13068
GAG	NFTALSEGA	13	23	VIPMFTALSEGAITQ	189	14	22	13069
GAG	WDRVHPVHA	13	23	AAEWDVHPVHVIAGPI	230	12	19	13070
GAG	IVRMYSPTS	14	22	LNKIVRMYSPTSILD	294	13	20	13071
GAG	LQEQIAWMT	14	22	SRELERFALNPOLLE	39	14	22	13072
GAG	LERFALNPO	14	22	TSTLQEQIAWMTGNP	261	05	8	13073
GAG	VHPVHAGPI	14	22	WDRVHPVHVIAGPIPG	233	11	17	13074
GAG	VIPMFTALS	14	22	SPEVIPMFTALSEGA	186	13	20	13075
GAG	VRMYSPTSI	14	22	NKIVRMYSPTSILDI	295	13	20	13076
GAG	LQKIWPSNK	13	20	ANFLQKIWPSNKGRRP	467	13	20	13077
GAG	LTSLSLFG	13	20	LYPLTSLSLFGNDP	544	04	7	13078
GAG	MYSPSILD	13	20	IVRMYSPTSILDIRQ	297	12	19	13079
GAG	YKLSHIVWA	13	20	KKKYKLSHIVWASRE	27	08	13	13080
GAG	YSPSILDI	13	20	VRMYSPTSILDIRQG	298	12	19	13081
GAG	LTSLSLFG	12	19	LYPLTSLSLFGNDP	544	04	7	13082
GAG	MMNLNIVGQH	12	19	DLNMMNLNIVGQHQA	204	12	19	13083
GAG	IDVKDTKEA	11	17	HQRIDVKDTKEALDK	91	03	5	13084
GAG	IGWMTSNPP	11	17	QEQIGWMTSNPPVP	265	09	14	13085
GAG	IPVODIYKR	11	17	NPPIPVODIYKRWII	277	08	13	13086
GAG	VHQALSPT	11	17	DKELYPLASLSLFG	541	06	10	13087
GAG	VNPOLLETS	11	17	QMVHQPALSPTLNA	161	07	11	13088
GAG	YPLASLSL	10	16	RFVNPGLLETSEGC	45	11	17	13089
GAG	FLQNRPEPT	10	16	KELYPLASLSLFGN	542	06	16	13090
GAG	IMMOKSNFK	10	16	PONFLQNRPEPTAPP	483	10	25	13091
GAG	LAEAMSQVQ	10	16	AAAIMMOKSNFKGPR	405	01	3	13092
GAG	LNPGLLETA	10	16	ARVLAEAMSQVQOSN	384	02	3	13093
GAG	WQNTTPOQ	10	16	ANFLGKIWPSSKGRP	467	10	16	13094
GAG	VPLRPMTYK	10	16	RFALNPGLLETAGOC	45	08	13	13095
NEF	WQNTTPOQ	07	15	KELYPLASLSLFGN	542	04	6	13096
NEF	VPLRPMTYK	48	83	FPDWQNTTGTQIRY	200	15	23	13097
NEF	LTFQWCFKL	46	75	GFVPRQVPLRPMTY	93	36	56	13098
NEF	WCFKLVPVD	39	73	RYPLTFQWCFKLVPV	216	15	24	13099
NEF	WVYHTQGY	34	61	RQELDLWVYHTQGY	182	12	19	13100
NEF	WKSISVIGW	26	41	TFQWCFKLVPVDPRE	222	07	11	13101
NEF	LLHPMSQHQ	21	33	ILDLWVYHTQGYFPD	186	21	33	13102
NEF	ITSSNTAAT	20	31	GGKWSKSSIVGWPAI	2	05	8	13103
NEF	LYPLTFGW	20	30	RQDILDLWVYHTQGY	182	05	8	13104
NEF	LEKHGAITS	19	25	NNCLLHPMSQHQMD	254	06	9	13105
NEF	LYPLTFGW	16	25	NSLLHPICQHQMED	234	04	6	13106
NEF	ITSSNTAAT	13	20	GGIRYPLTFGWCFK	210	06	9	13107
NEF	LEKHGAITS	13	20	HOATSSNTAATNAD	61	10	16	13108
NEF	WVYHTQGF	13	20	SRDLEKHGAITSNT	50	13	20	13109
NEF	MTYKGAFDL	12	20	ILDLWVYHTQGFDP	186	13	20	13110
NEF	LVPDPREV	11	17	LRPMTYKGAFDLSFF	103	06	9	13111
NEF				CFKLYPVPDPREVEEA	226	08	13	13112
NEF								13113

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
NEF	VGVPAIRER	10	17	SSVGVPAIRERMR	8	03	5	13114
NEF	WCFKLVPVE	11	17	TFGWCFKLVPVEK	222	04	6	13115
NEF	FDSRLAFH	10	16	EWRFSRLAFHHVAR	307	02	3	13116
NEF	FKLVDPDR	10	16	GWCFKLVPVDPREVE	224	10	16	13117
NEF	VPLRPMTFK	10	16	RQVFLRPMTFKGAF	98	04	6	13118
POL	LLDTAADT	63	98	KEALLDGTADDTVLE	107	37	58	13119
POL	WMGYELHPD	63	98	PFLWMGYELHPDKWT	415	60	94	13120
POL	YQYNVLPQG	63	98	GIRYQYNVLPQWKG	330	52	81	13121
POL	FRKYTAFTI	61	97	DKDFRKYTAFTPSI	310	10	16	13122
POL	WTVNDIQKL	62	97	KDSWTVNDIQKLVGK	438	43	67	13123
POL	LDCTHLEK	61	95	IWQLDCTHLEKIL	812	29	45	13124
POL	LDVGDAYFS	61	95	VTVLDVGDAYFSVPL	295	50	78	13125
POL	MDDL VVGSD	61	95	YQYMDL VVGSDFEI	370	57	89	13126
POL	VPAETQGE	61	95	EAEVIPAETGQETAY	837	57	90	13127
POL	WKGEQAVVI	61	95	KLLWKGEQAVVIQDN	992	53	83	13128
POL	WQLDCTHLE	61	95	PGIWQLDCTHLEGKI	810	32	50	13129
POL	VDRELNKR	60	94	RKLVDFRELNKRQTD	261	37	89	13130
POL	WPKMIGGI	60	94	PGKWKPKMIGGIGGF	126	39	61	13131
POL	IWQLDCTHL	59	92	SPGIWQLDCTHLEK	809	56	88	13132
POL	VAVHASOY	59	92	IILVAVHASGYEIA	824	26	41	13133
POL	IGUYSAGER	58	91	PGQWKGSPIFQSSM	339	42	66	13134
POL	FWEVQLQIP	57	89	KGGIGUYSAGERIID	940	37	59	13135
POL	IKKDKSTKW	57	89	DSQYALGIHQAPDK	690	39	61	13136
POL	LQIQAQPD	57	89	TQDFWEVQLQIPHPA	273	32	81	13137
POL	LGIHPAGL	56	89	VFAIKKDKSTKWRKL	249	36	56	13138
POL	VNTPLVKL	57	89	EVALGIHQAPDKSE	692	31	61	13139
POL	VTVLDVGDA	57	89	QVQLGIHPAGLKK	278	51	80	13140
POL	FPISPIETV	56	88	WEFVNTPLVKLWYQ	606	50	79	13141
POL	FVNTPLVK	54	86	KKSVTVLDVGDAYFS	292	49	77	13142
POL	LNFPISPIE	55	86	TLNFPISPIETVPVK	183	52	83	13143
POL	IQNFRVYVR	52	86	NFPISPIETVPVKLK	185	52	81	13144
POL	LVGPTPVI	54	84	EWEFVNTPLVKLWY	605	50	78	13145
POL	VQLQIPHPA	54	84	GCTLNFPISPIETVP	181	53	83	13146
POL	WQATWIPEW	54	84	IPWFEVNTPLVKL	603	49	77	13147
POL	IETVPVKLK	53	83	ITKQNFVRYRDSR	969	32	51	13148
POL	LOTVLVQPT	53	83	GTVLVQPTPVNIIGR	160	51	80	13149
POL	VLVQPTPVN	53	83	FWEVQLGIHPAGLK	276	53	83	13150
POL	YIEABVIPA	53	83	TEYWQATWIPEWEFV	595	19	30	13151
POL	VVGSDLBIG	53	83	ISPIETVPVKLKPGM	188	51	80	13152
POL	MDQPKVKQW	52	81	ASGYIAEIVPAETG	374	52	81	13153
POL	VASOYEAE	52	81	IGTVLVQPTPVNIIG	823	26	41	13154
POL	VQPTPVNII	52	81	KILVAVHASGYIE	156	22	34	13155
POL	VYVRSRDP	52	81	DDLYVGSDELKQHR	332	52	81	13156
POL	WGFTTPDKK	52	81	KFGMDQPKVKQWPLT	199	47	73	13157
POL		52	81	AVHASGYIEAIVP	828	51	80	13158
POL		52	81	TVLVQPTPVNIIGRN	161	45	70	13159
POL		52	81	GPVKQWPLTEEKIK	205	45	70	13160
POL		52	81	NFRVYVRSRDPPIWK	974	29	45	13161
POL		52	81	LLRWGFTTPDKKHQK	398	23	36	13162
POL		52	81					13163

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
POL	VIVQYMDL	51	80	PEIVQYMDLLVVG	365	23	36	13164
POL	LKKKSVTV	49	78	PAGLKKKSVTVLDV	286	46	72	13165
POL	VPRKAKII	50	78	IKVPRKAKIIRDY	1010	41	64	13166
POL	FPQITLWQR	49	77	SFSPQITLWQRLV	84	09	14	13167
POL	VIWGTPKF	47	73	ESVIWGTPKFRLP	570	23	37	13168
POL	YVDCGANRE	46	72	ETFYVDGAANRETKL	630	24	38	13169
POL	FNKLTKQY	45	70	QEPFNKLTKGYAKM	535	15	23	13170
POL	IQTKELQKQ	45	70	ATDIQTKELQKQITK	957	24	38	13171
POL	YQKQMGDD	45	70	IRDYQKQMGDDCYA	1021	41	64	13172
POL	WRAMASDFN	43	67	IISWRAMASDFNLPP	768	31	48	13173
POL	ISKIGPENP	42	66	EGKISKIGPENPYNT	233	40	63	13174
POL	LTIQIGCTLN	41	64	RNLLTIQIGCTLNPI	174	21	33	13175
POL	IIQAOPDKS	40	63	ALGIQAOPDKSEIE	694	38	59	13176
POL	LPEKDSWTV	40	63	PVLPKDSWTVNDI	432	13	20	13177
POL	FQSSMTKIL	38	59	PAIFQSSMTKILEPF	346	32	50	13178
POL	FTIPSINNE	38	59	YTAFTIPSINNETPG	316	36	56	13179
POL	IFOSSMTKI	38	59	SPAIFOSSMTKILEP	345	33	52	13180
POL	IIISQLIKKE	37	58	VSQIEQLIKKGVVY	710	19	30	13181
POL	LSWVPAHKG	37	58	KVYLSWVPAHKGIGU	722	23	37	13182
POL	YLSWVPAHK	37	58	EKVYLSWVPAHKGIG	721	15	24	13183
POL	YTAFTIPSI	37	58	FRKYTAFTIPSINNE	313	37	59	13184
POL	IIATDIQTK	35	55	IIIDIIATDIQTKELQ	952	22	34	13185
POL	INWGPAPLL	35	55	ADPIWGPAPKLLWKG	983	34	53	13186
POL	LOKQITKIQ	35	55	TKELQKITKIQNFR	962	29	46	13187
POL	LKEALLDTG	34	53	GGQLKEALLDTGADD	103	31	48	13188
POL	VYLSWVPAH	33	52	KEKYLSWVPAHKGDI	720	15	23	13189
POL	FILKLAGRW	32	50	TAYFILKLAGRWPVK	849	27	42	13190
POL	LEGKIILVA	31	48	CTIIEGKIILVAVHIV	817	30	47	13191
POL	YFILKLAGR	31	48	ETAYFILKLAGRWPV	848	30	47	13192
POL	IIIVAVHYA	30	47	EGKIILVAVHYASGY	821	30	47	13193
POL	INWGTPKFR	30	47	SIVIWGTPKFRLPI	571	22	34	13194
POL	LAGRWPVKV	30	47	ILKLAGRWPVKVHIT	853	19	30	13195
POL	VYAKEIVAS	30	47	LPPVYAKEIVASCDK	780	21	33	13196
POL	IIIDIIATDIQ	29	45	ERIIDIIATDIQTKG	950	22	34	13197
POL	IIIGRNMLTQ	29	45	GERIIDIIATDIQTK	949	23	36	13198
POL	IKYKQLCKL	29	45	PYNIIGRNMLTQIGC	168	11	17	13199
POL	VDKLVSSGI	29	45	YAGIKVKQLCKLLRG	460	18	28	13200
POL	IVQAETFFV	28	44	NEQVDKLVSSGIRKY	737	26	41	13201
POL	LPVYAKEI	28	44	KEPIVGAETFFYDGA	623	26	41	13202
POL	WTVPQIQLP	28	44	DFNLPPVYAKEIVAS	777	26	41	13203
POL	FNLPVYAK	27	42	PKWTVPQIQLPEKD	425	13	20	13204
POL	FTSAAYKAA	27	42	ASDFNLPPVYAKEIV	775	25	39	13205
POL	LALQDSGLE	27	42	GSNFTSAAYKAAACWW	870	25	39	13206
POL	LPPIVAKEI	27	42	AIHIALQDSGLEVNI	673	15	23	13207
POL	LQDSGLEVN	27	42	DFNLPPVYAKEIVAS	777	20	31	13208
POL	FNLPPIVAK	26	41	HLALQDSGLEVNI	675	13	20	13209
POL	IQHRAKIE	26	41	ASDFNLPPVYAKEIV	775	21	33	13210
POL	IIORNLLTQ	26	41	DLEIGQIRAKIEBLR	381	23	36	13211
POL	LEVINIVTDS	26	41	PVNIIGRNLLTQIGC	168	21	33	13212
POL		26	41	DSGLEVINIVTDSQYA	680	26	41	13213

Table XIXa
IIIY DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
POL	LRGAKALTD	26	41	CKLLRGAKALTDIVP	469	12	19	13214
POL	LVSSGIRKV	26	41	VDKLVSSGIRKVLFL	740	25	39	13215
POL	FLKLAGRW	25	39	TAYFLKLAGRWPKV	849	19	30	13216
POL	LALQDSSE	25	39	AIILALQDSSEVNI	673	08	13	13217
POL	LQDSGSEVN	25	39	ILALQDSGSEVNI	675	08	13	13218
POL	VKVIHTDNG	25	39	RWPVKVIHTDNGSNF	859	21	33	13219
POL	WPKVIHTD	25	39	AGRPVKVIHTDNGS	857	20	31	13220
POL	YFLKLGR	25	39	ETAYFLKLGRWPV	848	24	38	13221
POL	ICGKKAIGT	24	38	LIEICGKKAIGTVL	150	12	19	13222
POL	IVAKEIVAS	24	38	LPIIVAKEIVASCDK	780	22	34	13223
POL	LRWGFTPD	24	38	QILLRWGFTPDKKH	396	12	19	13224
POL	LEQKVILVA	23	36	CTHLEQKVILVAHV	817	23	36	13225
POL	LKWGFTPD	23	36	EIHLKWGFTPDKKII	396	13	20	13226
POL	VILVAIIVA	23	36	EGKVILVAIIVASGY	821	21	33	13227
POL	LAWVPAHKG	22	34	KVYLAWVPAHKGIGG	722	20	32	13228
POL	YDQILIEIC	22	34	VROYDQILIEICGKK	143	08	13	13229
POL	YLAWVPAHKG	22	34	EKVYLAWVPAHKGIG	721	20	30	13230
POL	ICQHRTKIE	21	33	DLICQHRTKIEELR	381	19	30	13231
POL	IGRNLTLQI	21	33	VNIQRNLTLQIGCT	169	21	33	13232
POL	LWQRPLVTI	21	33	QITLWQRPLVTIKIG	89	11	17	13233
POL	VSLTETTNQ	21	33	QKWSLTETTNQKTE	656	10	16	13234
POL	VYLAWVPAH	21	33	KEKVYLAWVPAHKG	720	20	31	13235
POL	ICGHKALTE	20	31	LIBICGHKALTEVL	150	10	16	13236
POL	LRGTKALTE	19	30	CKLLRGTKALTEVIP	469	11	17	13237
POL	LVNQIEQL	19	30	ESELVNQIEQLIKK	706	13	20	13238
POL	YFSVPLDKO	18	29	ESELVSIQIEQLKK	706	18	28	13239
POL	IGRNLTLQI	18	28	GDAYFSVPLDKDFRK	301	18	28	13240
POL	IKVRQLCKL	18	28	VNIQRNLTLQIGCT	169	12	19	13241
POL	LWKQPAKLL	18	28	YNGRNLTLQIGCT	460	13	20	13242
POL	LWQRPLVTI	18	28	YNGRNLTLQIGCT	983	13	20	13243
POL	YAGIKVKQL	18	28	RDPLWKQPAKLLWKG	89	09	14	13244
POL	WQKTPKFK	17	27	QITLWQRPLVTIKIG	457	18	28	13245
POL	LRHLLKRW	17	27	SQYAGIKVKQLCKL	571	17	27	13246
POL	VQIQLPEK	17	27	SIVIWQKTPKFKLPI	427	12	19	13247
POL	WQRPLVTIK	17	27	IEELREHLLKRWGFTT	391	13	20	13248
POL	WQRPLVTIK	17	27	KWTVQPIQLPEKDSW	427	13	20	13249
POL	WQRPLVTIK	17	27	ITLWQRPLVTIKIGG	90	11	17	13250
POL	WQRPLVTIK	17	27	ALGHIQAQPRSESE	694	12	19	13251
POL	WQRPLVTIK	17	27	KTELQAIIILALQDSG	668	15	23	13252
POL	WQRPLVTIK	17	27	IKALVEICTEMEKEG	218	15	23	13253
POL	WQRPLVTIK	17	27	IEELRQHILLRWGFTT	391	12	19	13254
POL	WQRPLVTIK	17	27	RNMLTLQGLCTLNPH	174	10	16	13255
POL	WQRPLVTIK	17	27	VDKLVSAQIRKVLFL	740	14	22	13256
POL	WQRPLVTIK	17	27	NEQVDKLVSAQIRKV	737	14	22	13257
POL	WQRPLVTIK	17	27	SQIYPGKVRQLCKL	457	12	19	13258
POL	WQRPLVTIK	17	27	LEPFRKQNPDIYIQ	357	14	22	13259
POL	WQRPLVTIK	17	27	TVSFEFQITLWQRP	77	05	10	13260
POL	WQRPLVTIK	17	27	GSNFTSTTVKAAACW	870	11	17	13261
POL	WQRPLVTIK	17	27	IIDIASDIQTKELQ	952	11	17	13262
POL	WQRPLVTIK	17	27	LLKLAGRWPKVTIHT	853	09	14	13263
POL	WQRPLVTIK	17	27	TEAVQKIATESIVW	561	10	16	13264

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
POL	FTPTSTNNE	13	20	YTAFTPTSTNNE	316	13	20	13264
POL	LBIDNLPK	13	20	DTVLEIDNLPKWK	117	13	20	13265
POL	LTDIVPLTE	13	20	AKALTDIVPLTEAE	475	08	13	13266
POL	LVTIKIGGQ	13	20	QRPLVTIKIGGQKE	94	13	20	13267
POL	MRAHTNDV	13	20	YARMRAHTNDVQKL	546	12	19	13268
POL	VKTIHTDNG	13	20	RWPVKTIHTDNGSNF	859	09	14	13269
POL	VQVPLPEK	13	20	KWTVQVPLPEKUSW	427	12	19	13270
POL	WPVKTIHTD	13	20	AGRWPKTIHTDNGS	857	09	14	13271
POL	WQRLPLTVK	13	20	ITLWQRLPLTVKIGG	90	09	14	13272
POL	WTQVIVLP	13	20	PKKWTVQVIVLPEKD	425	12	19	13273
POL	YTAFTPTST	13	20	FRKYTAFTPTSTNNE	313	13	21	13274
POL	IDIIASDIQ	12	19	ERIIDIIASDIQTK	950	11	17	13275
POL	IDIIASDI	12	19	GERIIDIIASDIQTK	949	11	17	13276
POL	TVDIATDI	12	19	GERIVDIATDIQTK	949	10	16	13277
POL	LEEINLPK	12	19	DTVLEEINLPKWK	117	11	17	13278
POL	LQAYLALQ	12	19	KTELQAYLALALQDSG	668	11	17	13279
POL	LQKQIKQ	12	19	TKELQKQIKQIKQNR	962	09	14	13280
POL	VDIATDIQ	12	19	ERIVDIATDIQTK	950	10	16	13281
POL	YDQIIEIC	12	19	VRQYDQIIEICGKK	143	05	8	13282
POL	FNFPQITLW	11	17	VPTFNFPQITLWQRP	79	01	17	13283
POL	IGRNMLTQL	11	17	VNIIGRNMLTQLGCT	169	10	16	13284
POL	ISRIQENP	11	17	EGKISRIQENPYNT	233	10	16	13285
POL	LTEVIPLTE	11	17	TKALTEVIPLTEAE	475	10	16	13286
POL	MESIVIWGK	11	17	KJAMESIVIWGKTPK	566	07	13	13287
POL	VPRKVKJI	11	17	IKVVPRKVKIIRDY	1010	08	13	13288
POL	VSFSPQIT	11	17	QGTVSFSFPQITLWQ	75	05	8	13289
POL	WYQLETEPI	11	17	VKLWYQLETEPIVGA	615	04	6	13290
POL	YPGIKYKQL	11	17	SOYTPGIKYKQLCKL	457	09	14	13291
POL	FFQGEAREF	10	16	NLAPFQGEAREFPE	5	05	8	13292
POL	LIEALLDTG	10	16	GGQLIEALLDTGADD	103	09	14	13293
POL	VSLTDTTNQ	10	16	QKVVSLTDTTNQKTE	656	09	14	13294
POL	WETWWTDYW	10	16	KETWETWWTDYWQAT	587	09	14	13295
POL	YAKMRTAHT	10	16	TOKYAKMRTAHTNDV	543	09	14	13296
POL	YKNLKTGKY	10	16	QEFYKNLKTGKYARM	535	03	5	13297
REV	LQLPLERL	36	56	PVPLQLPLERLTD	74	13	20	13298
REV	VPLQLPPLLE	36	56	AEPVQLPPLERLT	72	10	16	13299
REV	LYQSNPPPS	18	28	IKFLYQSNPPPSPEG	21	04	6	13300
REV	VRIIKILYQ	16	25	LKAVRIIKILYQSNP	13	06	9	13301
REV	YQSNPPPS	12	19	KFLYQSNPPPSPEGT	22	05	8	13302
REV	LQLPIERL	11	17	PVPLQLPIERLRLD	74	04	6	13303
REV	VPLQLPIE	11	17	AEPVQLPIERLRL	72	04	6	13304
TAT	WNHPSQPK	15	23	LEPNHPSQPKTAC	11	11	17	13305
TAT	FLNKGLOIS	14	22	QVCFLNKGLOISYGR	38	04	6	13306
TAT	WKHPGSPK	13	20	LEPWKHPGSPKTKAC	11	11	17	13307
TAT	YCKKCCFHC	11	17	NNCYCKKCCFHCQVC	26	04	6	13308
TAT	YCKKCCYHC	11	17	TNCYCKKCCYHCQVC	26	02	3	13309
TAT	WNHPSQPT	10	16	LEPNHPSQPTTAC	11	07	11	13310
VIF	MIVWQVDBM	46	72	WQVMIVWQVDBMRIR	5	28	44	13311
VIF	WQVDMWQV	43	67	ENRWQVDMWQVDRM	2	41	64	13312
VIF	WQVDMRIR	34	53	MIVWQVDMRIRTWK	8	14	22	13313

Table XIXa
IIIY DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
VIF	LQYLAL TAL	33	52	VGSLOYLALTALIKP	147	14	22	13314
VIF	LOHOVSIEW	31	48	DWHLGHGVSEWRRLR	81	11	17	13315
VIF	VDRMRRTW	31	48	VWQVDRMRRTWNSL	10	10	23	13316
VIF	YDFCSESA	28	44	HLYYDFCSESAIRN'	113	08	13	13317
VIF	YWGLHTGER	28	44	ITTYWGLHTGERDWH	68	14	22	13318
VIF	IRTYNSLVK	27	42	RMRTWNSLVKHHM	15	12	19	13319
VIF	LOQGVSEW	26	41	DWHLGGGVSEWRKK	81	07	11	13320
VIF	LVKHHMYVS	21	33	WNSLVKHHMYVSKKA	21	07	11	13321
VIF	IPLOEARLV	19	30	EVIIIPLGEARLVVKT	54	05	8	13322
VIF	LVKHHMYIS	19	30	WKS LVKHHMYISGKA	21	05	8	13323
VIF	YLALTALIK	16	25	SLOYLALTALIKPKK	11	11	17	13324
VIF	IRTWKSLVK	15	23	RMRTWKS LVKHHM	15	14	22	13325
VIF	LADQLIHLV	15	23	DPDLADQLIHLVYFD	104	07	11	13326
VIF	LALTALIKP	15	23	LQYLALTALIKPKKI	100	08	13	13327
VIF	VDPLADQL	14	22	STQVDFGLADQLIHL	111	04	6	13328
VIF	LYYDFCFSE	14	22	LIHLYYDFCFSESAL	117	10	16	13329
VIF	FSESAIRKA	13	20	FDFSESARIRKAILG	104	08	13	13330
VIF	LADQLIHHM	13	20	EPGLADQLIHHMIYFD	8	09	14	13331
VIF	WQVDRMKIR	13	20	LIVWQVDRMKIRTW	117	05	8	13332
VIF	FSDSAIRKA	12	19	FDFSESARIRKAILG	117	12	19	13333
VIF	FSESAIRNA	12	19	FDFSESARIRNAILG	130	06	9	13334
VIF	IVSPRCBYQ	12	19	LGHVSPRCBYQAGH	147	04	6	13335
VIF	LQYLALAL	12	19	VGSLOYLALALITP	10	12	19	13336
VIF	VDRMKIRTW	12	19	VWQVDRMKIRTWNSL	68	08	13	13337
VIF	YWGLQTGER	11	17	IKTYWGLQTGERDWH	54	06	9	13338
VIF	IPLODARLV	11	17	EVIIIPLODARLVTT	147	08	13	13339
VIF	LQYLALKAL	11	17	VGSLOYLALKALVTP	8	08	13	13340
VIF	WQVDRMRIN	10	16	MIVWQVDRMRINTWK	156	08	13	13341
VIF	IKPKKIKPP	10	16	TALIKPKKIKPPPS	10	09	14	13342
VIF	VDRMRINTW	10	16	VWQVDRMRINTWKS	71	08	13	13343
VPR	IGCQHSRIG	46	72	HFRIGCQHSRIGTR	15	12	19	13344
VPR	WTLELLEL	42	69	YNEWTLLELLEKSE	60	31	48	13345
VPR	ILQQLFIH	37	58	IIRILOQLFIHFRI	66	29	45	13346
VPR	FHFRIQCQ	30	47	QLLFHFRIQCQHSR	12	27	42	13347
VPR	YNEWTLLEL	30	47	REPYNEWTLLELLEL	31	12	19	13348
VPR	FPRPWHLQ	24	38	VRHFRPWHLQHQII	51	14	22	13349
VPR	WEGVEAIR	18	28	GDTWEGVEAIRILQ	20	15	23	13350
VPR	LEBLKSEAY	16	25	LELLELKSEAYRHF	51	15	23	13351
VPR	WAGVEAIR	16	25	GDTWAGVEAIRILQ	47	16	25	13352
VPR	YODTWAGVE	16	25	YETYGDTWAGVEAIR	66	03	5	13353
VPR	IGCRISRIQ	12	19	HFRIGCRHSRIGTR	71	11	17	13354
VPR	FIHFRIGCR	11	17	QLLFHFRIQCQHSR	66	10	16	13355
VPR	FVIFRIGQ	11	17	QLLFVHFRIQCQHSR	47	04	6	13356
VPR	YODTWTOVE	10	16	YETYGDTWTOVEAIR	31	05	8	13357
VPR	FPRWLHSL	09	15	VRHFRWLHSLGQII	15	03	5	13358
VPU	WALELLEL	01	50	YNEWALELLELKNE	87	01	2	13359
VPU	LVTLSSSK	01	50	EEWLVTLLSSSKLDQ	89	02	3	13360
VPU	VTLSSSK	01	36	EVLVTLLSSSKLDQ	20	01	1	13361
VPU	ILAIWVTI	01	33	VVALAIWVTIVFI	5	01	25	13362
VPU	VDYRIVIVA	01	33	LAKVDYRIVIVAFV	5	01	25	13363

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
VP1	LRQRKIDRL	17	27	RKILRQRKIDRLIDR	44	11	17	13364
VP1	IVVWTIVFI	15	23	IIAIVVWTIVFIEYR	27	07	11	13365
VP1	VVWTIVFIE	14	22	IAIVVWTIVFIEYRK	28	06	9	13366
VP1	IEYRKILRQ	13	21	IVFIEYRKILRQRKI	36	07	11	13367
VP1	ILAIVALVV	11	17	SLYLAIIVALVVAII	3	01	2	13368
VP1	WTIVFIEYR	10	16	IVVWTIVFIEYRKIL	30	05	8	13369
VP1	LAIVALVVA	09	15	LQILAIVALVVAIGH	4	02	3	13370

Table XIXb

[illegible]

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DRw19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VSTQLLNG	KPVVSTQLLNGSLA						12864
VYSTQLLN	IKPVVSTQLLNGSL						12865
LTWGIKQL	LLQLTYWGIKQLQAR		0.0180				12866
LLSGIVQQ	ARQLLSGIVQQSNL						12867
WATHACVPT	HNWATHACVPTDPN						12868
LGAGSTMG	LQFLGAGSTMGAAS						12869
VRQYSPLS	VNRVQYSPLSFQT		-0.0007				12870
LLNGSLAE	STQLLNGSLAEDEV						12871
VKLTPLCVT	KPCVKLTPLCVTLNC						12872
LRAIEAQH	NNLLRAIEAQHLLQ		0.0150				12873
VSTVQCTHG	CRNVSTVQCTHIGKP						12874
LGWGCSCG	QQLLGIWGCSCGLIC						12875
LWDQSLKPC	IISLWDQSLKPCVKL		0.0012				12876
LGFLGAUS	AVFLQFLGAAGSTMG						12877
VWATHACVP	VHNVWATHACVPTDP						12878
WGIKQLQAR	LTWVGIKQLQARVLA						12879
LWYIKIFM	TNWLWYIKIFMIVG						12880
FCASDAKAY	TTLFCASDAKAYDTE						12881
IVGGLIGLR	FIMIVGGLIGLRIVF						12882
IFIMIVGGL	YKIFIMIVGGLIGL						12883
VYGVCPVWK	WVTVYGVCPVWKEAT	-0.0004	0.0310	0.0049	0.4600		12884
IKQLQARVL	VWGKQLQARVLAVE						12885
IKFIMIVG	LWYIKIFIMIVGGLI						12886
MGAASLTLT	QSTMGAASLTLTVOA						12887
YIKIFIMIV	WLWYIKIFIMIVGGL						12888
ITQLLLTRO	SSNITGLLLTRDGGK						12889
IPHIYCAPA	FEPHIYCAPAGFA						12890
MIVGQLGL	IFIMIVGGLIGLRIV						12891
VQARQLSG	TLTVQARQLLSGIVQ						12892
FEPPIHYC	KVSFEPPIHYCAIPA						12893
LRSLCLFSY	WDDLRSCLFSYIIRL						12894
MKNMVEQ	NFMNWKNNMVEQMIHE						12895
VHNVWATHA	DTEVHNVWATHACVP						12896
WNNMVEQM	FNWNNMVEQMIED						12897
YGVCPVWKE	VTVYGVCPVWKEATT	0.0180	0.3900	0.0210	0.5100		12898
LEPLGVAPT	VVKIEPLGVAPTAK						12899
IKPVVSTQL	THQIKPVVSTQLLN						12900
LQARVLAVE	IKQLQARVLAVEVYL						12901
WDDLRSCL	ALA WDDLRSCLFSY						12902
INIHTPR	SRPINIHTPRREKR						12903
INHTPRE	RPINHTPRREKRA						12904
ITQACPKYS	TSVITQACPKVSFEP						12905
IVQQSNLL	LSQIVQQSNLLRAI						12906
LGNSTNST	NKTLGNSTNSTLGN						12907
VISTRTHRE	ARPVISTRTHREKRA						12908
WRWOTFLD	QNLWWRWOTFLDMLM						12909
WRWOTMLLG	QHLWRWOTMLLGLML						12910
FAVLSIVNR	RIVFAVLSIVNVRQ						12911
LLNGLAE	TQLLNGSLAEDEV						12912
							12913

Table XIXb

[illegible]

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LTPLCVTLN	CVKLTPLCVTLNCTD						12914
LYKYKVKYKI	RSELYKYKVVKIEPL						12915
VPWNSWSN	TTNPVPWNSWSNKS						12916
YRLNCTNS	YKEYRLNCTNSAIT						12917
IHYCAPAGF	PIPIHYCAPAGFAIL						12918
LKDDQLLGI	ERYLKDDQLLGIWGC						12919
YKYKVKIE	SELYKYKVVKIEPLG						12920
IRPVSTQL	THUIRPVSTQLLLN						12921
LDRWASLWN	LLALDKWASLWNWFD						12922
LRVFAVLS	LIGLRVFAVLSIVN						12923
LNGLAEIE	QLLLNGLAEIEVVI						12924
YKVVKIEPL	LYKYKVVKIEPLGVA						12925
LKGLRLGWE	RSSLKGLRLGWGLK						12926
FSYHRLKDL	LCLFSYHRLKDLII						12927
INCRPNNN	SYEINCRPNNNTRK						12928
VVKIEPLGV	KYKVVKIEPLGVAPT						12929
WKEATTLF	VPVWKEATTLFCAS						12930
IGLRVFAV	GGIGLRVFAVLSI				0.4700		12931
PFYCNTSGL	GGEFFYCNTSGLFNS						12932
FGLOALFLG	RAAFGLQALFLGFLQ						12933
FYCNTSGLF	GGEFFYCNTSGLFNST						12934
LIGLRVFA	VGGLIGLRVFAVLS						12935
VGLQAVFLG	KRAYGLGAVFLGFLG						12936
VGLQMLFLG	KRAVGLQMLFLGVLS						12937
ICTTAVPN	GKLICTTAVPNSSW						12938
ICTNVPWN	GKLICTNVPWNSSW						12939
LGVAFTKAK	IEPLGVAPTAKARR						12940
LICTTAVPW	SOKLICTTAVPWNS						12941
LRDQQLLGI	ERYLRDQQLGIWGC						12942
VFLGFLGAA	LOAVFLGFLGAAAGST						12943
FSYHRLRDF	LCLFSYHRLRDFIJI						12944
IPHYCTPA	FEPIPIHYCTPAGFA						12945
IVFAVLSIV	GLRIVEFAVLSIVNRV						12946
VFAVLSIVN	LRIVEFAVLSIVNRV						12947
VPWNASWSN	TTAVPWNASWSNKS						12948
IGLRVFAV	GGLIGLRVFAVLSI						12949
IRQAHCNIS	IGDIRQAHCNISRAK						12950
VAPTAKARR	PLGVAPTAKARRVVQ						12951
FNGTGPCKN	DKKFNGTGPCKNVST						12952
IGPGOTFYA	SVRIGPGOTFYATGD						12953
IGSGQAFYV	RYSGSQAFYVYTK						12954
IRYLNHVNQ	QTAIRYLNHVNQTN						12955
LIGLRIFA	VGGLIGLRIFA VLS						12956
LLQYWSEL	WWNLLQYWSELKNS						12957
LRNLCLFSY	WDDLRLNLCLFSYHRL						12958
LVSGFLALA	SIRLVSGFLALAWDD						12959
VSQFLALAW	IRLVSGFLALAWDDL						12960
FDPIHYC	KVTFDPIHYCTPA						12961
IIFAVLSIV	GLRIFA VLSIVNRV						12962
LINCNTSAI	EYRLINCNTSAITQA						12963

[illegible]

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LNATAIAV	AVSLNATAIAVAEG						12964
LRIFAIVLS	LIGLRIFAIVLSIVN						12965
VITQACPV	NTSVITQACPKVSFE						12966
YVWRLQYV	VLKYVWNLQYWSQE						12967
FAIKCNDK	PAGFAIKCNDKFN						12968
IFAVLSVN	LRIFAVLSIVNRVR						12969
INCHTSAT	YRLINCNTSAITQAC						12970
LNATAIAVA	VSLNATAIAVAEGT						12971
WNSSWSNKS	NVPWNSSWSNKSLE						12972
WNASWSNKS	NVPWNASWSNKSIED						12973
ICTTTVPV	GKLICTTTVPVNASW						12974
LLKLTYYGI	QQHLLKLTYYGIKQL						12975
LYKYVVEI	RSELYKYKVVEIKPL						12976
MELGLOAA	LGAMFELGLOAAGST						12977
MHSFCCGE	EIVMHSFNCGGEFFY						12978
YWSQELXNS	LLQYWSQELKNSAVS						12979
IGAVFLQL	AYGIGAVFLGLGAA						12980
LIARTVEL	DFILIAARTVELLGH						12981
LICTTTVPV	SOKLICTTTVPVNAS						12982
LLNGSLAEG	TQLLLNGSLAEGEII						12983
YWGQELKNS	LVWYWGQELKNSAIS						12984
IAARTVELL	FILIAARTVELLGHIS						12985
LFLFLGAA	IGALFLFLGAAAGST						12986
LKNSAVSL	SOELKNSAVSLNAT						12987
VGIGAVPLG	KRAVGIGAVFLGFLG						12988
VSLNATAI	NSAVSLNATAIAVA						12989
YATQDHDG	QTFYATQDHDGDIRI						12990
IAIAVAEGT	LDIAIAVAEGTDRI						12991
IHYCTPAOF	PIPIHYCTPAOFAIL						12992
ILGLVIICS	QTLILGLVIICSASN						12993
IWNNTWME	VDEIWNNTWMEWER						12994
LGLVICS	TLILGLVICSASN						12995
LRDFILAA	YHRLDFILIAARTV						12996
LTPLCVTLD	CVKLTPLCVTLDCLIN						12997
MLQTYWGI	QQHMLQLTWGIKQL						12998
VEINCTRN	NESVEINCTRPNNT						12999
VRQLLSGIV	TVQVRQLLSGIVQQQ						13000
LILGLVIIC	WGTLLILGLVIICSAS						13001
VGGHOAAQ	LNTYGGHOAAQMOMLK						13002
LLYQANPD	TETLLYQANPDCKT						13003
VQANPDCK	TLVQANPDCKTIL			0.2800	0.0024		13004
LGLNKIVRM	WIILGLNKIVRMYSF						13005
LSEGATPD	FSALSEGATPDQDNT			0.5400	0.6200		13006
WIILGLNKI	YKRWIILGLNKIVRM						13007
LEEMTACQ	GATLEEMTACQDVG						13008
YKRWIILQI	GEIYKRWIILQNLKI			0.7800	0.1400		13009
IYKRWIILQ	VOEIIYKRWIILQNLK						13010
VSQNYPIVQ	SSQYVSQNYPIVQNLQ						13011
WEKILRPG	LDKWEKILRPGGKK						13012
IAGTTSTLQ	QSDIAGTTSTLQEQI						13013

Table XIXb

[illegible]

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
WASRELERF	HLVWASRELERFALN						13014
IPMFSALE	PEVIPMFSALESEGAT						13015
MFSALSEGA	VIPMFSALESEGATPQ						13016
VIPMFSALE	SPVIPMFSALESEGA	0.0007	-0.0007	0.0130	0.0130		13017
MYSPVSLD	IVRMYSVPVSLDIRQ		-0.0007				13018
IVRMYSFVS	LNKIVRMYSFVSILDI						13019
VRMYSFVSI	NKIVRMYSFVSILDI						13020
YSPVSLDI	VRMYSFVSILDIRQG						13021
MTETLLVN	KNWMTETLLVQNANP						13022
WMTETLLVQ	VKNWMTETLLVQNAN						13023
ISPTLNAW	HQAISPTLNAAWKV	0.0032	0.0280	0.0008	0.0053		13024
VKNWMTETL	TQEVKNWMTETLLVQ						13025
IKCFNGCKE	QKRUKCFNGCKEGHL						13026
IPVGEIYKR	NPPIVGEIYKRWI						13027
YTAVFMRQG	KGGYTAVFMRQGNP						13028
VATLYCVHQ	YNTVATLYCVHQRIE						13029
WDLHPVHA	AAEWDLHPVHAGPI						13030
FLQSRPEPT	PGNFLQSRPEPTAIP		0.0130				13031
FKTLRAEQA	DRFFKTLRAEQATQE						13032
MVHQASIPR	QGMVHQASIPRTLNA	0.0083	0.0550	0.0067	0.6400		13033
VHQASIPRT	QGMVHQASIPRTLNA		-0.0007				13034
YKTLRAEQA	DRFYKTLRAEQASQE	-0.0001	0.0028		-0.0015		13035
VSILDRQG	YSPVSLDIRQGPKE						13036
LAEMASQVT	ARVLAEMASQVTNSA						13037
LCKVWPSHK	ANFLCKVWPSHKGRP						13038
VKCFNGCKE	RKTVKCFNGCKEGHI						13039
YNTVATLYC	RSLYNTVATLYCVIIQ						13040
LHPVHAGPI	WDLHPVHAGPIAPG						13041
LYNTVATLY	LRSLYNTVATLYCVH						13042
MTDTLLVQN	KNWMTDTLLVQNANP						13043
WMTDTLLVQ	VKNWMTDTLLVQNAN						13044
IEVKDTKEA	IQRIEVEKDTKEALDK						13045
LQQQMYVIOA	VQNLQQQMYVIOAISP						13046
MTNPNPIP	IQWMTNPNPIPVGEE						13047
WMTNPNPIP	QIGWMTNPNPIPVGEE						13048
IAPQMREP	AGPIAPQMREPGRCS						13049
VHAGPIAPQ	LHPVHAGPIAPQGMIR						13050
LQPGATLEE	LRALQPGATLEEMMT						13051
VHAGPIPPQ	VHPVHAGPIPPQGMIR						13052
IPQGMREP	AGPIQGMREPGRCS						13053
LSPTLNAAW	HQAISPTLNAAWKV						13054
YRLKHLVWA	KKKYRLKHLVWASRE						13055
LQPAATLEE	LKALQPAATLEEMMT						13056
LKALGPAAT	KTLKALGPAATLEE						13057
LSQGLDAW	QEQKLSQGLDAWEKI						13058
MTSNPIP	ASVLSQGLDAWEKI						13059
VKNWMTDTL	IQWMTSNPIPVGEE						13060
VSILDKQG	TQDVKNWMTDTLLVQ						13061
WMTSNPIP	YSPVSLDIRQGPKE						13062
	QIGWMTSNPIPVGEE						13063

[illegible]

Table XIXb
 IIIY DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
FNTVATLYC	KSLFNTVATLYCYHIQ						13064
IPMFTALSE	PEVPMFTALSEGAIT						13065
LASLSLFG	LYPLASLSLFGNDP						13066
LERFAYNPO	SRELERFAYNPGLE						13067
LFTVATLY	LRSLFNTVATLYCVH						13068
MFTALSEGA	VIPMFTALSEGATRO						13069
WDRVHPVHA	AAEWDRVHPVHAGHI						13070
IVRMYSPTS	LNKIVRMYSPTSILD						13071
LERFALNPG	SRELERFALNPGLE						13072
LQEQIAWMT	TSTLQEQIAWMTGNP						13073
VHPVIAGHI	WDRVHPVHAGRIIPG						13074
VIPMFTALS	SPEVIPMFTALSEGA						13075
VRMYSPTSI	NKIVRMYSPTSILDI						13076
LQKIWFSNK	ANFLQKIWFSNKGPR						13077
LTSLSLFG	LYPLTSLSLFGNDP						13078
MYSPSILD	IVRMYSPTSILDIRO						13079
YKLKHIVA	KKKYKLKHIVWASRE						13080
YSPSILDI	VRMYSPTSILDIROG						13081
LTSLSLFG	LYPLTSLSLFGNDP						13082
MMLNIVGQH	DLMMLNIVGQHQA						13083
IDVKDTKEA	HQRIDVKDTKEALDK						13084
IGWMTSNPP	QEIQWMTSNPPPV						13085
IPVGDIYKR	NPIPIVGDIYKKWII						13086
LYPLASLS	DKELYPLASLSLFG						13087
VHQALSPRT	QMVHQALSPRTLNA						13088
VNPGLLSTS	RFAYVNPGLLTSEGC						13089
YPLASLSL	KELYPLASLSLFGN						13090
FLQNRPEPT	PGNELQNRPEPTAPP						13091
IMMQKSNFK	AAIMMQKSNFKOPR						13092
LAEAMSQVQ	ARVLAEAMSQVQOSN						13093
LQKIWFSSK	ANFLQKIWFSSKGRP						13094
LNPGLLETA	REALNPGLLETAEGC						13095
YPLASLSL	KELYPLASLSLFGN						13096
WQNYTFPGG	FFDWQNYTFPGGIRY						13097
VRQVPLRP	QFEVRQVPLRPMTY						13098
VPLRPMTYK	RQVPLRPMTYKQAF						13099
LTFGWCFKL	RYPLTFGWCFKLVPV						13100
ILDWVYHT	RQEILDWVYHTQGY						13101
WCFKLVPVD	TFQWCFKLVPVDPLE						13102
LWVYHTQGY	ILDWVYHTQGYFPD						13103
WKSNSVQW	GGKWSKSNSVQWPAI						13104
LLHPMSQUG	RQDILDWVYNTQGY						13105
LLHPICQHG	NCLLIHPMSQUGMDIO						13106
IRYPLTFQW	NNSLLHPICQHGMDI						13107
ITSNTAAT	QPGIRYPLTFQWCFK						13108
LEKHGATTS	HGATTSNTAATNAD						13109
LWVYHTQGF	SRDLEKHGATTSNT						13110
MTYKGAFDL	ILDWVYHTQGFPPD						13111
LVPVDPREV	LRPMYKGFADLSFF						13112
	CFKLVPVDPREVEEA						13113

Core Sequence	Exemplary Sequence	DR1	DR2-wB1	DR2-wB2	DR3	DR4w4	DR4w15	DR5w11	DR3w12	SEQ ID NO.
VGIVPAIRER	SSINGVPAIRERMR									13114
WCFKLVPE	TFOWCFKLVPEPEK									13115
FSRLAFHH	EWRFDSRLAFHHVAR									13116
FKLVPDPDR	QWCFKLVDPDPREVE									13117
VPLRPMTEK	RQVPLRPMTEKGA									13118
LLDGTGADDT	KEALLDGTGADDTVLE									13119
WMGYELHPD	PFLWMGYELHPDKWT	0.0001		-0.0015		-0.0023		-0.0010		13120
YOYNVLPQG	QIRYQYNVLPQGWKO									13121
FRKYTAFTI	KDQFRKYTAFTIPSI									13122
WTVNDIQKL	KDSWTVNDIQKLVGK	0.0027		-0.0014		-0.0026		0.1200		13123
LDCTHLEK	IWQLDCTHLEKGIIL									13124
LDVGDAYFS	VTVLVDGDAYFSVPL	0.0003		-0.0014		-0.0026		-0.0007		13125
MDLDDYVGS	YQYMDLDDYVGSDEI	0.0006		-0.0014	-0.0160	0.0036		-0.0006		13126
VIPAETGQE	EAEPVIPAETGQETAY									13127
WKGGA VVI	KLLWKGGA VVIQDN	0.4600	0.0011	0.0058	-0.0043	0.0750	0.0200	0.0060	-0.0045	13128
WQLDCTHLE	PGIWQLDCTHLEGIKI									13129
WDFRELNR	RKLVDFRELNRKTQD									13130
WPKXMIIGI	PGKWKPKXMIIGIGGF	0.0013		-0.0021		0.0990		-0.0006		13131
WQLDCTHIL	SPGIWQLDCTHILEGK			-0.0021						13132
MAVHVASGY	IILVAVHVASGYIEA	0.0010		-0.0014		-0.0026		-0.0007		13133
WKGSPAIFQ	PQGWKGSPAIFQSSM									13134
IGOYSAGER	KGGIGOYSAGERIID									13135
YALGIIQAK	DSQYALGIIQAQPKD									13136
FWEVQLGIP	TQDFWEVQLGIPHPA									13137
KKKXDDTKW	VFAIKKXDDTKWRKL									13138
LGIIQAQPD	QYALGIIQAQPKDSE	0.0020		0.1300		-0.0026		-0.0007		13139
LGHPHPAGL	EVQLGHPHPAGLKKX	0.6900	0.0410	9.3000	0.0220	1.8000	1.9000	0.0630	0.2200	13140
WNTPLVLKL	WEFVNTPLVLKLWYQ	0.0019		-0.0014		0.0065		0.0030		13141
VTVLVDGDA	KKSVTVLVDGDAYFS	0.0190	0.0003	-0.0014	-0.0043			-0.0007	0.0170	13142
FPISPIETV	TLNFSPISPIETVPVK	0.0480	0.0013	0.0022	-0.0043	0.0810	0.0093	-0.0007	0.0460	13143
ISPIETVPV	NFPISPIETVPVKLK									13144
FVNTPLVLK	EWBEFVNTPLVLKLWY			-0.0014		-0.0026		-0.0006		13145
LNFFSPIE	GCTLNFFSPIETVP	0.0014		1.8000	0.0920	0.6600	1.6000	0.0830	0.0540	13146
WFEVNTPL	TEWFEVNTPLVLKL	1.1000	0.0089							13147
IQNFRVYR	ITKIQNFRVYRDSR									13148
LVQPTPNI	QTVLVQPTPNIHGR	0.0066	0.0061	-0.0014	-0.0043	-0.0026		0.0043	-0.0045	13149
VQLQIRHPA	FWEVQLQIRHPAGLK	0.0240		-0.0014		0.0033		-0.0006		13150
WQATWIPEW	TEYWQATWIPEWEFV									13151
IIETVPVKLK	ISPIETVPVKLKFGM					-0.0026		-0.0007		13152
IGTVLVQPT	KKAIGTVLVQPTPVN			0.0140						13153
LVAVHVASG	KIILVAVHVASGYIE									13154
IGTVLVQPTPN	IGTVLVQPTPNVNIIG	0.0120	0.0170	-0.0003		0.0008	0.0030	-0.0004		13155
YIEAEVIPA	ASGYIEAEVIPAETG	0.0230	-0.0003	-0.0021	-0.0043	0.2100		0.0020	-0.0045	13156
YVGSDEIG	DDLYVGSDEIGQHR									13157
ADDPKVKQW	KPOMDDPKVKQWFLT									13158
VASGYIEAE	AVIVASGYIEAEVIP									13159
VASGYIEAE	AVIVASGYIEAEVIP									13160
VGPTPVNII	TVLVGPTPVNIIQRN									13161
VKQWPLTEE	GPVKQWPLTEEKIK									13162
VYVYRDSRDP	NFRVYVYRDSRDPHWK	0.0010		-0.0014		-0.0026		0.0035		13163
WGFPTDCK	LLRWGFPTDCKKHQK									13163

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw33	SEQ ID NO.
VGWPAIRER	SSIVGWPAIRERMRR						13114
WCFKLVPVE	TCGWCFKLVPVEPEK						13115
FDSRLAPHH	EWRFDSRLAFIHVAR						13116
FKLVPVDR	GWCFKLVPVDPREVE						13117
VLRPMTEK	RQVPLRPMTEKGA						13118
LLDTGADDT	KEALLDTGADDTLE						13119
WMGYELIPD	PFLWMGYELHPDKWT		-0.0003				13120
YQYNVLPQG	GIRYQYNVLPQQWKG						13121
FRKYTAFTI	DKDFRYTAFTPSI						13122
WTYNDIQKL	KDSWTVNDIQKLVGK		-0.0005				13123
LDCTHLEK	IWQLDCTHLEKIL						13124
LDVGDAYFS	VTVLVDVGDAYFSVPL		-0.0005				13125
MDDLVYGS	YQYMDDLVYGSDEI		-0.0005				13126
VIPAEIQE	EAEVIPAEIQETAY						13127
WKDEGAVVI	KLLWKDEGAVVIQDN		0.2400	0.0450	0.2100		13128
WQLDCTHLE	PGIWQLDCTHLEKGI	0.0450					13129
VDFRELNRK	RKLVDRELNRKRTQD						13130
WPKMIGGI	PGKWKPKMIGGIGF		-0.0009				13131
IWQLDCTHL	SPGWQLDCTHLEK						13132
VAVHVASOY	IILVAVHVASGYIEA		0.0087				13133
WKGSPAIQ	PGGWKGSPAIQSSM						13134
IGGYSAGER	KGGIGGYSAGERIID						13135
YALGIIAQ	DSOYALGIIAQAPDK						13136
FWVQLGIP	TQDFWEVQLGIPHPA						13137
IKKDDTKW	YFAIKKDDTKWPKL						13138
LGIPHPAGL	EVQLGIPHPAGLKKX						13139
VNTPLVKL	WEFVNTPLVKLWYQ		-0.0005				13140
VTYLDVODA	KKSVTYLDVODAYFS	0.0390	1.7000	0.1400	1.9000		13141
FPISTPTV	TLNFPISPTPTPVK	0.0150	-0.0005	-0.0005	0.0016		13142
ISPIETPV	NFISPIETPVVKLK	0.0190	0.0640	0.0008	0.0046		13143
FVNTPLVK	EWFEVNTPLVKLWY		0.1500				13144
LNFPISPE	GCTLNFPISPIETVP		0.0380				13145
WEFVNTPL	IPWEFVNTPLVKL	0.0230	1.4000	0.2600	2.6000		13146
IQNFRVYR	ITKIQNFRVYRDSR						13147
LVGTPVNI	GTLYVGTPVNIOR	0.0290	0.0820	-0.0005	0.0180		13148
VQLGIPHPA	FWEVQLGIPHPAGLK		0.0024				13149
WQATWPEW	TBYWQATWPEWEFV						13150
IETPVKLL	ISPIETPVKLLKGM		0.0150				13151
IGTVLVGPT	KKAIGTVLVGPTPVN						13152
LVAVHVASQ	KILLVAVHVASGYIE						13153
VLGTPPVN	ICTVLVGPPTVNIIG						13154
YIAEVIPI	ASGYIEAEVIPIAETG	0.0400	0.0710	-0.0003	0.0320		13155
YVGSDEIG	DDLYVGSDEIGQHR	0.0006	0.0120	0.0097	0.0480		13156
MDGPKVKQW	KPGMDGPKVKQWPLT						13157
VASGYIEAE	AVHVASGYIEAEVIP						13158
VGPTTVNI	TVLVGPTTVNIORN						13159
VKQWPLTEE	GPVKQWPLTEEKIK						13160
VYTRDSRDP	NFRVYTRDSRDPWIK		0.0150				13161
WGFTTPDKK	LLRWGFTTPDKKIQQK						13162
							13163

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2-w01	DR2-w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
VIQYMDDL	PEIVYQYMDDL YVG	0.0060		-0.0014		-0.0026		-0.0006		13164
LKKKSVTV	PAGLKKKSVTVLDV	0.0003		0.0700		-0.0024		2.5000		13165
VPRRKAKII	IKVVPRRKAKIJDY	0.0027				0.0130				13166
FPQITLWOR	SFSFQITLWORPLV									13167
VIWGTPKF	ESIVYWGKTPKFLP									13168
YVDAANRE	ETFYVDAANRETKL									13169
FKNLKTGY	QEPFKNLKTGKYAKM									13170
IQTKELOQ	ATDIQTKELQKITK									13171
YGKQMGDD	IRDYQKQMGDDCVA									13172
WRAMASDFN	HSNWRAMASDFNLPP	0.1500	0.0004	0.1600	-0.0030	4.7000	2.6000	0.2100	-0.0045	13173
ISKIGPENP	EGKISKIGPENPYNT									13174
LTQIGCTLN	RNLLTQIGCTLNPI									13175
IIQAQPKS	ALGHQAQPKDSSE	0.0001		-0.0014		-0.0026		-0.0007		13176
LPEKDSWTV	PIVLPKDSWTVNDI									13177
FQSSMTKIL	PAIFQSSMTKILEPF	0.0320	0.0320	0.0200	-0.0043	0.0038	0.6500	0.0660	-0.0045	13178
FTFSINNE	YTAFTFSINNETPG									13179
IFQSSMTKI	SIFQSSMTKILEP	0.0140	0.0420	0.0300	-0.0043	0.0140	0.3500	0.0270	0.0122	13180
IEQLIKKE	VSQIEQLIKKEKVV									13181
LSWVPAHG	KVYLSWVPAHGIGG									13182
YLSWVPAHK	EKVYLSWVPAHKIGG	0.0270	0.1300	0.0048	-0.0043	0.1700	0.2800	0.0110	0.0039	13183
YTAFTFSI	FRKYTAFTFSINNE									13184
IIADIQTK	IIADIADIQTKELQ									13185
IKWGPAKLL	RDPIWKGPAPAKLLWKG									13186
LQKQITKIQ	TKELQKQITKIQNFR	0.0071	0.0210	0.0350		0.0540	0.0200	0.0530		13187
LKEALLDTG	GGQLKEALLDTGADD	0.0001		-0.0021		-0.0024		-0.0005		13188
VYLSWVPAH	KEKVYLSWVPAHKG									13189
FILKLAGRW	TATYFILKLAGRWPK									13190
LEGKILVA	CTIILEGKILVAHYV									13191
YFILKLAGR	ETAYFILKLAGRWPV									13192
IILVAHVIA	EGKIILVAHVIVASQY									13193
IWGTTPKFR	SIVIWGTTPKFERLPI									13194
LAKRWPKV	ILKLAKRWPKVYHIT									13195
VVAKEIVAS	LPPVVAKEIVASCOK	0.0001		-0.0021		0.0043		-0.0010		13196
IIIDIAIDQ	ERIIDIAIDQITKE									13197
IIIDIAIDQ	GERIIDIAIDQITK									13198
IIGNMLTQ	PVNIIGNMLTQIGC									13199
IKVKQLCKL	YAGIKVKQLCKLLRG									13200
VDKLYSSGI	NEQVDKLYSSGIRKV									13201
IVGAETFYV	KEPVGAETFYVDGA									13202
LPPVVAKEI	DFNLPPVVAKEIVAS	0.0042		-0.0021		-0.0024		0.0036		13203
WTVQPIQLP	PDKWTVPQIQLPEKD									13204
FNLPVPAK	ASDFNLPPVVAKEIV	0.0026		-0.0021		-0.0028		-0.0006		13205
FTSAAVKAA	QSNFTSAAVKAAACWV									13206
LALQDSGLE	AIHLALQDSGLEVNI									13207
LPPIVAKEI	DFNLPPVVAKEIVAS									13208
LQDSGLEVN	HLALQDSGLEVNIVT									13209
FNLPPIVAK	ASDFNLPPVVAKEIV									13210
IGQHRKIE	DLEIGQHRKIEELR									13211
IIGNLLTQ	PVNIIGNLLTQIGC	0.0039		-0.0014		0.0043		0.0990		13212
LEVNIIVTDS	DSGLEVNIVTDSQYA	0.0001		-0.0014		0.0350		-0.0007		13213

Table XIXb
 HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VITYMDLL	PEIYQYMDLLVYG						13164
LKKKSVTV	PAGLKKKSVTVLDV		0.0140				13165
VPRKAKI	IKVYPRKAKIURDY		0.0030				13166
FQITLWQR	SFSFPQITLWQRPLV		0.0006				13167
VIWGTPKF	ESIYVIWGTPKFRLP						13168
YVDAANRE	ETFYVDAANRETKL						13169
FNKLTKY	QEPFNKLTKYAKM						13170
IQTKELQK	ATDIQTKELQKQITK						13171
YKQMAQDD	IRDYKQMAQDDCYA						13172
WRAMASDN	HSNWRAMASDNLP	0.0008	0.0530	0.0250	0.0860		13173
ISKIGENP	EGKISKIGENPYNT						13174
LTQIGCTLN	RNLLTQIGCTLNFI						13175
IQAOPDKS	ALGIQAOPDKSESE		-0.0005				13176
LFQDSWTV	PIVLFQDSWTVNDI						13177
FQSSMTKIL	PAIFQSSMTKILEFP	0.1100	0.7300	0.0140	0.9100		13178
FTIPSNNE	YTAFTIPSNNETFG	0.2800	0.3700	0.0150	2.3000		13179
IFQSSMTKI	SPAFQSSMTKILEP						13180
IEQLIKKE	VSQIEQLIKKEKYY						13181
LSWVPAHKG	KVYLSWVPAHKGIGG						13182
YLSWVPAHK	EKVYLSWVPAHKGIG						13183
YTAFTPSI	FRKYTAFTPSINNE	-0.0004	0.8400	0.0610	1.9000		13184
IATDIQTK	IIDIATDIQTKELQ						13185
IWRQPAKLL	RDPWRQPAKLLWKG						13186
LQKQITKIQ	TKELQKQITKIQNFR	0.0050	0.0055	0.0250	0.0028		13187
LKEALLDTG	GGQLKEALLDTGADD		-0.0009				13188
YLSWVPAHI	KEKYYLSWVPAHIKGI						13189
FILKLAGRW	TAYFILKLAGRWPKV						13190
LEGKILVA	CTHLEGKILVAVHV						13191
YFILKLAGR	ETAYFILKLAGRWPV						13192
IILVAVHVA	EGKILVAVHVASOY						13193
IWGTTPKFR	SIVIWGTTPKFRPLI						13194
LAGRWPKVY	ILKLAGRWPKVVIIT						13195
VYAKEIVAS	LPPVYAKEIVASCDK		-0.0009				13196
IDIIATDIQ	ERIIIDIIATDIQTK						13197
IIDIATDI	GERIIDIATDIQTK						13198
IIGRNMLTQ	PVNIIGRNMLTQIGC						13199
IKVKQLCKL	YAGIKVKQLCKLLRG						13200
VDKLVSQI	NEQVDKLVSSGIRKV						13201
IVQAEIFYV	KEPIVGAETIFYVDGA						13202
LPVPVAKEI	DRNLPPVPVAKAIVAS		0.0530				13203
WTYQHQPL	FDKWTYQHQPLPEKD						13204
FNLPVPYAK	ASDFNLPVPYAKEIV		0.0840				13205
FTSAAVKAA	GSNFTSAAVKAAACWW						13206
LALQDSGLE	AHLALQDSGLEVNI						13207
LPPIVAKEI	DFNLPIVAKAIVAS						13208
LQDSGLEVN	IILALQDSGLEVNI						13209
FNLPPIVAK	ASDFNLPPIVAKAIV						13210
IQHRAKIE	DLEIQHRAKIEELR						13211
IIGRNMLTQ	PVNIIGRNMLTQIGC		-0.0005				13212
LEVNIIVTDS	DSGLEVNIIVTDSQYA		-0.0005				13213

Table XIXb

[illegible]

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw33	SEQ ID NO.
LRGAKALTD	CKLLRGAKALTDIVP						13214
LVSSGIRKV	VOKLYSSGIRKVLFL						13215
FLKLGRW	TAYFLKLGRWVPVK						13216
LALQDSGE	AHLALQDSGEVNI						13217
LQDSGEVN	HLALQDSGEVNI						13218
VKVIITDNG	RWPVKVIITDNGSNF						13219
WPKVVIHTD	ACRPVKVIHTDNGS						13220
YFLKLAGR	ETAYFLKLAGRWPV						13221
ICOKKAGT	LIEICGKKAIGTVLV		0.0041				13222
IVAKEIVAS	LPIIVAKEIVASCDK						13223
LRWGFITPD	QHLLRWGFITPDKKH						13224
LECKVILVA	CTNLECKVILVAVIV						13225
LKWOFITPD	EHLLKWOFITPDKKH						13226
VILVAVHVA	EGKVILVAVHVASGY						13227
LAWVPAHKG	KVYLAWVPAHKGIGG			0.2500	0.3000		13228
YDQILIEC	VRQYDQILIEICGKK		0.1400				13229
YLAWVPAHK	EKYVLAWVPAHKIGG		1.4000	1.6000	0.5200		13230
ICQHRKIE	DLEIQHRKIEELR	0.0010					13231
IGNMLTQI	VNIORNLLTQIGCT						13232
LWORPLVTI	QITLWORPLVTIKIG		0.0012				13233
VSLTEITNQ	QKVSLEITNQKTE						13234
VYLAWVPAH	KEKYVLAWVPAHKG						13235
ICGIKAIGT	LIEICGHKAIGTVLV						13236
LRGTALTE	CKLLRGTKALTEVIP						13237
LVNQIEQL	ESELVNQIEQLIKK						13238
LVSQIEQL	ESELYSQIEQLIKK						13239
YFSVPLDK	GDAYFSVPLDKDFRK		0.0040				13240
IGRNMLTQI	VNIORNMLTQIGCT						13241
IKVRQLCKL	YPIKVRQLCKLLRG						13242
LWKQPAKLL	RDPLWKQPAKLLWKQ						13243
LWQRPLTVY	QITLWQRPLTVYKIG						13244
YAGIKVKQL	SQYAGIKVKQLCKL						13245
IWKTPPKK	SIVIWKTPPKKLP						13246
LRHLLKWW	IEELRHLLKWWGFT						13247
VQIQLPEK	KWTVQIQLPEKDSW						13248
WORPLVTIK	ITLWQRPLVTIKIG						13249
IIQAQDRS	ALGHQAQDRSESE						13250
LQAIHLAQ	KTELOAIHLALQDSG						13251
LVEICTEMB	IKALVEICTEMEG						13252
LRQHLLRWG	IEELRQHLLRWGFT						13253
LTQLGCTLN	RNMLTQLGCTLNFI						13254
LVSAIRKV	VOKLYSAIRKVLFL						13255
VOKLYSAGI	NEQVOKLYSAGIRKV		0.0120				13256
YPIKVRQL	SQYPIKVRQLCKL		0.0028				13257
FRKQNPDI	LEPFRKQNPDIYQ						13258
FSPQTILW	TVSFSPTILWQRP						13259
FTSTTVKAA	QSNFTSTTVKAAWW						13260
TIASDIQTK	IIDIASDIQTKELQ						13261
LACRWPKVT	LLKLACRWPKVTIHT						13262
VQKIATESI	TEAVQKIATESIVW						13263

[illegible]

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
FTIPSTNNE	YTAFITPSTNNEPQ						13264
LEDINLPGK	DTVLEDINLPGKWKP						13265
LTDIVPLTE	AXALTDIVPLTEAE						13266
LVTKIGGQ	QRPLVTIKIGGQKE						13267
MRGAIITNDV	YAMRGAITNDVQKL						13268
VKTIHTDNG	RWPVKTIHTDNGSNF						13269
VQPIVLPEK	KWTQVQPIVLPEKDSW						13270
WPVKTIHTD	AGRWPVKTIHTDNGS						13271
WQRLVTVK	ITLWQRLVTVKIGG						13272
WTVQPIVLP	PDKWTVQPIVLPKED						13273
YTAFITPST	FRKYTAFTIPSTNNE						13274
IDIASDIQ	ERIDIIASDIQTK						13275
IIDIASDI	GERIIDIASDIQTK						13276
IVDIATDI	GERIVDIIATDIQTK						13277
LEENLPGK	DTVLEENLPGKWKP						13278
LQAIYLALQ	KTELQAIYLALQDSG						13279
LQKQIKIQ	TKELQKQIKIQIFR						13280
VNIATDIQ	ERIVDIIATDIQTK						13281
YDQIPIEC	VRQYDQIPIECGKK						13282
FNFPQITLW	VPTFNFPQITLWQRP						13283
IGRNMLTQL	VNIGRNMLTQLGCT						13284
ISRGFENP	ECKISRGFENPYNT						13285
LTEVPLTE	TKALTTEVPLTEAE						13286
MESIVWGK	KIAMESIVWGKTPK						13287
VPRKVKII	IKVVPKVKIIRDY						13288
VSFSPQIT	QQTVSFSPQITLWQ						13289
WYQLETEH	VKLWYQLETEHVG						13290
YPOIKVKQL	SNYPGKIKVKQLCKL						13291
FPQGEAREF	NLAFPQGEAREFPE						13292
LIBALLDTG	GGQLEALLDTGADD						13293
VSLDTITNQ	QKVVSLDTITNQKTE						13294
WETWWTDYW	KETWETWWTDYWQAT						13295
YAKMRTAHT	TGKYAKMRTAHTNDV						13296
YKNLTKGY	QEPYKNLTKGYABM						13297
LQLPPLERL	PVPLQLPPLERLTD						13298
VPLQLPPL	AEPVPLQLPPLERLT						13299
LYQSNPPPS	IKFLYQSNPPPSPEG						13300
VRIKILYQ	LKAVRIKILYQSNP						13301
YQSNPPSP	KFLYQSNPPSPSPEGT						13302
LQLPPIERL	PVPLQLPPIERLALD						13303
VPLQLPIE	AEPVPLQLPPIERLR						13304
WNHPSQPK	LEPNHPSQPKTAC						13305
FLNKGLIS	QVCFLNKGLISYGR						13306
WZHPQSQPK	LEPNHPSQPKTAC						13307
YCKKCCFHC	NNCYCKKCCFHCQVC						13308
WNHPSQPT	TNCKKCCFHCQVC						13309
WVWQVDMR	LEPNHPSQPTTAC						13310
WQVDMRIR	WQVDMIRVQVDMRIR						13311
	ENRWQVDMIRVQVDMR						13312
	MIWVQVDMIRJRTWK						13313

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2-w01	DR2-w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LQYLALTAL	VGSQYLALTALIKP									13314
LGHGVSEW	DWHLGHGVSEWRRL									13315
VDRMRRTW	VWQVDRMRRTWNSL									13316
YDFCFESA	HLYYDFCFSESAIN									13317
YWGHTGER	ITTYWGLHTGERDWH									13318
IRTWNSLVK	RMJRTWNSLVKHHM									13319
LQGVSEW	DWHLQGVSEWERKK									13320
LVKHHMYYS	WNSLVKHHMYYSKKA									13321
IPLEEARLV	EVHIFLGEARLVYRT									13322
LVKHHMYIS	WKSLLVKHHMYISGKA									13323
YLALTALIK	SLQYLALTALIKPKK									13324
IRTWKSLVK	RMJRTWKSLLVKHHM									13325
LADQLIILY	DFDLADQLIHLYYFD									13326
LALTALIKP	LQYLALTALIKPKKI									13327
VDPGLADQL	STQVDPGLADQLIHL									13328
LYYDFCFSE	LIHLYYDFCFSESAL									13329
FSESAIRKA	DFCFSESARLKALG									13330
LADQLIIMH	EPGLADQLIIMHYFD									13331
WQVDRMKIR	LIVWQVDRMKIRWTN									13332
FSDSAIRKA	DFCFSDSAIRKALG									13333
FSESAIRNA	DFCFSESARNAALG									13334
IVSPCEYQ	LGHVSPCEYQAGH									13335
LQYLALAL	VGSQYLALALALITP									13336
VDRMKRTW	VWQVDRMKRTWNSL									13337
YWGLQTGER	IKTYWGLQTGERDWH									13338
IPGDARLV	EVHIFLGDARLVIT									13339
LQYLALIKAL	VGSQYLALIKALVTP									13340
WQVDRMRIN	MIVWQVDRMRINTWK									13341
IKPKKIKPP	TALIKPKKIKPPPS									13342
VDRMRNTW	VWQVDRMRNTWKSLL									13343
IGCQHSRIG	IIFRIGCQHSRIGTR									13344
WTLELLEL	YNEWTLLELLELKS									13345
ILQQLLFH	IRILQQLLFHFR									13346
FIHFRIGCQ	QLLFHFRIGCQHSR									13347
YNEWTLLEL	REPYNEWTLLELLEL									13348
FRPVLHGL	VRHFRPVLHGLQGH									13349
WEGVEAIR	GDTWEGVEAIRILQ									13350
LEELKSEAY	LELLELKSEAYRHF									13351
WAGVEAIR	GDTWAGVEAIRILQ									13352
YGDTWAGVE	YETYGDTWAGVEAIL									13353
IGCRHSRIG	HFRIGCRHSRIGTR									13354
FIHFRIGCR	QLLFHFRIGCRHSR									13355
FVHFRIGCQ	QLLFVHFRIGCQHSR									13356
YGDTWGVGE	YETYGDTWGVGEAIL									13357
FPRIWLHSL	VRHFRPWLHSLQGH									13358
WALELLEL	YNEWALELLELKNE									13359
LYTLSSSK	EEWLYTLSSSKLDQ									13360
VTLSSSKL	EWLYTLSSSKLDQD									13361
IIAIVVWTI	VVAIAIVVWTIVFI									13362
VDRIVIVA	LAKVDYRIVIVAFIV									13363

0.0200

0.0034

Table XIXb
 HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LQYLALAL	VGSLOYLALTALIKP						13314
LGHGVSIEW	DWRLGHGVSEWRLR						13315
VDRMBIRTW	VWQVDRMBIRTWNSL						13316
YFDCFSEA	HLVYFDCFSEAIRN						13317
YWGLHTGER	ITTYWGLHTGERDWH						13318
IRTWNSLVK	RMRIKRTWNSLVKHIM						13319
LQQGVSEW	DWHLGQQGVSEWRKK						13320
LVKHMYYS	WNSLVKHYHMYYSKKA						13321
IPLGEARLV	EVHPLGEARLVVRT						13322
LVKJHMYIS	WKSLSVKHYHMYISOKA						13323
YLALTALIK	SLQYLALTALIKPKK						13324
IRTWKSLVK	RMRIKRTWKSLSVKHIM						13325
LAQQLILY	DPDLADQLILHYFED						13326
LALTALIKP	LQYLALTALIKPKKI						13327
VDPLADQL	STQVDFGLADQLIHL						13328
LYYDFCSE	LHLVYDFCSESAL						13329
FSESARKA	FDCFSESARKAILG						13330
LADQLIIMH	EPGLADQLIIMHYFD						13331
WQVDRMKIR	LIVWQVDRMKIRTW						13332
FSDSARKA	FDCFSDSARKAILG						13333
FSESARNA	FDCFSESARNAILG						13334
IVSPRCYQ	LGHVSPRCYQAOH						13335
LQYLALAL	VGSLOYLALALALTP						13336
VDRMKRTW	VWQVDRMKRTWNSL						13337
YWGLQTOER	IKTYWGLQTOGERDWH						13338
IPLGDAFLV	EVHPLGDAFLVIT						13339
LQYLALAL	VGSLOYLALALALVTT						13340
WQVDRMRIN	MIVWQVDRMRINTWK						13341
IKPKKKKPP	TALIKPKKIKPKPLPS						13342
VDRMRINTW	VWQVDRMRINTWKSIL						13343
IGQHSRIG	IFRIGQHSRIGITR						13344
WTLELLEL	YNEWTLLELELKE						13345
ILQQLFIH	IIRILQQLFIHIFRI						13346
FIHFRIGCQ	QLLFIHFRIGCQHSR						13347
YNEWTLLEL	REPYNEWTLLELEL						13348
FRPWHLHOL	VRIHFRPWHLHOLQII						13349
WEGVEAIR	GDWVEGVEAIRILQ						13350
LEELKSEAV	LELLLELKSEAVRIH						13351
WAGVEAIR	GDWVAGVEAIRILQ						13352
YGDWAGVE	YETYGDWAGVEAIL						13353
IGCRHSRIG	IFRIGCRHSRIGITR						13354
FIHFRIGCR	QLLFIHFRIGCRISR						13355
FVFRIGCQ	QLLFVHFRIGCQISR						13356
YGDWTGTVE	YETYGDWTGTVEAIL						13357
FRPWHLHSL	VRHFRPWHLHSLGQH						13358
WALELLEL	YNEWALELLELKE						13359
LVTLSSSK	EEWLVTLSSSKLDQ						13360
VTLLSSSKL	EWLVTLSSSKLDQO						13361
IIAVVWTI	VVARIAVVVWTIFI						13362
VDRIRIVA	LAKYDRIIRIVAFIV						13363

0.0084

Table XIXb
IIIV DR Super Motif Peptides with Binding Information

[illegible]

Table XIXb
 HTV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LQRKIDRL	RKILRQRKIDRLIDR						13364
IVVWTIVFI	ILAIIVVWTIVFIEYR						13365
VVWTIVFIE	IAIVVWTIVFIEYRK						13366
IEYRKILRQ	IVFIEYRKILRQRKI						13367
ILAIVALVY	SLYILAIIVALVYALI						13368
WTIVFIEYR	IVVWTIVFIEYRKIL						13369
LAIVALVA	LQILAIIVALVYAGII						13370

Table XXa
HIV DR 3a Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	VPTDPNQE	53	83	HACVPTDPNQEVL	85	12	19	13371
ENV	YLDQQLLG	31	48	VERYLDQQLLGWG	669	18	28	13372
ENV	MHEDIISLW	29	45	VEQMHEIISLWDQS	114	17	27	13373
ENV	VSFEPPIH	29	45	CPKVSFEPPIHYCA	250	18	28	13374
ENV	LAVERYLKD	26	41	ARVLAVERYLKDQQL	664	15	23	13375
ENV	VKIEPLGVA	23	36	YKVKIEPLGVAPTK	564	15	23	13376
ENV	VWKEATTLT	22	34	GVPVWKEATTLTFC	52	22	34	13377
ENV	LAWDDLRL	20	31	FLALAWDDLRLSLCF	849	19	30	13378
ENV	LIESONQQ	20	31	IYTLIESONQKEKN	737	07	11	13379
ENV	LGWGLKYL	09	29	GLRLGWGLKYLWNL	892	07	23	13380
ENV	LELDKWASL	18	28	QELLELDKWASLWNW	722	07	11	13381
ENV	YLDQQLLG	18	28	VERYLDQQLLGWG	669	11	17	13382
ENV	MWQEVGKAM	15	23	IINMWQEVGKAMYAP	492	12	19	13383
ENV	IBEEGERD	13	20	PEGIEEGGERDRDR	827	08	13	13384
ENV	MNNENNGTN	01	20	INEMNNENNGTSTW	212	01	2	13385
ENV	IBEEGBQD	12	19	LORIEEGGBQDKNR	827	02	3	13386
ENV	LAEEVVIR	12	19	NGSLAEEVVIRSEN	309	04	6	13387
ENV	LALDKWASL	11	17	QDLALDKWASLWNW	753	05	8	13388
ENV	LAVERYLRD	11	17	ARVLAVERYLRDQQL	664	10	16	13389
ENV	IRSENLTNN	10	16	FIIRSENLTNNVKT	317	03	5	13390
ENV	MWEREDIN	10	16	MTWMEWEREDINYTS	721	03	5	13391
GAG	INEAAEWD	55	86	KETINEEAAEWDRLLH	223	18	28	13392
GAG	FSPEVPMF	54	84	EKAFSPEVPMFESAL	182	36	56	13393
GAG	VLAEAMSVQ	33	52	KARVLAEAMSVQVTS	383	09	14	13394
GAG	MLKDTINEE	32	50	AMQMLKDTINEEAAE	218	30	47	13395
GAG	VVEEKAFSP	28	44	WVKVVEEKAFSPEVI	176	28	44	13396
GAG	LRAEQATQB	27	42	FKTLRAEQATQBEVKN	325	09	14	13397
GAG	MLKETINEE	23	36	AMQMLKETINEEAAE	218	22	34	13398
GAG	VIEEKAFSP	21	33	WVKVIEEKAFSPEVI	176	20	31	13399
GAG	VLAEAMSDA	16	25	KARVLAEAMSDASGA	383	03	5	13400
GAG	IEEONKSK	15	23	LDKIEEONKSKKKA	103	09	14	13401
GAG	LRAEQATQD	14	22	FKTLRAEQATQDVKN	325	10	16	13402
GAG	LRAEQASQE	12	19	YKTLRAEQASQEVKN	325	12	19	13403
NEF	YFPDQWNT	36	56	TQGYFPDQWNTTPCP	195	33	52	13404
NEF	FLKEKGLE	30	47	LSHFLKEKGGLDGLI	114	15	23	13405
NEF	FLKEGGGLD	26	41	LSFELKEGGGLDGLI	114	14	22	13406
NEF	FFPDWQNT	17	27	TQGFPPDWQNTTPCP	195	17	27	13407
NEF	VSRDLKKG	11	17	VGAVSRDLKKGHAT	46	11	17	13408
POL	YMDLLYVGS	62	97	IYQYMDLLYVGSdle	369	59	92	13409
POL	IGPENFYNT	60	94	ISKIGPENFYNTPFV	236	28	44	13410
POL	LHPDKWTVQ	60	94	GYELHFPDKWTVQPIQ	420	29	45	13411
POL	IVTDSQYAL	59	92	EVNIVTDSQYALGII	684	58	91	13412
POL	IPATGGET	58	91	AEVIPAETGGETAYF	838	35	86	13413
POL	LTEEKIKAL	56	88	QWPLTEEKIKALTEI	210	26	41	13414
POL	IEAEVIPAE	55	86	SOYIEAEVIPAEETGQ	833	51	80	13415
POL	LFLDGIDKA	55	86	RKVLFDGIDKAEQE	749	32	50	13416
POL	VAKBIVASC	54	86	PPVVAKEIVASCDC	781	22	34	13417
POL	LKGEAMHGG	53	83	KCOLKGEAMHGGVDC	794	47	73	13418
POL	VGSDLEIGQ	53	83	DLVVGSDLEIGQHRA	375	28	44	13419
POL	IRDYGKQM	50	78	KAKIIRDYGKQMAQD	1017	36	56	13420

Table XXa
 IIIV DR 3a Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
POL	MASDFNLPT	47	73	WRAMASDFNLPPVA	771	24	38	13421
POL	FYYDGAANR	43	67	AETFYVDGAANRETK	629	33	52	13422
POL	IHTDNGSNF	42	66	VKVIHTDNGSNFSA	862	17	27	13423
POL	ILKEPVHGV	41	64	NREILKEPVHGVYVD	495	36	56	13424
POL	IYQEPFKNL	40	63	TYQYQEPFKNLKTG	530	39	61	13425
POL	VYDPSKDL	39	61	VIQGYVYDPSKDLIAE	506	26	41	13426
POL	YVTDGRGRQK	39	61	KAGYVTDGRGRQKVVS	646	19	30	13427
POL	LTEEALEL	37	58	IVPLTEEALELAEN	481	12	19	13428
POL	VIQNSDIK	37	58	GAVVIQNSDIKVVP	999	37	58	13429
POL	IATDIQTKE	35	55	IDIAITDIQTKELOK	953	22	34	13430
POL	INNETPGR	32	51	IPSNNETPGRYQY	321	31	48	13431
POL	LIAEIQKQG	30	47	SKDLIAEIQKQCGQ	514	09	14	13432
POL	ICTEMEKEG	28	44	LVEICTEMEKEGKIS	221	14	22	13433
POL	VGAETFYVD	28	44	EPVGAETFYVDGAA	624	20	31	13434
POL	IQKETWETW	27	42	RLPIQKETWETWTD	582	09	14	13435
POL	IKQEGIPY	26	41	WAGIKQEGIPYNPQ	884	21	33	13436
POL	MAGDDCVAG	25	39	GKQMAGDDCVAGRQD	1025	23	36	13437
POL	IKKEKYTLA	20	31	EQLIKKEKYTLAWVP	715	19	30	13438
POL	VPLDKDFRK	18	30	GKQMAGDDCVASRQD	1025	19	30	13439
POL	IQKEFGIPY	16	25	WAGIQKEFGIPYNPQ	884	11	17	13441
POL	LEKEPVQA	16	25	WYQLEKEPVQAE	616	16	25	13442
POL	IQKETWEAW	15	23	KLPIQKETWEAWWTE	582	05	8	13443
POL	FSSEOTRAN	14	22	AREFSSEOTRANSFT	14	10	16	13445
POL	IASDIQTKE	14	22	IDIASDIQTKELOK	953	09	14	13446
POL	IATESIVW	14	22	VOKIATESIVWQKT	564	11	17	13447
POL	ILEIQGKK	14	22	YDQILIBICOKKAIQ	146	13	20	13448
POL	VLEENLPO	14	22	DDTVLEENLPOKWK	116	11	17	13449
POL	IKKEKYLS	13	20	EQLIKKEKYLSWVP	715	07	11	13450
POL	VLEDINLNG	13	20	DDTVLEDINLPOKWK	116	13	20	13451
POL	VLEKDSWT	12	20	QPIVLEKDSWTVND	431	13	20	13452
POL	VIQDNSEIK	12	19	GAVVIQDNSEIKVVP	999	12	19	13453
POL	IKDYGKQM	11	17	KAKIUDYGKQOMAGA	1017	06	9	13454
TAT	VRETETDTP	11	17	KEKVERETETDPAVQ	95	01	2	13455
VIF	YVYDFCES	11	17	VKKLTEDRWNKPKQT	175	09	14	13456
VIF	LVEDRWKPK	11	17	IILYVYDFCESAIR	112	14	22	13457
VIF	IDPDLADQL	10	16	VQKLVEDRWNKPKQT	175	04	6	13458
VPR	LKNEAVRHF	18	28	STQIDPDLADQLIIL	100	10	16	13459
VPR	LKSEAVRIIF	15	23	LEELKNEAVRHFPRP	23	07	11	13461
VPR	YIYETYGDT	14	22	LEELKSEAVRIIFRI	23	07	11	13462
VPR	LKQEAVRHF	11	17	LQQYIYETYGDTWAG	42	06	9	13463
VPR	LKQEAVRHF	11	17	LEELKQEAVRIFPRP	23	06	9	13463

Table XXb

[illegible]

Table XXb
HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw33	SEQ ID NO.
VPTDPNPE	HACVPTDPNPEVVL						13371
YLDQQLLG	VERYLKDQQLGIWG						13372
MIEDISLW	VEQMHEIISLWDQS						13373
VSFERIPH	CPKVSFPIPIHYCA						13374
LAVERYLKD	ARVLAVERYLKDQQL						13375
VKIERLOVA	YKVVKEIPLGVAPTK						13376
VWKEATTL	GVPVWKEATTLFLCA						13377
LAWDDLRL	FLALA WDDLRLSLCF						13378
LIEESQNO	ITYLIEESQNOQEK						13379
LOWEGLKYL	QLRLGWELKYLWNL						13380
LELDKWSL	QELLELDKWSLWNV						13381
YLRDQQLG	VERYLKDQQLGIWG						13382
MWQEVKAM	IINMWQEVGKAMTAP						13383
IEEGGERD	PEGIEEGGERDRDR						13384
MNNENNGTN	INENNNENNGTNTW						13385
IEEGGEDD	LGRIEIEEGGEDKNR						13386
LAEEVVR	NGSLAEEVVRSEN						13387
LALDKWSL	QDLALDKWSLWNV						13388
LAVERYLKD	ARVLAVERYLKDQQL						13389
IRSENLTNN	ELIIRSENLTNNVKT						13390
MEWREIDN	MTWMEWREIDNNTS						13391
INEEAAEWD	KETINEEAAEWDRLH		0.0023				13392
FSPEVPMF	EKAFSPEVPMFSAL		0.0025				13393
VLAEMSQV	KARVLAEMSQTNS		0.0003				13394
MLKDTNBE	AMQMLKDTNBEAAE						13395
VVEEKAFSP	WVKVVEEKAFSFEVI						13396
LRAEQATQE	FKTLRAEQATQEVKN						13397
MLKGTNBE	AMQMLKETINEEAAE						13398
VIEEKAFSP	WVKVIEEKAFSFEVI						13399
VLAEMSQA	KARVLAEMSQAQSA						13400
IEEQNKSK	LKIEEQNKSKKKA						13401
LRAEQATQD	FKTLRAEQATQDVKN						13402
LRAEQASQE	YKTLRAEQASQEVKN						13403
YFPDWQNT	TQGYFPDWQNTTGP						13404
FLKEKGLE	LSIFLKEKGLEGLI						13405
FLKEKGULD	LSFFLKEKGULDGLI						13406
FPDWQNTY	TQGFPPDWQNTTGP						13407
YMDLIVGCS	IYQYMDLIVGSDLE						13408
IGFENPTNT	ISKIGFENPTNTPVF		-0.0005				13409
LHPDKWTVQ	GYELHDPDKWTVQPIQ	0.0108	-0.0014	-0.0009			13410
IVTDSOVAL	EVNIIVTDSOVALGII						13411
IPATQGET	AEVIPAETQGETAYF						13412
LTEBKIKAL	QWPLTEBKIKALTEI						13413
IEAEVPAE	SOYIEAEVPAETQO						13414
LFLLDIDKA	RKVLFLDIDIDKAQEE						13415
VAKETVASC	PPVVAKETVASCDC						13416
LKQEAMHGG	KCOLKQEAMHGGVDC		0.0015				13417
VGSLEIGQ	DLYVGSLEIGQHR						13418
IIRDYKQKM	KAKIIRDYKQKMAQD						13419
							13420

Table XXb
HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
MASDFNLPP	WRAMASDFNLPPVVA						13421
FYVDGAANR	AETFYVDGAANRETK	-0.0002	-0.0014	0.0035			13422
IHTDNGSNF	YKVHTDNGSNFTSA						13423
ILKEPVHGV	NREILKEPVHGVYD	0.0120	0.0033	0.0010	0.0210		13424
YQEFKNL	TYQIQEFKNLKTG						13425
VYDFPSKDL	VHGYYDFPSKDLIAE						13426
YVDRGRQK	KAGYVDRGRQKVVS						13427
LTEEALEL	IVPLTEEALELAEN						13428
VIQDNSDIK	QAVVIQDNSDIKVYP	0.0447	-0.0014	-0.0009			13429
IATDIQTKB	IDIATDIQTKELQK						13430
INNETPGIR	IPSINNETPGIRYQY						13431
LIAEQKG	SKDLIAEQKGQGGQ						13432
ICTEMEKEG	LVEICTEMEKEGKIS						13433
VGAETFYVD	EPIVGAETFYVDGAA						13434
IQKETWETW	RLPIQKETWETWTD						13435
IKQEFQIPY	WAGIKQEFQIPYNPQ	0.0123	-0.0014	-0.0009			13436
MAGDDCVAG	QKQMAQDDCVAGRQD						13437
IKKEKVTLA	EQLIKKEKVTLAVVP	-0.0003	-0.0005	-0.0015	0.0011		13438
MAGDDCVAS	QKQMAQDDCVASRQD						13439
VPLDKDFRK	YFSVPLDKDFRKYTA						13440
IQKEFQIPY	WAGIQKEFQIPYNPQ						13441
LEKEPIVGA	WYQLEKEPIVGAETE						13442
YQLEKEPIV	KLWYQLEKEPIVGAE						13443
IQKETWEAW	KLPIQKETWEAWWTE						13444
FSSEQTRAN	AREFSSEQTRANSTPT						13445
IASDIQTKB	IDIIASDIQTKELQK						13446
LATESIVW	VQKIATESIVWQKT						13447
ILIBICOKK	YDQILIBICOKKAIQ						13448
VLEENLPQ	DDTVLEENLPQKWK						13449
IKKEKVYLS	EQLIKKEKVYLSWVP						13450
VLEDNLPQ	DDTVLEDNLPQKWK						13451
VLPKDSWT	QPIVLPKDSWTVND						13452
VIQDNSEIK	GAVVIQDNSEIKVVP						13453
IKDYCKQM	KAKIKDYCKQMAGA						13454
VERETETDP	KEKVERETETDPVAVQ						13455
LTEDRWKRP	VKKLTEDRWKRPQKT						13456
VYFDCFSB	IHLVYFDCFSBSAIR						13457
LVFEDRWKRP	VQKLVFEDRWKRPQKT						13458
IDPDLADQL	STQIDPDLADQLIHL						13459
LKNEAVRIIF	LEELKNEAVRIIFRP						13460
LKSEAVRH	LEELKSEAVRHFRP						13461
YIVETGDT	LQQYIVETGDTWAG						13462
LKQEAVRHF	LEELKQEAVRHFPRP						13463

Table XXc
HIV DR 3b Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
ENV	MRDNWRSEL	40	63	GGDMRDNRSELYKY	550	37	38	13464
ENV	LTQARQLL	36	56	SITLTQARQLLSGI	620	27	42	13465
ENV	IEAQHLLQ	35	55	LRAIEAQHLLQLTV	642	34	53	13466
ENV	IGDIRQAH	27	44	TGEIGDIRQAHCNI	582	07	11	13467
ENV	VEREKRAVG	23	37	RRVVEREKRAVGIGA	582	11	17	13468
ENV	MVEQMHEDI	23	36	KNNMVEQMHEDIISL	110	19	30	13469
ENV	AWDDLRLC	20	31	LALAWDDLRLSLCLS	850	18	28	13470
ENV	LEITHSFN	20	31	GGDLLEITHSFNCRG	426	10	16	13471
ENV	YDTEVHNW	18	28	AKAYDTEVINWVATH	71	15	23	13472
ENV	AEQTDRIE	17	27	IYAEQTDRIEVVQ	927	02	3	13473
ENV	VQREKRAVG	17	27	RRVYVQREKRAVGIGA	582	05	8	13474
ENV	AEQTDRIE	15	23	IYAEQTDRIEVVQ	927	07	11	13475
ENV	IEAQHLLK	12	19	LRAIEAQHLLKLT	642	08	13	13476
ENV	LKNDKKFN	12	19	FAILKNDKKFNGTG	269	05	8	13477
GAG	ANPDCKTL	45	70	VQNANPDCKTLKAL	347	27	42	13478
GAG	FYKTLRAEQ	28	44	VDREYKTLRAEQASQ	321	19	30	13479
GAG	APQMRER	27	42	GPIAPQMRERPGSD	242	19	30	13480
GAG	FKTLRAEQ	27	42	VDRFFKTLRAEQATQ	321	26	41	13481
GAG	IPWSHKGR	23	36	LGKIWPSHKGKRGNE	470	22	34	13482
GAG	LARNCRAPR	20	32	EGHLARNCRAPRKG	431	19	30	13483
GAG	LAKNCRAPR	18	29	EGHLAKNCRAPRKG	431	10	16	13484
GAG	ATQDVKNWM	18	28	AEQATQDVKNWMTET	330	14	22	13485
GAG	LARNCRAPR	13	21	EGHLARNCRAPRKG	431	13	20	13487
GAG	IPWNSKGR	13	20	LGKIWPSKGRGKGF	470	13	20	13488
GAG	ANPDCKSIL	11	17	VQNANPDCKSILRAL	347	06	9	13489
GAG	ASQEVKNWM	11	17	AEQASQEVKNWMTET	330	11	17	13490
GAG	IPWSSKGR	10	16	LGKIWPSKGRGKGF	470	10	16	13491
NEF	LYSKKRQE	18	28	LDGLYSKKRQREILD	171	11	17	13492
NEF	VPVDFREVB	11	17	FKLVVPVDFREVEAN	227	06	9	13493
NEF	MARELHPEY	10	16	FHHMARELHPEYKID	316	04	6	13494
POL	MGVELHPDK	60	94	FLWMGVELHPDKWTY	416	60	94	13495
POL	FIHNPXRKO	58	91	MAYFIHNPXRKOGIO	930	57	89	13496
POL	MNKLKKII	56	89	VESMKNKLKKIIQOV	903	45	70	13497
POL	IIGQVRDQA	44	69	LKKIIGQVRDQAEHL	910	43	67	13498
POL	YISNWRAMA	39	61	HEKYIISNWRAMASDF	764	23	36	13499
POL	MEKEQKISK	36	56	CTEMEKEQKISKGP	225	22	34	13500
POL	YVRDSRDP	34	53	FRYYVRDSRDPFWKG	975	34	54	13501
POL	ANRETKLGI	30	47	DGAANRETKLGKAGY	635	28	44	13502
POL	IGGQLKEAL	25	39	TIKIGGQLKEALLDT	99	17	27	13503
POL	LDRDFRKYT	19	30	SVPLDRDFRKYTAFT	306	17	27	13504
POL	YVRDSRDP	14	22	FRYYVRDSRDPFWKG	975	13	21	13505
POL	IIGQVREQA	13	20	LKKIIGQVREQAEHL	910	13	20	13506
POL	YHNNWRAMA	10	16	HEKYHNNWRAMASDF	764	06	9	13507
REV	ARNRRRRW	39	61	TRQARNRRRRWRAR	38	18	28	13508
REV	ARKNRBRW	18	28	TRQARNNRBRWRAR	38	13	20	13509
REV	LLKTVRLIK	10	16	DEELLKTVRLIKFLY	9	08	6	13510
VIF	ISSBVHPL	27	42	HPRISSBVHPLGDA	48	04	13	13511
VIF	VSSBVHPL	27	42	HPKVSSBVHPLGEA	48	11	17	13512
VIF	VSIEWRLRR	11	17	OHGVSIEWRLRRYST	85	05	8	13513

Table XXg
HIV DR3b Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
VPR	LPSNTRGRG	01	50	IGILPSNTRGRGRN	82	01	2	13514
VPR	LLEELKNEA	17	27	TLELLEELKNEAVRH	19	12	19	13515
VPR	LLEELKSEA	16	25	TLELLEELKSEAVRH	19	15	23	13516
VPU	AKVDYRNI	01	33	DLLAKVDYRIVVAF	3	01	2	13517
VPU	AKVDYRLGV	01	33	NFLAKVDYRLGVGAL	3	01	2	13518
VPU	ILRQRKIDR	13	23	YRKILRQRKIDRLID	42	12	19	13519

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
MRDNWRSEL	QDDMRDNWRSELYKY						13464
LTVAQRQLL	SITLTVAQRQLLSGI						13465
IEAQQLLQ	LEAQQLLQLTLV						13466
IIGDIRQAH	TGEIGDIRQAHCHN						13467
VEREKRAVG	RRVVEREKRAVGIGA						13468
MVEQMIEDI	KNNMVEQMIEDIISL						13469
AWDDLRLC	LALAWDDLRLSLCLS						13470
LETTITISFN	QODLEITTHSFNCRG						13471
YDTEVHNW	AKAYDTEVHNWATH						13472
AEGTDRIE	IAVAEGTDRIEVVQ						13473
VQREKRAVG	RRVYQREKRAVGIGA						13474
AEGTDRIE	IAVAEGTDRIEVVQ						13475
IEAQQLLK	LEAQQLLKLTLV						13476
LKNDCKFN	FAILKNDCKKFNQGT						13477
FYKTLRAEQ	VQNAFQCMREPRGSD						13478
APQCMREPR	VDRFFKTLRAEQATQ						13479
FFKTLRAEQ	LGKIWPSSHKGKGFNF						13480
TPWSHKGRF	EGHLARNCRATPKKG						13481
LARNCRAPR	EGHLARNCRAPRKKG						13482
IAXNCRAPR	AEQATQBYKXNWMET						13483
ATQBYKXNM	AEQATQBYKXNWMET						13484
ATQBYKXNM	EGHLARNCRAPRKKG						13485
IARNCRAPR	EGHLARNCRAPRKKG						13486
IPSNKORP	LGKIWPSSKGRPCNF						13487
ANPDCSKL	VQNAFQCMREPRGSD						13488
ASQEVKNWM	AEQATQBYKXNWMET						13489
IPSSKORP	LGKIWPSSKGRPCNF						13490
LIYSKKRQE	LDOLYSKKRQEILD						13491
VPVDPREVE	FKLPVPDPREVEEAN						13492
MARELHPEY	PHIMARELHPEYTKD						13493
MGYELHPDK	FLWMGYELHPEYTKD						13494
FJNFKXAG	MAVFIJNFKXAGGIG						13495
IKQVRDQA	VBSNMKELKIIQGY						13496
YHSNWRAMA	LKKIIGQVRDQAHL						13497
MEKEOKISK	HEKYIHSNWRAMASDF						13498
YRDSRDPI	CTEMEKEOKISKIGP						13499
ANRETKLCK	FRVYRDSRDPIWKD						13500
IGGQLKEAL	DGAANRETKLCKAGY						13501
LKDKFRKTY	TIKIGGQLKEALLDT						13502
YRDSRDPI	SVPLDKDFRKYTAFT						13503
IGQVRDQA	FRVYRDSRDPIWKD						13504
YHNNWRAMA	LKKIIGQVRDQAHL						13505
ARKNRRRW	HEKYIHSNWRAMASDF						13506
LLKTVRLK	TRQARKNRRRWWRAR						13507
ISSEVHIPL	DEELLKTVRLKFLY						13508
VSEVHIPL	HPKVSSEVHIPLQDA						13509
VSEVHIPL	HPKVSSEVHIPLQDA						13510
VSEVHIPL	HPKVSSEVHIPLQDA						13511
VSEVHIPL	HPKVSSEVHIPLQDA						13512
VSEVHIPL	HPKVSSEVHIPLQDA						13513

0.0048

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w01	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LPSNTRGRG	IGLPSNTRGRGRBN									13514
LLEELKNEA	TLLEELKNEAVRH									13515
LLEELKSEA	TLLEELKSEAVRH									13516
AKVDYRIV	DLLAKVDYRIVAF									13517
AKVDYRLGV	NFLAKVDYRLGVGAL									13518
ILRQRKIDR	YRILRQRKIDRLID	0.0024	0.0740	0.0410	11.0000	-0.0055		0.1500		13519

Table XXd
HTV DR 3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LPSNTRGRQ	IGILPSNTRGRGRN						13514
LLEELKNEA	TLEELLEELKNEAVRII						13515
LLEELKSEA	TLEELLEELKSEAVRII						13516
AKVDYRIV	DLLAKVDYRIVIVAF						13517
AKVDYRLGV	NFLAKVDYRLGVGAL						13518
ILAQRKIDR	YRKILRQRKIDRLID	0.0016	-0.0014	0.0270			13519

TABLE XXI. Population coverage with combined HLA Supertypes

<u>HLA-SUPERTYPES</u>	<u>PHENOTYPIC FREQUENCY</u>					
	Caucasian	North American Black	Japanese	Chinese	Hispanic	Average
<u>a. Individual Supertypes</u>						
A2	45.8	39.0	42.4	45.9	43.0	43.2
A3	37.5	42.1	45.8	52.7	43.1	44.2
B7	38.6	52.7	48.8	35.5	47.1	44.7
A1	47.1	16.1	21.8	14.7	26.3	25.2
A24	23.9	38.9	58.6	40.1	38.3	40.0
B44	43.0	21.2	42.9	39.1	39.0	37.0
B27	28.4	26.1	13.3	13.9	35.3	23.4
B62	12.6	4.8	36.5	25.4	11.1	18.1
B58	10.0	25.1	1.6	9.0	5.9	10.3
<u>b. Combined Supertypes</u>						
A2, A3, B7	83.0	86.1	87.5	88.4	86.3	86.2
A2, A3, B7, A24, B44, A1	99.5	98.1	100.0	99.5	99.4	99.3
A2, A3, B7, A24, B44, A1, B27, B62, B58	99.9	99.6	100.0	99.8	99.9	99.8

Table XXIII: Immunogenicity of HIV peptides

	Peptide	Sequence	Protein	Immunogenicity	
				patients	transgenic
A2 Supermotif	1261.04	LTFGWCFKL	HIV nef 221	4/12	3/3
	1261.15	MASDFNLPPV	hiv pol 774	1/15	2/6
	1069.32	VLAEAMSQV	hiv gag 386	6/19	3/3
	1261.16	CTLNFPISPI	hiv pol 182	0/1	1/6
	1261.02	LLQLTVWGI	HIV env 651	2/8	1/6
	1261.13	KLVGKLNWA	HIV pol 448	3/15	3/3
	1211.04	KLTPLCVTL	HIV env 134	2/12	2/6
	1261.08	ALVEICTEM	HIV pol 220	0/2	1/6
	1261.11	AIIRILQQL	HIV vpr 59	5/9	0/6
	1261.09	LVGPTPVNI	HIV pol 163	1/9	1/6
	1261.12	RILQQLLFI	HIV vpr 62	6/20	2/6
	1261.05	TLNFPISPI	HIV pol 183	1/7	0/6
	1261.03	MTNNPPIPV	HIV gag 271	2/17	4/6
	1261.17	KMIGGIGGFI	HIV pol 132	2/7	0/6
	941.03	ILKEPVHGV	HIV pol 498	8/19	3/6
	1261.10	RAMASDFNL	HIV pol 772	2/9	0/6
	1261.07	KAACWWAGI	HIV pol 879	1/8	0/6
A3 Supermotif	1211.32	KIQNFRVYYR	HIV pol 971	4/6	
	1193.03	AVFIHNFKR	HIV pol 931	3/6	
	1069.49	QMAVFIHNFK	HIV pol 929	3/6	
	1150.14	MAVFIHNFK	HIV pol 930	6/6	
	1069.42	KVYLAWVPAHK	HIV pol 722	6/6	
	966.01	AIFQSSMTK	HIV pol 347	5/6	1/6
	940.03	QVPLRPMTYK	HIV nef 100	0/6	6/10
	1273.07	TTLFCASDAK	HIV env 61	3/6	
	1273.09	VTIKIGGQLK	HIV pol 98	6/6	
	1069.43	TVYYGVPVWK	HIV env 48		28/33
	1069.47	VTVYYGVPVWK	HIV env 47	6/6	
DR Supermotif	27.0313	KRWILGLNKIVRMY	HIV gag 298	3/13	
	27.0311	GEIYKRWILGLNKI	HIV gag 294	2/13	
	27.0354	WEFVNTPLVKLWYQ	HIV pol 596	2/13	
	27.0377	QKQITKIQNFRVYYR	HIV pol 956	3/13	
	1280.03	KVYLAWVPAHKGIGG	HIV pol 712	3/13	
	27.0361	EKVYLAWVPAHKGIG	HIV pol 711	1/13	
	27.0304	QGQMVHQAI SPRTL N	HIV gag 171	4/13	
	27.0344	SPAIFQSSMTKILEP	HIV pol 335	3/13	
	27.0341	FRKYTAFTIPSINNE	HIV pol 303	3/13	
	27.0364	HSNWRAMASDFNLPP	HIV pol 758	3/13	
	27.0373	KTAVQMAVFIHNFKR	HIV pol 915	4/13	

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays				Radiolabeled peptide	
Species	Antigen	Allele	Cell line	Source	Sequence
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0207	21.221 (transfecta	HBVc 18-27 F6->Y	FLPSDYFPSV
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK
	A11		BVR	non-natural (A3CON1)	KVFPYALINK
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK
	A28/68	A*6801	CIR	HBVc 141-151 T7->Y	STLPETYVVR
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTLVL
	B8	B*0801	Steinlin	(Vgp 586-593 Y1->F, Q5->	FLKDYQLL
	B27	B*2705	LG2	R 60s	FRYNGLIHR
	B35	B*3501	CIR, BVR	non-natural (B35CON2)	FPEKYAAAF
	B35	B*3502	TISI	non-natural (B35CON2)	FPEKYAAAF
	B35	B*3503	EHM	non-natural (B35CON2)	FPEKYAAAF
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY
	B51		KAS116	non-natural (B35CON2)	FPEKYAAAF
	B53	B*5301	AMAI	non-natural (B35CON2)	FPEKYAAAF
	B54	B*5401	KTJ	non-natural (B35CON2)	FPEKYAAAF
	Cw4	Cw*0401	CIR	non-natural (C4CON1)	QYDDAVYKL
	Cw6	Cw*0602	'21.221 transfecte	non-natural (C6CON1)	YRHDGGNVL
	Cw7	Cw*0702	'21.221 transfecte	non-natural (C6CON1)	YRHDGGNVL
Mouse	D ^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI
	K ^b		EL4	VSV NP 52-59	RGYVFQGL
	D ^d		P815	HTV-IIIB ENV G4->Y	RGPYRAFVTI
	K ^d		P815	non-natural (KdCON1)	KFNPMKTYI
	L ^d		P815	HBVs 28-39	IPQSLDSYWTSL

B. Class II binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide	
				Source	Sequence
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAFAAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIAFDEEARR
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE
	DR51	DRB5*0101	3M3107 or L416.:	Tet. tox. 830-843	QYIKANAKFIGITE
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT
	DQ3.1	QA1*0301/DQB1*0301	PF	non-natural (ROIV)	AHAAHAAHAAHAAHAA
Mouse	IA ^b		DB27.4	non-natural (ROIV)	AHAAHAAHAAHAAHAA
	IA ^d		A20	non-natural (ROIV)	AHAAHAAHAAHAAHAA
	IA ^k		CH-12	HEL 46-61	YNTDGSTDYGILQINSR
	IA ^s		LS102.9	non-natural (ROIV)	AHAAHAAHAAHAAHAA
	IA ^u		91.7	non-natural (ROIV)	AHAAHAAHAAHAAHAA
	IE ^d		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK
	IE ^k		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK

Table XXV. Monoclonal antibodies used in MHC purification.

Monoclonal antibody	Specificity
W6/32	HLA-class I
B123.2	HLA-B and C
IVD12	HLA-DQ
LB3.1	HLA-DR
M1/42	H-2 class I
28-14-8S	H-2 D ^b and L ^d
34-5-8S	H-2 D ^d
B8-24-3	H-2 K ^b
SF1-1.1.1	H-2 K ^d
Y-5	H-2 K ^b
10.3.6	H-2 I A ^k
14.4.4	H-2 IE ^d , IE ^K
MKD6	H-2 I A ^d
Y3JP	H-2 I A ^b , I A ^s , I A ^u

Table XXVI. The table lists the 64 fully represented aligned amino acid sequences that were identified for Motif analysis. Included are the aligned amino acid sequence ID number, the complete nucleotide sequence name it was derived from, the accession numbers for the sequence, the subtype, country and the total length of all nine sequences.

	ID Number	Name	Accession Numbers	Subtype	Country	Length
1	A.KE.Q23-CxC-CG	HIVQ2317	AF004885	A	KE	3584
2	A.SE.UGSE8891	AUGSE8891	AF069673	A	SE	3584
3	A.UG.92UG037	H92UG037	U51190	A	UG	3584
4	A.UG.U455	HIVU455A	M62320	A	UG	3584
5	AC.IN.21301	21301	AF067156	AC	IN	3584
6	AC.RW.92RW009	92RW009	U88823	AC	RW	3584
7	AC.ZM.ZAM184	ZAM184	U86780	AC	ZM	3584
8	ADI.ZR.MAL	HIVMALCG	K03456, X04415	ADI	ZR	3584
9	AE.CF.90CF402	HIV90CF402	U51188	AE	CF	3584
10	AE.TH.93TH253	H93TH253	U51189	AE	TH	3584
11	AE.TH.CM240	HIV1CM240	U54771	AE	TH	3584
12	AG.DJ.DJ263	DJ263	AF063223	AG	DJ	3584
13	AG.DJ.DJ264	HDJ264	AF063224	AG	DJ	3584
14	AG.NG.92NG003	92NG003	U88825	AG	NG	3584
15	AG.NG.92NG083	H92NG083	U88826	AG	NG	3584
16	AG.NG.IBNG	HIVIBNG	L39106	AG	NG	3584
17	AGI.CY.94CY0323	94CY032-3	AF049337	AGI	CY	3584
18	AGI.ZR.Z321	HIVU76035, Z321B	U76035	AGI	ZR	3584
19	AGJ.AU.BFP90	HIVBFP90	AF064699	AGJ	AU	3584
20	B.CN.RL42	HCHRL42CG	U71182	B	CN	3584
21	B.DE.D31	HIV1D31	U43096	B	DE	3584
22	B.DE.HAN	HIVHAN2	U43141	B	DE	3584
23	B.FR.HXB2R	HIVHXB2	AF033819, K03455, M38432	B	FR	3584
24	B.GA.OYI	HIVOYI	M26727	B	GA	3584
25	B.GB.CAM1	HIVCAM1	D00917, D10112	B	GB	3584
26	B.GB.MANC	HIV1MANC	U23487	B	GB	3584
27	B.NL.ACH32OA	HIV1ACH32OA	U34604	B	NL	3584
28	B.US.ADA	HIV1AD8	AF004394	B	US	3584
29	B.US.DH123	HIV1DH123	AF069140	B	US	3584
30	B.US.JRCSF	HIVJRCSF	M38429	B	US	3584
31	B.US.JRFL	HIVJRFL	U63632	B	US	3584
32	B.US.MN	HIVMN	M17449	B	US	3584
33	B.US.P896	HIV1896	M96155, U39362	B	US	3584
34	B.US.RF	HIVRF	M12508	B	US	3584
35	B.US.SF2	HIVSF2CG	K02007	B	US	3584
36	B.US.WEAU160	HIVWEAU160	U21135	B	US	3584
37	B.US.WR27	HIV1WR27	U26546	B	US	3584
38	B.US.YU2	HIVYU2	M93258	B	US	3584
39	BF.BR.93BR029.4	93BR029	AF005495	BF	BR	3584
40	C.BR.92BR025	H92BR025	U52953	C	BR	3584
41	C.BW.BW96BW0502	96BW0502	AF110967	C	BW	3584
42	C.ET.ETH2220	HIVETH2220	U46016	C	ET	3584
43	C.IN.11246	1N11246	AF067159	C	IN	3584
44	C.IN.21068	C1N21068	AF067155	C	IN	3584
45	C.IN.301904	301904	AF067157	C	IN	3584
46	C.IN.301905	CIN301905	AF067158	C	IN	3584
47	C.IN.301999	CIN301999	AF067154	C	IN	3584
48	D.UG.94UG1141	94UG114	U88824	D	UG	3584
49	D.ZR.84ZR085	84ZR085	U88822	D	ZR	3584
50	D.ZR.ELI	HIVELICG	K03454, X04414	D	ZR	3584
51	D.ZR.NDK	HIVNDK	M27323	D	ZR	3584
52	F.BR.93BR0201	93BR020	AF005494	F	BR	3584
53	F.FN.FIN9363	FIN9363	AF075703	F	FN	3584
54	G.BE.DRCBL	DRCBL	AF084936	G	BE	3584
55	G.FI.HH87931	HH8793	AF061640, AF061641	G	FI	3584
56	G.SE.SE6165	SE6165	AF061642	G	SE	3584
57	H.BE.VI991	VI991	VI991	H	BE	3584
58	H.BE.VI997	VI997	VI997	H	BE	3584

	ID Number	Name	Accession Numbers	Subtype	Country	Length
59	H.CF.90CF056	90CF056	AF005496	H	CF	3584
60	J.SE.SE91733	SE91733	AF082395	J	SE	3584
61	J.SE.SE92809	SE92809	AF082394	J	SE	3584
62	N.CM.YBF3O	NCMYBF3O	AJ006022	N	CM	3584
63	O.CM.ANT7OC	HIVANT7OC	L20587	O	CM	3584
64	O.CM.MVP518O	HIVMVP518O	L20571	O	CM	3584

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TABLE XXVII
in vitro binding of conserved HIV derived peptides to HLA-A2 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%)		A2-supertype binding capacity (IC50 nM)						alleles	
					total	B	A*0201	A*0202	A*0203	A*0206	A*6802	bound		
1261.14	10	NEF	221	LTFGWCFKLV	55	74	294.1	48.9	185.2	57.8	6.2	5		
1261.04	9	NEF	221	LTFGWCFKL	61	74	35.7	33.1	4545.5	205.6	5.6	4		
1261.06	9	POL	316	YTAFTPSI	58	68	26.3	6.1	9.1	7	16.7	5		
1261.15	10	POL	774	MASDFNLPPV	39	68	62.5	22.6	55.6	33.6	18.2	5		
1069.32	9	GAG	386	VLAEMSQV	52	74	66.6	82.7	15.2	115.6	363.6	5		
1261.16	10	POL	182	CTLNFPISPI	94	100	147	23.9	30.3	8.4	100	5		
1261.02	9	ENV	651	LLQLTVWGI	53	63	9.8	21.5	43.5	24.7	645.2	4		
1261.13	9	POL	448	KLVGKLNWA	95	95	59.5	12.6	5.9	39.8	3076.9	4		
1211.04	9	ENV	134	KLTPLCVTL	81	95	102	126.5	66.7	185	20000	4		
1261.08	9	POL	220	ALVEICTEM	23	79	217.3	187	140.8	264.3	2857.1	4		
1261.11	9	VPR	59	AIIRILQQL	61	74	333.3	22.6	41.7	38.5	547.9	4		
1261.09	9	POL	163	LVGPTPVNI	84	100	454.5	153.6	19.2	2846.2	67.8	4		
1261.12	9	VPR	62	RILQQLFI	56	74	19.2	1535.7	125	37	1818.2	3		
1261.05	9	POL	183	TLNFPISPI	97	100	75.7	1482.8	1.1	1947.4	57.1	3		
1261.03	9	GAG	271	MTNNPPIPV	31	89	166.6	7166.7	33.3	1608.7	12.1	3		
1261.17	10	POL	132	KMIGGIGGFI	97	95	172.4	54.4	4.8	770.8	3333.3	3		
941.03	9	POL	498	ILKEPVHGV	64	79	192.3	2388.9	6.7	37000	363.6	3		
1260.10	9	POL	772	RAMASDFNL	64	79	217.3	116.2	25000	52.1	3076.9	3		
1261.07	9	POL	879	KAACWVAGI	49	79	277.7	1075	83.3	160.9	2666.7	3		
1211.09	10	ENV	814	SLLNATDIAV	22	68	9.8	1303	238.1	28.5	5479.4	3		
1211.05	9	ENV	608	FLQAAAGSTM	86	100	73.5	3583.3	1.5	4111.1	66666.7	2		
25.0053	9	VPR	66	QLLFIHRI	69	89	94.3	21500	25000	1608.7	476.2	2		
25.0139	10	GAG	270	WMTNPPIPV	31	89	98	3071.4	16.9	18500	2222.2	2		
1069.33	10	POL	993	LLWKGEHAV	95	100	111.1	632.4	25	770.8	3636.4	2		
25.0142	10	NEF	219	PLTFGWCFKL	61	74	142.8	741.4	4761.9	3700	47.6	2		
1069.34	9	POL	993	LLWKGEHAV	97	100	172.4	10750	21.7	1608.7	2666.7	2		
25.0161	10	POL	452	KLNWASQIYA	42	84	217.3	3909.1	400	6166.7	3076.9	2		
1211.082	9	GAG	79	SLYNTVATL	34	58	277.7	3583.3	50	37000	100000	2		
25.0037	9	GAG	486	FLQSRPEPT	44	68	454.5	10750	32.3	18500	3076.9	2		
25.0046	9	POL	91	TLWQRPLVT	61	68	270.2	21500	2500	18500	2857.1	1		

TABLE XXVIII
in vitro binding of conserved HIV derived peptides to HLA-A3 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%)		A3-supertype binding capacity (IC50 nM)						alleles bound
					total	B	A*0301	A*1101	A*3101	A*3301	A*6801		
1273.01	9	GAG	163	MVHQALSPR	42	58	61.1	89.6	18.0	13.8	9.5	5	
1193.0200	9	POL	572	IVIWGKTPK	75	79	129.4	16.2	18.2	96.7	242.4	5	
1193.03	9	POL	931	AVFIHFKR	97	100	64.7	3.3	5.1	107.4	4.2	5	
1193.01	9	POL	724	YLAWVPAHK	34	95	142.9	105.3	327.3	33.0	2.0	5	
1211.32	10	POL	971	KIQNFRVYYR	81	95	343.8	28.6	2.7	341.2	210.5	5	
1069.49	10	POL	929	QMAVFIHFK	94	100	9.2	6.5	268.7	432.8	400.0	4	
1273.03	10	GAG	162	QMVHQALSPR	42	58	42.3	6000.0	243.2	290.0	186.0	4	
1193.09	9	POL	353	MTKILEPFR	67	84	13750.0	375.0	81.8	69.0	25.8	4	
966.01	9	POL	347	AIQSSMTK	56	79	10.0	10.0	12000.0	96666.7	242.4	3	
940.03	10	NEF	100	QVPLRPMTYK	72	79	18.0	9.5	1836.7	2230.8	131.3	3	
1069.43	10	ENV	48	TVYYGVVWVK	64	95	11.0	3.5	1636.4	10357.1	14.5	3	
1069.48	10	POL	931	AVFIHFKRK	91	100	114.6	20.7	1125.0	5000.0	307.7	3	
1273.05	9	POL	99	TIKIGGQLK	27	63	40.7	181.8	18000.0	36250.0	72.7	3	
1273.06	9	ENV	64	TLFCASDAK	81	84	118.3	11.3	10588.2	22307.7	190.5	3	
1273.07	10	ENV	61	TTLFCASDAK	78	84	119.6	27.3	9473.7	14500.0	140.4	3	
1273.04	9	ENV	878	RIVELLGRR	34	89	200.0	600.0	138.5	13809.5	444.4	3	
1273.09	10	POL	98	VTIKIGGQLK	27	63	297.3	28.6	10588.2	11600.0	125.0	3	
1273.02	9	POL	246	NTPVFAIKK	58	94.7	333.3	100.0	30000.0	48333.3	4.7	3	
1150.14	9	POL	930	MAVFIHFK	94	100	647.1	20.0	375.0	517.9	2.5	3	
1273.08	9	VIF	7	VMIVWQVDR	69	95	3235.3	272.7	3.8	5.3	2424.2	3	
1069.47	11	ENV	47	VTVYYGVVWVK	64	94	84.6	11.3	4615.4	36250.0	170.2	3	
1069.42	11	POL	722	KVYLAWVPAHK	32	89	3.5	7.6	163.6	3580.2	8000.0	3	
1069.44	9	POL	855	KLAGRWPVK	78	68	8.5	133.3	500.0	72500.0	80000.0	3	

TABLE XXIX

in vitro binding of conserved HIV derived peptides to HLA-B7 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%)		B7-supertype binding capacity (IC50 nM)					alleles	
					total	B	B*0702	B*3501	B*5101	B*5301	B*5401	bound	bound
1146.01	9	NEF	94	FPVRPQVPL	75	74	15.7	43.0	11.6	481.9	71.4	5	5
1296.01	9	ENV	259	IPIHYCAPA	56	42	423	343	153	-	3.7	4	4
15.0268	10	GAG	545	YPLASLRSLF	15	32	392.9	480.0	39.3	150.0	714.3	4	4
1261.01	9	POL	186	FPISPIETV	88	95	3437.5	1043.5	148.6	251.4	9.1	3	3
1296.02	9	ENV	250	CPKVSFEPI	47	79	100.0	5142.9	161.8	2447.4	100.0	3	3
1296.03	11	POL	893	IPYNPQSQGVV	92	89	458.3	72000.0	119.6	46500.0	66.7	3	3
29.0028	8	REV	75	VPLQLPPL	56	68	112.2	6000.0	0.8	46500.0	270.3	3	3
1292.13	9	GAG	237	HPVHAGPIA	30	74	50.0	11.6	13750.0	4428.6	4.3	3	3

Table XXX: A1-motif peptides

Peptide	Sequence	Protein	Conservancy		IC50 nM
			Total	Clade B	
1.0431	EVNIVTDSQY	HIV pol 1187	83	93	472
1.0014	FRDYVDRFY	HIV gag 298	51	96	278
2.0129	IYQYMDDL	HIV pol 359	78	87	391
1069.27	VIYQYMDDL	HIV pol 358	78	87	446
1069.26	VTVLVDVGDAY	HIV pol 265	96	93	439

Table XXXI: A24-motif peptides

Peptide	Sequence	Protein	Conservancy		IC50 nM
			Total	Clade B	
25.0113	IWGCSGKLI	HIV env 69	69	91	444
25.0127	IYETYGDTW	HIV vpr 92	92	100	207
1069.60	IYQEPFKNL	HIV pol 1036	74	87	444
25.0128	PYNEWTLEL	HIV vpr 56	56	71	86
25.0123	PYNTPVFAI	HIV pol 74	74	100	387
1069.57	RYLKDQQLL	HIV env 2778	40	53	43
1069.58	RYLRDQQLL	HIV env 2778	23	32	52
1069.59	TYQIQEPPF	HIV pol 1033	78	93	67
25.0115	VWKEATTTL	HIV env 47	47	85	400
25.0218	VWKEATTTLF	HIV env 47	47	85	44
25.0219	YWQATWIPEW	HIV pol 96	96	93	182

Table XXXII: Immunogenicity of A2-supertype cross-reactive binding peptides

Peptide	Sequence	Protein	Conservancy		Immunogenicity		
			Total	Clade B	XRN	patients	transgenic
1261.14	LTFGWCFKLV	HIV nef221	55	74	5	0/1	0/6
1261.04	LTFGWCFKL	HIV nef221	61	74	4	4/12	3/3
1261.06	YTAFTIPSI	HIV pol 316	58	68	5	0/1	0/6
1261.15	MASDFNLPPV	HIV pol 774	39	68	5	1/15	2/6
1069.32	VLAEMSQV	HIV gag 386	52	74	5	6/19	3/3
1261.16	CTLNFPISPI	HIV pol 182	94	100	5	0/1	1/6
1261.02	LLQLTVWGI	HIV env 651	53	63	4	2/8	1/6
1261.13	KLVGKLNWA	HIV pol 448	95	95	4	3/15	3/3
1211.04	KLTPLCVTL	HIV env 134	85	95	4	2/12	2/6
1261.08	ALVEICTEM	HIV pol 220	23	79	4	0/2	1/6
1261.11	AIIRILQQQL	HIV vpr 59	61	74	4	5/9	0/6
1261.09	LVGPTPVNI	HIV pol 163	84	100	4	1/9	1/6
1261.12	RILQQLLFI	HIV vpr 62	56	74	3	6/20	2/6
1261.05	TLNFPISPI	HIV pol 183	97	100	3	1/7	0/6
1261.03	MTNNPPIPV	HIV gag 271	31	89	3	2/17	4/6
1261.17	KMIGGIGGFI	HIV pol 132	97	95	3	2/7	0/6
941.03	ILKEPVHGV	HIV pol 498	64	79	3	8/19	3/6
1261.10	RAMASDFNL	HIV pol 772	64	79	3	2/9	0/6
1261.07	KAACWWAGI	HIV pol 879	49	79	3	1/8	0/6
1211.09	SLLNATDIIV	HIV env 814	22	68	3		

Table XXXIII: Immunogenicity of HIV-derived A3-supertype peptides

Peptide	Sequence	Protein	Conservancy		Immunogenicity	
			Total	Clade B	transgenic	patients
1211.32	KIQNFRVYYR	HIV pol 971	81	95	5	4/6
1193.02	IVIWGKTPK	HIV pol 572	75	79	5	0/6
1193.03	AVFIHNFKR	HIV pol 931	97	100	5	3/6
1069.49	QMAVFIHNFK	HIV pol 929	94	100	4	3/6
1150.14	MAVFIHNFK	HIV pol 930	94	100	3	6/6
1069.48	AVFIHNFKRK	HIV pol 931	91	100	3	0/6
1273.01	MVHQAI SPR	HIV gag 163	42	58	5	0/6
1273.03	QMVHQAI SPR	HIV gag 162	42	58	4	0/6
1193.01	YLA WVP AHK	HIV pol 724	34	95	5	0/6
1069.42	KVYLA WVP AHK	HIV pol 722	32	89	3	6/6
1193.09	MTKILEPFR	HIV pol 353	67	84	4	0/8
966.01	AIFQSSMTK	HIV pol 347	56	79	3	5/6
940.03	QVPLRPMTYK	HIV nef 100	72	79	3	0/6
1069.44	KLGRWPVK	HIV pol 855	78	68	3	
1273.02	NTPVFAIKK	HIV pol 246	58	95	3	0/6
1273.08	VMIVWQVDR	HIV vif 7	69	95	3	0/6
1273.04	RIVELLGRR	HIV env 878	34	89	3	
1273.07	TTLFCASDAK	HIV env 61	78	84	3	3/6
1273.06	TLFCASDAK	HIV env 62	81	84	3	0/6
1273.09	VTIKIGGQLK	HIV pol 98	27	63	3	6/6
1273.05	TIKIGGQLK	HIV pol 99	27	63	3	0/6
1069.43	TVYGVVPVWK	HIV env 48	64	95	3	28/33
1069.47	VTYGVVPVWK	HIV env 47	64	94	3	6/6

Screening Panel	Antigen	Alleles	Representative Assay		Phenotypic Frequencies					
			Allele	Alias	Cauc.	Blk.	Jpn.	Chn.	Hisp.	Avg.
Primary	DR1	DRB1*0101-03	DRB1*0101	(DR1)	18.5	8.4	10.7	4.5	10.1	10.4
	DR4	DRB1*0401-12	DRB1*0401	(DR4w4)	23.6	6.1	40.4	21.9	29.8	24.4
	DR7	DRB1*0701-02	DRB1*0701	(DR7)	26.2	11.1	1.0	15.0	16.6	14.0
	Panel total				59.6	24.5	49.3	38.7	51.1	44.6
Secondary	DR2	DRB1*1501-03	DRB1*1501	(DR2w2 B1)	19.9	14.8	30.9	22.0	15.0	20.5
	DR2	DRB5*0101	DRB5*0101	(DR2w2 B2)	-	-	-	-	-	-
	DR9	DRB1*09011,09012	DRB1*0901	(DR9)	3.6	4.7	24.5	19.9	6.7	11.9
	DR13	DRB1*1301-06	DRB1*1302	(DR6w19)	21.7	16.5	14.6	12.2	10.5	15.1
Panel total				42.0	33.9	61.0	48.9	30.5	43.2	
Tertiary	DR4	DRB1*0405	DRB1*0405	(DR4w15)	-	-	-	-	-	-
	DR8	DRB1*0801-5	DRB1*0802	(DR8w2)	5.5	10.9	25.0	10.7	23.3	15.1
	DR11	DRB1*1101-05	DRB1*1101	(DR5w11)	17.0	18.0	4.9	19.4	18.1	15.5
	Panel total				22.0	27.8	29.2	29.0	39.0	29.4
Quaternary	DR3	DRB1*0301-2	DRB1*0301	(DR3w17)	17.7	19.5	0.4	7.3	14.4	11.9
	DR12	DRB1*1201-02	DRB1*1201	(DR5w12)	2.8	5.5	13.1	17.6	5.7	8.9
	Panel total				20.2	24.4	13.5	24.2	19.7	20.4

Table XXXV: cross-reactive HLA-DR binding peptides

Peptide	Sequence	Protein	Binding Capacity (IC50 nM)										DR Alleles				
			DR1	DR2w201	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	DR6w19	DR7	DR8w2	DR9	DR53	bound	
27.0313	KRWILGLNKIVRMV	HIV gag 298	4.2	5.1	24	188	613	404	54	124	0.36	379	49	58		12	
27.0354	WEFVNITPLVKLWYQ	HIV pol 596	7.2	222	2.1	13636	28	20	317	1355	90	15	350	39		10	
27.0377	QKQTKIQNFRVYYR	HIV pol 956	2.9	3.4	80	-	357	49	53	124	25	25	75	577		11	
1280.03	KVYLAWVPAHKGG	HIV pol 712	8.3	25	24	-	156	165	71	12598	2500	179	196	250		9	
27.0311	GEYKRWIILGLNKI	HIV gag 294	82	138	225	-	1667	380	213	1656	98	192	63	536		9	
27.0361	EKVYLAWVPAHKGG	HIV pol 711	3.6	21	4.9	3226	9.3	27	37	6478	3500	18	31	144		9	
27.0297	QHLLQLTVWGKQLQ	HIV env 729	6.1	21	690	-	1316	345	2128	1064	350	44	907	375		8	
27.0304	QQQMVHQAIPTLN	HIV gag 171	72	65	13	17647	60	400	-	-	412	455	7313	117		8	
27.0344	SPAIFQSSMTKILEP	HIV pol 335	357	217	667	-	3571	109	741	-	13	68	3267	33		8	
F091.15	IKQFINMWQEVGKAMY	HIV env 566	128	217	206	-	417	271	4878	-	1000	-	350	5769	104	8	
27.0341	FRKYTAFTIPSINNE	HIV pol 303	185	70	4167	-	294	136	1818	-	-	30	803	39		7	
27.0364	HSNWRAMASDFNLPP	HIV pol 758	33	-	125	-	11	15	95	-	4375	472	1960	872		7	
27.0373	KTAVQMAVFIHNFKR	HIV pol 915	161	650	690	-	909	452	182	18625	125	1786	1441	2586		7	

A dash indicates IC50>20µM

Table XXXVI: DR3 binding peptides

Peptide	Sequence	Protein	DR3
35.0135	YRKILRQRKIDRLID	HIV vpu 31	23
35.0131	WAGIKQEFGIPYNPQ	HIV pol 874	300
35.0127	EVNIVTDSQYALGII	HIV pol 674	732
35.0125	AETFYVDGAANRETK	HIV pol 619	769
35.0133	GAVVIQDNSDIKVVP	HIV pol 989	1000

TABLE XXXVII
Immunogenicity of HIV-derived DR-superinfectif peptides

Peptide	Sequence	Protein	conservation (%)		DR Alleles bound	Patient Immunogenicity
			total	clade B		
27.0313	KRWILGLNKIVRMY	HIV gag 298	85 [89] ¹	94 [95]	12	3/13
27.0311	GEYKRWILGLNKI	HIV gag 294	58 [86]	95 [95]	9	2/13
27.0354	WEFVNTPLVLKLWYQ	HIV pol 596	79 [89]	84 [95]	10	2/13
27.0377	QKQITKIQNFRVYYR	HIV pol 956	56 [67]	95 [95]	11	3/13
1280.03	KVYLAWVPAHKGIGG	HIV pol 712	32 [34]	89 [95]	9	3/13
27.0361	EKVYLAWVPAHKGIG	HIV pol 711	32 [34]	94 [95]	9	1/13
27.0304	QGQMVHQAIPTLN	HIV gag 171	41 [42]	52 [58]	8	4/13
27.0344	SPAIFQSSMTKILEP	HIV pol 335	52 [59]	79 [78]	8	3/13
27.0341	FRKYTAFTIPSINNE	HIV pol 303	59 [58]	68 [68]	7	3/13
27.0364	HSNWRAMASDFNLPP	HIV pol 758	48 [67]	68 [79]	7	3/13
27.0373	KTAVQMAVEIHNFKR	HIV pol 915	87 [95]	94 [100]	7	4/13

1: conservation of core region

Table XXXVIII. Candidate CTL Epitopes

Restriction	Peptide	Protein	Sequence
HLA-A2	1069.32	HIV gag 386	VLAEAMSQV
"	1261.03	HIV gag 271	MTNNPPIPV
"	1261.15	HIV pol 774	MASDFNLPPV
"	1261.13	HIV pol 448	KLVGKLNWA
"	1261.09	HIV pol 163	LVGPTPVNI
"	941.03	HIV pol 498	ILKEPVHGV
"	1261.07	HIV pol 879	KAACWWAGI
"	1261.17	HIV pol 132	KMIGGIGGFI
"	1261.10	HIV pol 772	RAMASDFNL
"	1261.05	HIV pol 183	TLNFPISPI
"	1211.04	HIV env 134	KLTPLCVTL
"	1261.02	HIV env 651	LLQLTVWGI
"	1211.09	HIV env 163	SLLNATDIIV
"	1261.04	HIV nef 221	LTFGWCFKL
"	1261.11	HIV vpr 59	AHRLQQL
"	1261.12	HIV vpr 62	RILQQLFI
HLA-A3	1069.49	HIV pol 929	QMAVFIHNFK
"	1069.42	HIV pol 722	KVYLAWVPAHK
"	1211.32	HIV pol 971	KIQNFRVYYR
"	1193.09	HIV pol 353	MTKILEPFR
"	966.01	HIV pol 347	AIFQSSMTK
"	1273.09	HIV pol 98	VTIKIGGQLK
"	1273.07	HIV env 61	TTLFCASDAK
"	1069.47	HIV env 47	VTVYYGVPVWK
"	940.03	HIV nef 100	QVPLRPMTYK
"	1273.08	HIV vif 7	VMIVWQVDR
"	1273.03	HIV gag 162	QMVHQAIAPR
HLA-B7	15.0268	HIV gag 545	YPLASLRSLF
"	1292.13	HIV gag 237	HPVHAGPIA
"	1261.01	HIV pol 186	FPISPIETV
"	1296.03	HIV pol 893	IPYNPQSQGVV
"	1296.01	HIV env 259	IPIHYPAPA
"	1296.02	HIV env 250	CPKVSFEPI
"	1146.01	HIV nef 94	FPVRPQVPL
"	29.0028	HIV rev 75	VPLQLPPL
HLA-A1	1.0431	HIV pol 684	EVNIVTDSQY
"	1.0014	HIV gag 317	FRDYVDRFY
"	1069.27	HIV pol 368	VITYQYMDLY
"	1069.26	HIV pol 295	VTVLDVGDAY
HLA-A24	1069.60	HIV pol 533	IYQEPFKNL
"	25.0123	HIV pol 244	PYNTPVFAI
"	1069.59	HIV pol 530	TYQIYQEPF
"	25.0219	HIV pol 597	YWQATWIPEW
"	25.0113	HIV env 681	IWGCSGKLI
"	1069.57	HIV env 671	RYLKDQQLL
"	25.0115	HIV env 55	VWKEATTLF
"	25.0127	HIV vpr 46	IYETYGDTW
"	25.0128	HIV vpr 14	PYNEWTLEL

Table XXXIX: HTL Candidate Epitopes

Selection Criteria	Peptide	Sequence	Protein
DR	27.0313	KRWIILGLNKIVRMY	HIV gag 298
	27.0354	WEFVNTPLVLWYQ	HIV pol 596
	27.0377	QKQITKIQNFRVYYR	HIV pol 956
	1280.03	KVYLAWVPAHKGIGG	HIV pol 712
	27.0311	GEIYKRWIILGLNKI	HIV gag 294
	27.0361	EKVYLAWVPAHKGIG	HIV pol 711
	27.0297	QHLLQLTVWGIKQLQ	HIV env 729
	27.0304	QGQMVHQAISPRTLN	HIV gag 171
	27.0344	SPAIFQSSMTKILEP	HIV pol 335
	F091.15	IKQFINMWQEVGKAMY	HIV env 566
	27.0341	FRKYTAFTIPSINNE	HIV pol 303
	27.0364	HSNWRAMASDFNLPP	HIV pol 758
	27.0373	KTAVQMAVFIHNFKR	HIV pol 915
DR3	35.0135	YRKILRQRKIDRLID	HIV vpu 31
	35.0131	WAGIKQEFGIPYNPQ	HIV pol 874
	35.0127	EVNIVTDSQYALGII	HIV pol 674
	35.0125	AETFYVDGAANRETK	HIV pol 619
	35.0133	GAVVIQDNSDIKVVP	HIV pol 989

TABLE XL
Estimated population coverage by a panel of HIV derived HTL epitopes

Antigen	Alleles	Representative assay	No. of epitopes ²	Population coverage (phenotypic frequency)					
				Cauc.	Blk.	Jpn.	Chn.	Hisp.	Avg.
DR1	DRB1*0101-03	DR1	13	18.5	8.4	10.7	4.5	10.1	10.4
DR2	DRB1*1501-03	DR2w2 β1	12	19.9	14.8	30.9	22.0	15.0	20.5
DR2	DRB5*0101	DR2w2 β2	12	-	-	-	-	-	-
DR3	DRB1*0301-2	DR3	5	17.7	19.5	0.40	7.3	14.4	11.9
DR4	DRB1*0401-12	DR4w4	10	23.6	6.1	40.4	21.9	29.8	24.4
DR4	DRB1*0401-12	DR4w15	13	-	-	-	-	-	-
DR7	DRB1*0701-02	DR7	11	26.2	11.1	1.0	15.0	16.6	14.0
DR8	DRB1*0801-5	DR8w2	9	5.5	10.9	25.0	10.7	23.3	15.1
DR9	DRB1*09011,09012	DR9	11	3.6	4.7	24.5	19.9	6.7	11.9
DR11	DRB1*1101-05	DR5w11	9	17.0	18.0	4.9	19.4	18.1	15.5
DR13	DRB1*1301-06	DR6w19	8	21.7	16.5	14.6	12.2	10.5	15.1
Total ¹				98.5	95.1	97.1	91.3	94.3	95.1

1. Total opulation coverage has been adjusted to account for the presence of DRX in many ethnic populations. It has been assumed that the range of specificities represented by DRX alleles will mirror those of previously characterized HLA-DR alleles. The proportion of DRX incorporated under each motif is representative of the frequency of the motif in the remainder of the population. Total coverage has not been adjusted to account for unknown gene types.

2. Number of epitopes represents a minimal estimate, considering only the epitopes shown in Table 13. Additional alleles possibly bound by nested epitopes have not been accounted.

WHAT IS CLAIMED IS

1. A composition comprising a prepared human immunodeficiency virus-1 (HIV-1) epitope consisting of an amino acid sequence selected from the group consisting of:

VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
QMVHQAISPR,	PYNTPVFAI,	YWQATWIPEW
IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
PYNEWTLEL,	KIQNFRVYYR,	IPYNPQSQGVV,
EVNIVTDSQY,	FRDYVDRFY,	VITYQYMDDLY,
VTVLDVGDAY,	IYQEPFKNL,	TYQIYQEPF,
QMAVFIHNFK	QKQITKIQNFRVYYR,	IKQFINMWQEVGKAMY,
WAGIKQEFGIPYNPQ,	GAVVIQDNSDIKVP	WEFVNTPLVLKLWYQ,
KVYLAWVPAHKGIGG,	GEIYKRWILGLNKI,	EKVYLAWVPAHKGIG,
QHLLQLTVWGIKQLQ,	QGQMVHQAISPRTLN,	SPAIFQSSMTKILEP,
FRKYTAFTIPSINNE,	HSNWRAMASDFNLPP,	KTAVQMAVFIHNFKR,
YRKILRQRKIDRLID,	EVNIVTDSQYALGIL, and	AETFYVDGAANRETK.

2. The composition of claim 1, wherein the epitope is selected from the group consisting of:

VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
QMVHQAISPR,	PYNTPVFAI,	YWQATWIPEW
IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
PYNEWTLEL,	WEFVNTPLVLKLWYQ,	KVYLAWVPAHKGIGG,
GEIYKRWILGLNKI,	EKVYLAWVPAHKGIG,	QHLLQLTVWGIKQLQ,

QGQMVHQAI SPRTL N, SPAIFQSSMTKILEP, FRKYTAFTIPSINNE,
HSNWRAMASDFNLPP, KTAVQMAVFIHNFKR, YRKILRQRKIDRLID,
EVNIVTDSQYALGII, and AETFYVDGAANRETK.

3. The composition of claim 1, comprising two epitopes selected from the group in claim 1.

4. The composition of claim 3, comprising three epitopes selected from the group in claim 1.

5. The composition of claim 1, wherein the composition further comprises a cytotoxic T lymphocyte (CTL) epitope selected from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMIVWQVDR, FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWIILGLNKIVRMY, MASDFNLPPV, KAACWWAGI, RAMASDFNL, YPLASLRSLF, HPVHAGPIA, IPIHYCAPA, and VPLQLPPL.

6. The composition of claim 1, wherein the composition further comprises a helper T lymphocyte (HTL) epitope.

7. The composition of claim 6, wherein the HTL epitope is a pan DR binding molecule.

8. The composition of claim 1, wherein the epitope is on or within a liposome.

9. The composition of claim 1, wherein the peptide is joined to a lipid.

10. The composition of claim 1, wherein the epitope is bound to an HLA heavy chain, β 2-microglobulin, and strepavidin complex, whereby a tetramer is formed.

11. The composition of claim 1, wherein the epitope is bound to an HLA molecule on an antigen presenting cell.
12. The composition of claim 1, wherein the antigen presenting cells is a dendritic cell.
13. The composition of claim 1, the composition further comprising a pharmaceutical excipient.
14. The composition of claim 1, wherein the epitope is in a unit dose form.
15. The composition of claim 1, wherein the epitope is expressed from a recombinant nucleic acid molecule that encodes the epitope.
16. A composition comprising a prepared peptide of less than 500 amino acid residues comprising at least two human immunodeficiency virus-1 (HIV-1) peptide epitopes selected from the group consisting of:

VLAEAMSQV,	MTNNPIPV,	KLVGKLNWA,
LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
LTFGWCFKL,	AIRILQQL,	RILQQLLFI,
KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
QMVHQAISPR,	PYNTPVFAI,	YWQATWIPEW
IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
PYNEWTLEL,	KIQNFRVYYR,	IPYNPQSQGVV,
EVNIVTDSQY,	FRDYVDRFY,	VITYQYMDDL,
VTVLDVGDAY,	IYQEPFKNL,	TYQIYQEPF,
QMAVFIHNFK	QKQITKIQNFRVYYR,	IKQFINMWQEVGKAMY,
WAGIKQEFGIPYNPQ,	GAVVIQDNSDIKVP	WEFVNTPLVLKLYQ,
KVYLAWVPAHKGIGG,	GEIYKRWILGLNKI,	EKVYLAWVPAHKGIG,
QHLLQLTVWGIKQLQ,	QGQMVHQAISPRTLN,	SPAIFQSSMTKILEP,
FRKYTAFTIPSINNE,	HSNWRAMASDFNLPP,	KTAVQMAVFIHNFKR,

YRKILRQRKIDRLID, EVNIVTDSQYALGII, and AETFYVDGAANRETK, wherein the peptide comprises less than 50 contiguous amino acids that have 100% identity with a native peptide sequence.

17. The composition of claim 16, wherein at least two epitopes are linked via a spacer.
18. The composition of claim 16, further comprising a third epitope.
19. The composition of claim 18, wherein the third epitope is selected from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMIVWQVDR, FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWIILGLNKIVRMY, MASDFNLPPV, KAACWWAGI, RAMASDFNL, YPLASLRSLF, HPVHAGPIA, IPIHYCAPA, and VPLQLPPL.
20. The composition of claim 16, further comprising a third epitope that is a helper T lymphocyte (HTL) epitope.
21. The composition of claim 20, wherein the HTL epitope is a panDR binding molecule.
22. The composition of claim 16, wherein the peptide is on or within a liposome.
23. The composition of claim 16, wherein the peptide is joined to a lipid.
24. The composition of claim 16, wherein the peptide further comprises at least three of the epitopes in the group of claim 16.
25. The composition of claim 16, wherein the peptide further comprises at least four of the epitopes in the group of claim 16.

26. The composition of claim 16, wherein the peptide further comprises at least five of the epitopes in the group of claim 16.
27. The composition of claim 16, wherein the peptide further comprises at least six of the epitopes in the group of claim 16.
28. The composition of claim 16, the composition further comprising a pharmaceutical excipient.
29. The composition of claim 16, further wherein the peptide is in a unit dose form.
30. The composition of claim 16, wherein the peptide is expressed from a recombinant nucleic acid that encodes the peptide.

AMENDED CLAIMS

[received by the International Bureau on 12 March 2001 (12.03.01);
original claims 1-30 replaced by new claims 1-36 (6 pages)]

1. A composition comprising a prepared human immunodeficiency virus-1 (HIV-1) epitope, said epitope consisting of an amino acid sequence selected from the group consisting of the sequences:
- | | | | |
|----|------------------|--------------------|----------------------|
| 5 | VLA EAMSQV, | MTNNPPIPV, | KL VGKLNWA, |
| | LVGPTPVNI, | KMIGGIGGFI, | TLNFPISPI, |
| | KLTPLCVTL, | LLQLTVWGI, | SLLNATDIAV, |
| | LTFGWCFKL, | AIRILQQL, | RILQQLFI, |
| 10 | KVYLAWVPAHK, | MTKILEPFR, | AIFQSSMTK, |
| | VTIKIGGQLK, | TTLFCASDAK, | VTVYYGVPVWK, |
| | QMVHQAI SPR, | PYNTPVFAL, | YWQATWIPEW |
| | IWGCSGKLI, | VWKEATTTLF, | IYETYGDTW, |
| | PYNEWTLEL, | KIQNFRVYYR, | IPYNPQSQGVV, |
| 15 | EVNIVTDSQY, | FRDYVDRFY, | VYQYMDDL Y, |
| | VTVLDVGDAY, | IYQEPFKNL, | TYQIYQEPF, |
| | QMAVFIHNFK | QKQITKIQNFRVYYR, | IKQFINMWQEVGKAMY, |
| | WAGIKQEFGIPYNPQ, | GAVVIQDNSDIKVVP | WEFVNTPLVLKLYQ, |
| | KVYLAWVPAHKGIGG, | GEIYKRWILGLNKI, | EKVYLAWVPAHKGIG, |
| 20 | QHLLQLTVWGIKQLQ, | QGQMVHQAI SPRTL N, | SPAIFQSSMTKILEP, |
| | FRKYTAFTIPSINNE, | HSNWRAMASDFNLPP, | KTAVQMAVFIHNFKR, |
| | YRKILRQRKIDRLID, | EVNIVTDSQYALGIL, | and AETFYVDGAANRETK. |

2. The composition of claim 1, comprising two epitopes selected from the group in claim 1.

3. The composition of claim 1, comprising three epitopes selected from the group in claim 1.

4. The composition of claim 1, wherein the composition further comprises a cytotoxic T lymphocyte (CTL) epitope selected from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMVWQVDR, FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWILGLNKIVRMV, MASDFNLPPV, 5 KAACWWAGI, RAMASDFNL, YPLASLRSLF, HPVHAGPIA, IPIHYCAPA, and VPLQLPPL.
5. The composition of claim 1, wherein the composition further comprises a helper T lymphocyte (HTL) epitope.
- 10 6. The composition of claim 5, wherein the HTL epitope is a pan DR binding molecule.
7. The composition of claim 1, wherein the epitope is on or within a 15 liposome.
8. The composition of claim 1, wherein the peptide is joined to a lipid.
- 20 9. The composition of claim 1, wherein the epitope is bound to an HLA heavy chain, β 2-microglobulin, and strepavidin complex, whereby a tetramer is formed.
10. The composition of claim 1, wherein the epitope is bound to an 25 HLA molecule on an antigen presenting cell.
11. The composition of claim 1, wherein the antigen presenting cells is a dendritic cell.
- 30 12. The composition of claim 1, the composition further comprising a pharmaceutical excipient.

13. The composition of claim 1, wherein the epitope is in a unit dose form.

5 14. The composition of claim 1, wherein the epitope is expressed from a recombinant nucleic acid molecule that encodes the epitope.

15. An expression vector comprising a recombinant nucleic acid molecule encoding a prepared epitope set out in claim 1.

10

16. A composition comprising a prepared peptide of less than 500 amino acid residues comprising at least two human immunodeficiency virus-1 (HIV-1) peptide epitopes selected from the group consisting of:

	VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
15	LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
	KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
	LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
	KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
	VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
20	QMVHQAISPR,	PYNTPVFAI,	YWQATWIPEW
	IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
	PYNEWTLEL,	KIQNFRVYYR,	IPYNPQSQGVV,
	EVNIVTDSQY,	FRDYVDRFY,	VTYQYMDDLTY,
	VTVLDVGDAY,	IYQEPFKNL,	TYQIYQEPF,
25	QMAVFIHNFK	QKQITKIQNFRVYYR,	IKQFINMWQEVGKAMY,
	WAGIKQEFGIPYNPQ,	GAVVIQDNSDIKVP	WEFVNTPLVKLWYQ,
	KVYLAWVPAHKGIGG,	GEIYKRWILGLNKL,	EKVYLAWVPAHKGIG,
	QHLLQLTVWGIKQLQ,	QGQMVHQAISPRTLN,	SPAIFQSSMTKILEP,
	FRKYTAFTIPSINNE,	HSNWRAMASDFNLPP,	KTAVQMAVFIHNFKR,

YRKILRQRKIDRLID, EVNIVTDSQYALGII, and AETFYVDGAANRETK,
wherein the peptide comprises less than 50 contiguous amino acids that have 100%
identity with a native peptide sequence.

- 5 17. The composition of claim 16, wherein at least two epitopes are
linked via a spacer.
18. The composition of claim 16, further comprising a third epitope.
- 10 19. The composition of claim 18, wherein the third epitope is selected
from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMIVWQVDR,
FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWIILGLNKIVRMY,
MASDFNLPPV, KAACWWAGI, RAMASDFNL, YPLASLRSLF, HPVHAGPIA,
IPIHYCAPA, and VPLQLPPL.
- 15 20. The composition of claim 16, further comprising a third epitope
that is a helper T lymphocyte (HTL) epitope.
21. The composition of claim 20, wherein the HTL epitope is a panDR
20 binding molecule.
22. The composition of claim 16, wherein the peptide is on or within a
liposome.
- 25 23. The composition of claim 16, wherein the peptide is joined to a
lipid.
24. The composition of claim 16, wherein the peptide further
comprises at least three of the epitopes in the group of claim 16.
- 30

25. The composition of claim 16, wherein the peptide further comprises at least four of the epitopes in the group of claim 16.

26. The composition of claim 16, wherein the peptide further
5 comprises at least five of the epitopes in the group of claim 16.

27. The composition of claim 16, wherein the peptide further comprises at least six of the epitopes in the group of claim 16.

10 28. The composition of claim 16, the composition further comprising a pharmaceutical excipient.

29. The composition of claim 16, further wherein the peptide is in a unit dose form.

15 30. The composition of claim 16, wherein the peptide is expressed from a recombinant nucleic acid that encodes the peptide.

31. An expression vector comprising a recombinant nucleic acid
20 encoding a prepared peptide as set out in claim 16.

32. A composition comprising a prepared human immunodeficiency virus-1 (HIV-1) epitope, said epitope consisting of an amino acid sequence selected from the group consisting of the sequences set forth in Tables VII-XX.

25 33. A composition of claim 32, wherein the composition comprises a further epitope consisting of an amino acid sequence selected from the group consisting of the sequences set forth in Tables VII-XX.

30 34. The composition of claim 32, wherein the epitope is expressed from a recombinant nucleic acid molecule that encodes the epitope.

35. A composition comprising a prepared peptide of less than 500 amino acid residues comprising at least two human immunodeficiency virus-1 (HIV-1) peptide epitopes selected from the group consisting of the sequences set out in Tables VII-XX.

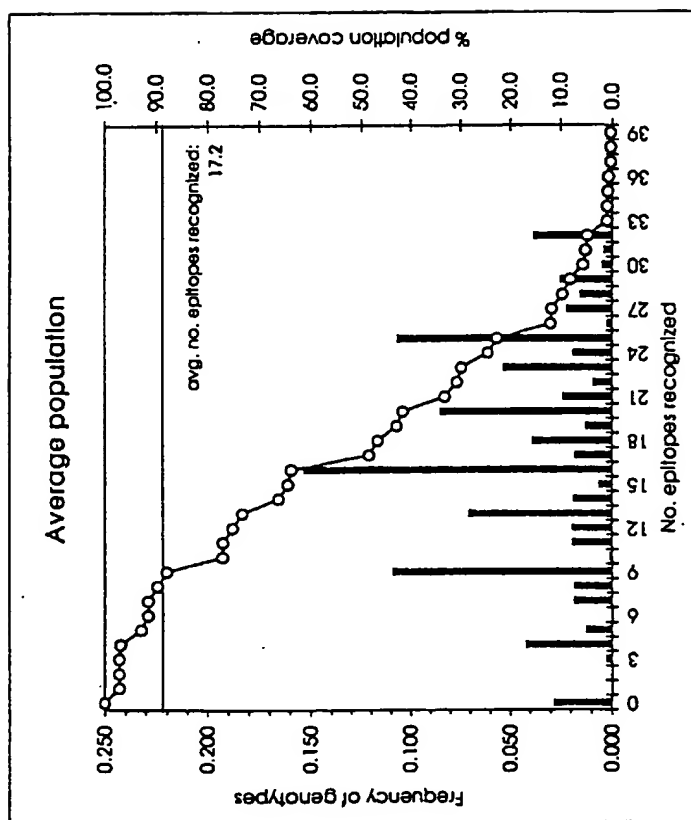
36. The composition of claim 35, wherein the prepared peptide is expressed from a recombinant nucleic acid molecule that encodes the peptide.

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Figure 1



Plot of total frequency of genotypes as a function of the number of candidate epitopes bound by HLA-A and B alleles, in an average population. Genotype values were derived by averaging the gene frequencies in Caucasian, North American Black, Japanese, Chinese, and Hispanic populations. Also shown is the cumulative frequency of genotypes.

Using currently available HLA typing data, a residual fraction (about 15%) of the genes, in an average population, are unspecified. To arrive at 100% accounting of genes, a fraction of the residual has been added for each hit population cluster in proportion to the relative frequency of the cluster within the HLA specified population.

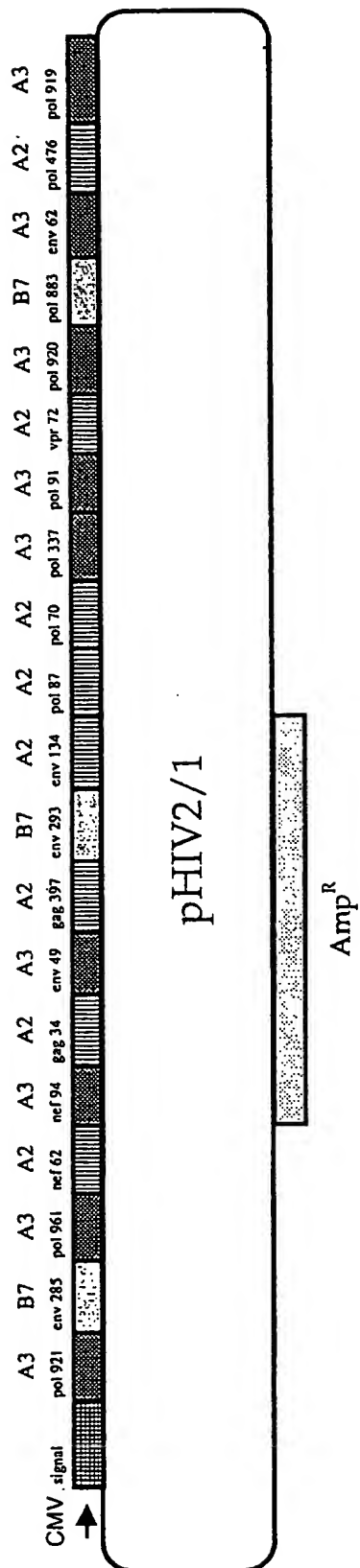


FIGURE 2

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/27766

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : A61K 38/08, 38/10, 38/16, 39/295, 39/21; C07K 7/00, 9/00, 14/155

US CL : 530/328,327,326,325,324; 424/188.1, 208.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/328,327,326,325,324; 424/188.1, 208.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE, WEST 2.0 search terms: author names, hiv, peptid?, hla, mhc, t cell, vaccine, polyvalent, ctl

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	RAMMENSEE et al. MHC ligands and peptide motifs: first listing. Immunogenetics. 1995, Vol 41, pages 178-228, see entire document.	1-30
Y	US 5,683,701 (MCMICHAEL et al.) 04 November 1997, see entire document.	1-30
Y	WO 94/20127A1 (CYTEL COEPORATION) 15 September 1994, see entire document.	1-30
Y	US PATENT 5,756,666 A (TAKIGUCHI et al.) 26 May 1998, see entire document.	1-30



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*G* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

14 DECEMBER 2000

Date of mailing of the international search report

12 JAN 2001

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

RON SCHWADRON

Telephone No. (703) 308-0196

TECHNOLOGY CENTER 1600
PARALEGAL SPECIALIST
DELTA MAE COLLINS